

5	452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	3.17
	451230	BE546208	Hs.26090	hypothetical protein FLJ20272	3.16
	418000	R82342	Hs.79856	ESTs, Weakly similar to S65657 alpha-1C-	3.16
	444823	BE262989	Hs.12045	putative protein	3.15
	446528	AU076640	Hs.15243	nucleolar protein 1 (120kD)	3.15
	430388	AA356923	Hs.240770	nuclear cap binding protein subunit 2, 2	3.15
	447801	H85923	Hs.270247	Homo sapiens cDNA FLJ11977 fis, clone HE	3.15
	424188	AW954552	Hs.142634	zinc finger protein	3.15
10	436941	AA860383	Hs.292791	ESTs	3.15
	400592			Target Exon	3.15
	437842	AL079309		gb:Homo sapiens mRNA full length insert	3.15
	450406	A1894913	Hs.279637	ESTs	3.15
	414161	AA138106	Hs.184852	KIAA1553 protein	3.15
15	440129	AA865818		ESTs, Weakly similar to S71886 Ste20-lik	3.14
	438538	AA832203	Hs.291955	ESTs	3.14
	441013	A126252	Hs.126419	ESTs	3.14
	450431	AW136797	Hs.266041	ESTs	3.14
	423755	AB037735	Hs.132560	hypothetical protein FLJ10312	3.13
20	434768	AA648884	Hs.134278	Homo sapiens cDNA FLJ12676 fis, clone NT	3.13
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	3.12
	410704	BE076754		gb:CM1-BT0601-180200-121-b10 BT0601 Homo	3.12
	412673	AL042957	Hs.31845	ESTs	3.11
	420507	AF093408	Hs.96397	A kinase (PRKA) anchor protein 3	3.11
25	423419	R55336	Hs.23539	ESTs	3.11
	428925	AW242474	Hs.98960	ESTs	3.11
	426108	AA622037	Hs.166468	programmed cell death 5	3.10
	439398	AA284267	Hs.221504	ESTs	3.10
	449138	AW294215	Hs.195831	ESTs	3.10
30	441785	N58115	Hs.21137	AD024 protein	3.10
	458053	S57488	Hs.76252	endothelin receptor type A	3.10
	403610			C3001199:gl[7494834]pirjT15308 hypothet	3.10
	421261	A1299139	Hs.17517	ESTs	3.10
	429274	A1379772	Hs.99206	ESTs	3.10
35	438243	A1581311		ESTs	3.10
	424800	AL036588	Hs.153203	MyoD family inhibitor	3.09
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	3.08
	418443	N59469	Hs.194225	ESTs	3.08
	421230	AW958439	Hs.105633	ESTs	3.07
40	427906	AA864330	Hs.166520	ESTs	3.07
	414706	AW340125	Hs.76889	KIAA0097 gene product	3.06
	441703	AW390054	Hs.192843	leucine zipper protein FKSG14	3.06
	445679	A1343688	Hs.301059	hypothetical protein FLJ12488	3.06
	434456	AW452621	Hs.116832	ESTs	3.05
45	433228	F28212	Hs.14953	KIAA1491 protein	3.05
	419335	AW960146	Hs.284137	hypothetical protein FLJ12888	3.05
	415227	AW821113	Hs.72402	ESTs	3.05
	421184	NM_003616	Hs.102456	survival of motor neuron protein interac	3.05
50	438869	AF076009		gb:Homo sapiens full length insert cDNA	3.05
	422726	U11690	Hs.1572	faciogenital dysplasia (Aarskog-Scott sy	3.04
	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	3.04
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	3.04
	433914	AF108138	Hs.112160	Homo sapiens DNA helicase homolog (PIF1)	3.04
	411365	M76477	Hs.289082	GM2 ganglioside activator protein	3.04
55	435725	BE535787	Hs.113170	ESTs	3.03
	426386	AA748850	Hs.125830	bladder cancer overexpressed protein	3.03
	420598	NM_002692	Hs.99185	polymerase (DNA directed), epsilon 2	3.02
	427953	AA417944	Hs.44331	ESTs	3.01
	433612	AF078164	Hs.61188	Homo sapiens Ku70-binding protein (KUB3)	3.01
60	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	3.00
	448048	BE281291	Hs.170408	ESTs, Moderately similar to A47582 B-cell	3.00
	434776	AA648988		gb:ns41f1.s1 NC1_CGAP_GCB1 Homo sapiens	3.00
	414132	A1801235	Hs.48480	ESTs	3.00
	430491	AL109791	Hs.241559	Homo sapiens mRNA full length insert cDN	3.00
65	433493	AA594915	Hs.155087	ESTs	3.00
	452606	N45202	Hs.90012	hypothetical protein FLJ23441	3.00
	453416	NM_003037	Hs.32970	signalling lymphocytic activation molecu	3.00

TABLE 53B

Key: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

75	Key	CAT Number	Accession
	432666	144_7	AA558585 AA565499 A1360576 AW204069 AA991648 AA884939
	423458	30480_1	BC018070 BG702493 A1204212 AA460929 AA993605 BF926635 AA226938 BG190705 BG186496 AW291865 BG183340 BG195301 BG214539
			BG215094 BG198867 BG196532 BG208220 BG212418
	430676	60836_2	BG433950 BE061583 T05808 BE144813 AW812038 BE144812 AW812040 AW812041 AU124350 BE061602 BE061604 BF922596 BE061803
			A1352469 BE061601 B1062752 AW818206 BF887722
80	422828	227063_1	BE671981 BE503379 A1655440 A1337054 A1288920 A1242370 A1825182 AA758081 BF855141 BF081068
	418477	4172_1	BC022538 A190847 BF478249 BG217995 BG212702 BG182057 AW589883 BF000085 AA993969 BG479023 BG220014 BG679466 BE907092
			A1623855 AA223956 AA223917 AW022983 AW090580 AW573219 BF514491 BF445397 AA884705 A1910424
	443068	18595_17	AW752763 A1032142 N30308 N22181 H95390 AW675632
	436812	659779_1	AW978773 AW298067 AA810101 AW194180 AA731645 A1690873

5	427521	513212_1	AW973352 BF222929 AW016853 BF059130 AI651829 BE551767 AA550414 AJ339359 BF059601 AJ961162 AI341422 AI206248 AI206165 AA548736 AA768578 AI539081 AW025957 AA736837 N79575 AW594357 AA480892 AA764852 AA736937 AW954733 AA315005 AW856665 AI964001 AI634418 AW236545 AI824860 BF223710 AW139686 AI672051 AI655566 AW025712 N36327 BF222876 N34083 AA911045 N40303 AW835451
10	427486	584159_1	BF510715 BE673055 BE464111 AW590520 AI637939 AA404324 AW236441 AI650952 BF056796 AA974433 AA301270 AA301379 AA301366 AA683356 AW592804 AI150267 AF147390 R76593 R76594
15	421974	864120_1	AJ420453 AL526740 AW968449 AA459140 AA843893 AI568516 AW971760 AA430089 AI753216 AA854268 AA743075 AI864957 AA458920 AI566634 AA211796 BG616512 BE169275 BF983253 BF969462 AA766261 AI769894 AA135933 AI831542 N63376 AA274392 AI154486 AW605017 AW460072 AA446459 BE881875 AI061423 AA598549 AW439151 AA426273 Z40087 AA812434 AA135965 H04812 BF666746 D59356 BG678312 N56840 AA166861 AA917062 AA757369 AW592218 AL109688 R23665 R26578 BC009612 NM_Q03526 BI597616 AV761592 AV760377 AL601008 BI604131 BE545918 BG187760 BG181525 BG210634 BG192899 AI263307 AA344186 AW952966 AA033609 AA037562 AA722183 R79452 H70775 BF674991 BE769437 BG007856 AA037483 AW572536 AI143991 AA084581 AA033610 AV742510 AV735788 R08336 AA210987 D57294 AA214584 AA207006 D56572 AK025201 AA425472 AI694282 BG057305 AA907787 AI288170 AI694577 AJ420494 AI809865 BF058095 AI478773 AI160445 AL044114 AW665529 AI129239 AW297152 AI268215 AI469807 AI969353 BE552356 N66509 AA736741 AA382655 AW075811 AV759188 BI259364 BF445142 BG232065 AI141758 AI631202 AI167565 AI208445 AA889823 BF982682 N90322 BI090882 BF208005 AW953918 AL044113 AI016793 AA382556 AW235763 AA927051 AI862075 BE886691 BE619282 AA906366 AA938956 AI910938 AW102570 AA907160 AA907120 AA737188 AI248890 AW977353 BG576155 BM005591 AI479075 AI025794 AI017957 AA448270 BE466812 AA853422 AI392649 BG952034 AA513384 BF840124 BE714620 AW969505 AI553633 BM453041 AA760783 BE218582 AI340046 AW166131 BF515854 AI630295 AA461307 AI090881 AW023059 AA156797 AA115486 AL597396 AW889004 AW937420 AA137082 AA013374 BG619478 BG401839 BE072634 BE072653 AA830615 AA214736 AA331718 AA218925 AW962081 AA354237 BG570706 BG572749 AW606284 H04021 AA151166 AW954405 AA131254 BG056461 W46291 H01532 H04384 H03231 AA852876 H04410 H58605 BE157601 AA113758 NM_Q00363 X54183 M64247 AI265781 AI760600 AI367238 BE140258 AW207185 AI857074 C03333 AI193911 C05024 C03193 AI950215 C05070 C05613 W17389 C06351 AA311399 C04180 C04896 C05502 C05482 C04456 C04543 C04558 C04551 C09114 C03103 AI669979 AI652255 T12391 T12073 W19390 C02994 C02730 C04434 W07136 R57607 C03339 AK056686 BG399272 AA187835 BF821903 AV660550 AV660556 AV660602 BG564397 BE379584 BF446961 AI653056 AW973709 AI653173 BG054997 AI266043 BI054879 AI658750 AA92830 AW021142 AI472184 AW170066 AI092443 AI167921 D59940 BI492086 H74180 AW130886 AI348677 AI278577 AA761517 AI698203 AA115535 AI264790 AW205074 AA860452 AA554902 AI000715 D62102 BE544768 AI376090 D59939 AW242249 AA525421 R34211 R34328 BF248064 BF241437 BF572759 BF218832 BI015205 AI761324 AW880937 AW880941 AA338252 AA338213 AK055748 AA039909 BE183282 W60721 AA464867 AA398986 T67280 BF959651 AI675065 BG001061 BF764727 BF766707 BF764717 BF764852 BF173139 BE010038 AA933717 BF061897 AW628327 AA641788 AA400495 BE065183 AI144398 BE085367 BF377924 NM_Q58168 AF220030 AL043894 AW974257 AA625445 AU153502 AI650537 AW612116 AI672377 AW772451 BE092241 BE501740 AA718936 AI650276 AI654206 BE503226 AI651327 AW873562 AW271269 AW271565 AI873518 AI207150 AI338926 AI650258 AI628362 AA227117 AI207149 AW052076 AI470776 AA588100 AW235852 AA769791 AI701653 AK027664 AI984770 AU153469 BE222316 AA609539 BE220093 AA608112 BI054316 AF080229 AF080232 U87593 U87592 U87591 U87590 AI636743 AI633818 AW206802 AI583718 AF080231 AF080234 AF080233 AI635594 AI818326 AF080230 S46404 AI970376 AA463992 AW665466 BF512210 U87695 U87589 BE550633 AI672574 BE467547 AI680833 AW614951 N25986 N25695 H69001 U87596 BE573974 AI97498 AI701526 AA703396 AW139734 H92278 N68048 BE219539 BE871865 AI624817 BE466611 AI206344 AA574387 BF593413 BG231271 BF773517 U87594 BF062180 BE466420 AI887798 BF674385 AA204735 AW496803 AA204833 AA207156 BI004766 AA206282 AI355204 H77808 AW590511 T39328 T39310 T39303 T39284 BE893356 AA625304 AI765607 AI624898 R76600 AA069661 BG998885 R35783 BF086499 AA428755 AI245055 BC013389 BC017308 AI023543 AA191424 AI287700 AI669633 AW958486 AW953397 AA172056 BE940298 BF909208 BF909980 BF095153 BG285837 AI720344 BF541715 AA365086 AA172236 N50454 AA620999 T16375 AW958037 R42557 AI337047 AA946360 AI638005 AA459950 AI624915 AI638047 AI467856 AI521828 AA860305 AI932315 AW003092 AW271756 AW779380 AA609879 AI634781 AI493770 AI565211 Z41145 AI627952 AA303734 BE349457 AW198765 AA256527 BE089727 T65754 AA229658 AA229857 AK056550 AK056356 AI928212 AI742073 AW300558 BG058755 AA058343 AI554842 AW207438 BF509981 BF444964 AW028234 AI620104 AA973460 AI370934 N63066 AA493129 AW590888 AI682952 AI167202 AA831394 AI421915 AI222883 BF477519 AI208777 AA765849 AI676076 AI370922 AI339579 AA486224 AA453624 AW771805 AI492842 H54679 AA961022 AW023555 H06192 AA910222 AI650021 AI032525 AI375480 AI361860 AI032919 AA833589 BG057928 AA553913 AW235737 AA002124 AA913636 F04607 AI657699 AA648100 BE091446 AA486378 BE002022 H84627 BI059837 BF917659 BF917100 BF917043 BF917104 BF916878 BG290981 AW954251 AA757128 H11545 AA353384 N48448 AA379845 AA004943 AA378928 AA002123 BM470118 AL598847 AI598830 BG899239 R57470 BF939179 AI650642 AI758851 BF352505 W68422 W36297 H11435 AA937499 AI783996 R12500 AI819557 N39083 Z41819 H22849 AA004942 R09436 R02403 T90942 T85823 BG028683 AI248120 BI650480 AW779829 N22494 BE155042 BE155040 BE154987 BE155012 BG110129 AW749287 BE535498 AW749299 AW749293 AW749302 AW749298 AW749291 AW749294 AW749289 AW749288 AW749286 AW769294 AW749297 AW749295 AW749292 BE002573 AW813110 BF771370 BF771371 AW813113 AW003381 BI862319 AA204955 BF240507 BG212143 AW205739 BI760647 BM129481 BI760482 AW300025 AI288591 AW236114 AI302852 AI038548 AI797207 AA534496 BG188194 AA921877 BG191845 BG182959 BE620243 BF217428 BC009514 BM463015 AL529077 BM051874 BG773269 BM314351 BM314660 AW628666 AA316207 AI623431 AA504153 AA314700 BG195449 BG614101 BI999967 BF438599 AW864793 AI802899 BE815132 AW468888 AI672189 AI052004 BF112024 AA772335 AW275054 AA573845 AI144148 AI968683 AA846576 AA927355 H00424 AW973295 R88209 F29868 BE928871 AA846804 AA757581 AI050950 AI092024 AA838807
20	417886	1031334_1	
	412537	14066_1	
25	440801	2635916_1	
	436909	586835_1	
	429228	215430_1	
30	451050	11847_4	
	418235	886897_1	
	418378	1227421_1	
	450375	16559_3	
35	409517	4537_1	
	442582	39593_1	
40	451105	1145037_1	
	424281	892055_1	
	430183	17316_1	
45	427298	115241_1	
	444386	1490237_1	
	414725	19377_1	
50	438641	35983_1	
55	418768	2293204_1	
	409268	109625_1	
	415989	10194_1	
60	439979	2076469_1	
	420218	191547_1	
65	418866	245947_1	
	449587	25369_2	
70	445685	381678_1	
	413646	1525656_1	
	437834	294580_1	
75	454679	174325_1	
	440840	29886_1	
80	433023	3970_8	
	437440	2497201_1	

5	417553	258857_1	AL545411 AI096369 BF431750 AI130946 W60065 W80663 AA258580 W73279 W76156 W80662 AW058658 AI204599 W60115 N56751 N30878
	408065	101881_1	AI769345 R71250 AI363766 R22777 R17009 R27985 R28243
	418049	12052_4	BI603077 AW954272 BI598724 AI003154 AA059300 AAD46911 BI669907 BI600966 BI669987
	430968	1237115_1	AJ314647 NM_052888 BI494693 AA835065 AI634477 AJ336678 AI807698 BF477887 AF011147 Z39187 R38979 F02234 AA984711 BI222234
	400268	840_4	AV731417 R42405 H04996 T98498 R12489 R12577 R42405
10			AW972830 AA489820 AA527647 AA570362
			U69868 AA448366 X63105 BC016514 BE694436 AI655584 AW235355 BG427984 AA612862 AA448223 BM145813 BM194555 AI870824 BE973573
			BM148408 AA448232 AA454176 AA740959 AA884391 AA808545 AW070759 BM144223 N75518 BE542983 BE241942 AI124022 AA761687
			BF908518 BF907890 R11490 AI536642 BF109180 AA953881 AJ783716 BE622908 AI621005 AW148784 AI690114 AW275000 AI765790 BF222859
			AW167268 AIS90460 AW300443 AA779660 AI620588 BF115024 BE504703 AW626332 AI922851 BE006636 AU158376 AI168279 AA809916
			AI469757 AA830828 AA830388 N64324 AI049683 AA970275 BF477354 BG261301 AA328388 AU159374 AA687987 N58510 AI650450
			AI549572 BF349280 BF349269 BM463016 AW836798 AL120958 AW836891 AW385525 BE175733 BE175727 BE175723 BF092430 BI061782
			AU135358 BE175731 BE175754 BE175756 BE841747 BF798384 AU128251 BF095246 BG223262 AW847833 AL536643 AW365516 AW391532
			BE934857 BF925057 AW438446 R86245 AW178270 BE087782 BI832144
15	440605	10075_1	BC017350 BC021031 AI220219 AI828751 AW134498 BE138642 AA894554 AI278594 AV747315 BE561749 BI085890 TB0117 H69682 N70904
	427239	20459_2	AV741999 H70098
20			AL532360 BE794750 AA582905 AI015057 AW271034 BG271636 AW075177 AW071374 AI345565 AI307208 BE138953 BE049086 AI334881
			AW075006 AW075181 AA464019 AW302733 AW075100 AW073433 AI802854 AI334909 AI802853 AI345036 AI348921 AI340734 AI307478
			AI251289 AW302327 AW072520 AI312145 AW073856 AW072513 AW071289 AI307558 AA876188 T29587 AI307493 AI255068 AI252868 AI252839
			AW074809 AI252926 AI252160 AI251662 AI251262 AI610913 AI270787 AI270156 AI252075 AW073459 AW072901 AW072495 AW071420
			AI305762 AI254764 AI802837 AI251264 AW073049 AW071311 AI340643 BE138955 BE138502 AW073455 AI334733 AI054335 BE139260
			AI054302 AI054060 AI054057 AI053722 AI289711 BE139228 AW470478 AW271039 AW302085 BE041872 AI254494 AI271496 AI252427
			BF18773 BF718645 AW074866 BE857822
25	445093	175983_1	AJ207197 BF773544 AW195462
	456505	15472_2	BC017955 AW969075 AA279982 AA504511 AI219979 AA504595 AI245579 AA278181 BG485019 BI049312
	428612	1383189_1	AA770001 AA431112 AA432126
	437642	77594_1	AL079308 AA281819
	440129	2607882_1	AI732597 AA977633 AA855818
30	410704	1054673_1	AW877458 AW877524 BE076922 BE166912 AW840534 BE076754 AW797829 BE166905 BE166926 AW877462 BE166927 BE166932 AW877523
			BE166917 AW877529 BE166928 BF351394 AW877522 AW877528 BE166861 BE166865 BE166913 BE166919 AW877456 AW877537 BE076866
			AW840571
	438243	2532601_1	AI581311 AA781682 AA781678
	438869	52134_1	AF075009 R63109 R63068
35	434776	118129_1	AW974599 AA548988 R98760

TABLE 53C

40	Pkey:	Unique number corresponding to an Eos probe set
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
	Strand:	Indicates DNA strand from which exons were predicted.
	Nt_position:	Indicates nucleotide positions of predicted exons.

45	Pkey	Ref	Strand	Nt_position
	408547	7711513	Minus	172780-174358
	404996	6007890	Plus	37999-38145,38652-38998,39727-39872,4055
	402199	8576116	Minus	84187-84744
	402145	8018280	Plus	113086-114800
50	401837	7630990	Minus	120993-121095,121660-121729
	403780	8076989	Plus	93160-93408
	402299	6693370	Plus	23367-25175
	401435	8217934	Minus	54508-55233
	401454	6682291	Minus	170688-170834
55	402098	8117697	Minus	44186-44330
	404287	2326514	Plus	53134-53281
	406367	9256126	Minus	58313-58489
	403137	9211494	Minus	92349-92572,92958-93084,93579-93712,9394
	402178	8575912	Plus	391138-391711
60	403433	9719611	Minus	72225-72437
	402408	9798239	Minus	110325-110491
	405935	6758795	Minus	163112-163652
	406542	7711499	Plus	117335-118473
	402099	8117697	Plus	121553-121742,123265-123423
65	404068	3168621	Minus	18123-18766
	401644	8576138	Plus	82655-83959
	402680	8113438	Plus	137634-137768,139702-139893,140475-14059
	401091	9958240	Plus	94760-94898
	400587	9887626	Plus	25435-25588,25668-25747
70	401148	2547238	Minus	22521-23053
	403432	9719611	Minus	68204-68392
	400592	9887642	Minus	24642-24815
	403610	8308286	Plus	157705-157860

75	TABLE 54A:
	Pkey: Unique Eos probe set identifier number
	ExAccn: Exemplar Accession number, Genbank accession number
	UnigeneID: Unigene number
	Unigene Title: Unigene gene title
80	R1: Ratio of normal testis to normal adult tissues
	R2: Ratio of "average" normal testis to "average" testicular cancer

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
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	401979		C17000767.gj11990770[amb]CAC19651.1] (A	10.08	43.3	
	421825	AA298758	Hs.183747	ESTs, Moderately similar to CALB_HUMAN C	10.35	36.8
	408493	BE206854	Hs.46039	phosphoglycerate mutase 2 (muscle)	5.74	32.0
5	441728	A1797395	Hs.169797	Homo sapiens BOULE (BOULE) mRNA, complet	10.54	24.5
	452215	AK002043	Hs.28472	hypothetical protein FLJ11181	4.86	22.0
	415211	R64730.	Hs.155986	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	6.93	19.8
	418677	S83308	Hs.87224	SRV (sex determining region Y)-box 5	4.94	18.5
	449108	A1140683	Hs.98328	hypothetical protein MGC13040	7.94	17.5
10	420437	AA992768	Hs.97633	A kinase (PRKA) anchor protein 4	16.75	15.6
	438632	AA724299	Hs.304020	ESTs, Weakly similar to CRTG_HUMAN CALRE	6.51	14.9
	418409	AA219332	Hs.120869	ESTs, Weakly similar to R107_HUMAN H-REV	4.96	14.6
	406409			Target Exon	3.98	14.3
	427060	AW378993	Hs.90286	ESTs	3.56	14.2
	427310	A1613480	Hs.47152	teklin 3	4.50	14.0
15	427166	AA431576	Hs.99154	ESTs	4.28	13.9
	427178	AA398868	Hs.97542	Homo sapiens testis-development related	10.19	13.7
	410694	AL137538	Hs.85500	Homo sapiens mRNA; cDNA DKFZp434N2019 (f	5.76	13.4
	424310	AA338648	Hs.50334	testes development-related NYD-SP22	5.24	13.3
20	427441	AA412605	Hs.343879	SPANX family, member C	10.45	12.6
	438057	AW294544	Hs.125785	ESTs, Weakly similar to CORB_MOUSE CORNI	18.57	12.3
	422183	AA431698	Hs.112794	Human DNA sequence from clone 1058E13 on	5.18	12.3
	427293	AA705799	Hs.183714	ESTs	10.79	12.1
	444963	A1916973	Hs.213603	ESTs	3.18	12.1
25	428608	A1699329	Hs.99168	ESTs, Weakly similar to AF132972 1 CGI-3	15.40	11.8
	453178	AA496088	Hs.61648	ESTs	4.13	11.8
	428618	AA885360		Target CAT	7.53	11.5
	401741			Target Exon	10.41	11.5
	422086	AW182930	Hs.250182	ESTs	4.39	10.7
30	426604	H53354	Hs.97141	ESTs, Weakly similar to hypothetical pro	7.04	10.6
	442373	A5377758	Hs.164799	testes development-related NYD-SP17	8.23	10.3
	427455	AF173081	Hs.178215	Vertebrate LIN7 homolog 1, Tax Interact	3.03	10.1
	437248	AW449340	Hs.93090	ESTs	9.06	10.1
	426808	AA444162	Hs.99344	hypothetical protein PRD-NY3	3.68	10.0
35	427297	AW292593	Hs.334907	Homo sapiens, clone MGC:17333, mRNA, com	9.70	9.8
	422358	AL133030	Hs.115429	Homo sapiens mRNA for KIAA1666 protein,	11.85	9.7
	451610	AW118604	Hs.207126	ESTs	5.63	9.7
	410630	BE044562	Hs.266847	ESTs, Weakly similar to KIAA1214 protein	4.38	9.5
	426677	AW949858	Hs.97165	ESTs	6.58	9.3
40	437558	A1126471	Hs.124112	ESTs, Moderately similar to HSI2_HUMAN D	4.47	9.2
	423088	NM_006687	Hs.123530	actin-like 7A	15.07	8.9
	426476	NM_003296	Hs.2042	taste specific protein 1 (probe H4-1 p3	18.55	8.9
	421952	AA300900	Hs.98849	dynein light chain 2B (DNLC2B)	13.93	8.8
	429877	W37337	Hs.103014	ESTs	6.97	8.7
45	413114	A1825838	Hs.75206	protein phosphatase 3 (formerly 2B), cat	3.78	8.6
	412026	AA383618	Hs.73073	testis-specific ankyrin motif containing	22.03	8.5
	411844	A1807661	Hs.144658	ESTs, Weakly similar to T17257 hypotheti	7.34	8.3
	436898	AA974253	Hs.120319	Homo sapiens autoimmune infertility-rela	4.16	8.2
	426599	AW183674		ESTs	6.29	8.1
50	426683	A1073430	Hs.146775	ESTs, Weakly similar to T30993 hypotheti	10.89	8.0
	426930	AA393442		ESTs	5.06	8.0
	427836	AA416842	Hs.116176	ESTs	4.79	8.0
	407721	Y12735	Hs.38018	dual-specificity tyrosine-(Y)-phosphoryl	5.11	7.9
55	430822	AJ005371	Hs.248017	glyceraldehyde-3-phosphate dehydrogenase	21.26	7.6
	434150	BE047007	Hs.116116	taste specific, 10	4.85	7.6
	422789	AK001113	Hs.120842	hypothetical protein FLJ10251	10.28	7.5
	422116	H84205	Hs.111850	mitochondrial capsule selenoprotein	9.12	7.5
	433724	A1827749	Hs.144924	serine/threonine protein kinase SSTK	22.24	7.4
	410187	AA860341	Hs.104680	ESTs	3.03	7.4
60	419584	AF063356	Hs.283764	F-box only protein 24	6.43	7.4
	456182	A1147998	Hs.155833	ESTs, Weakly similar to spliceosomal pro	9.90	7.3
	418665	T19204	Hs.185685	ESTs	7.14	7.3
	426646	AA382787	Hs.122713	ESTs	7.03	7.3
	420349	NM_016811	Hs.97174	potassium inwardly-rectifying channel, s	14.80	7.3
65	428624	A1125222	Hs.98712	hypothetical protein DKFZp434H0311	3.71	7.1
	420710	NM_007009	Hs.99875	zona pellucida binding protein	20.78	7.1
	434317	A1674095		ESTs	3.98	7.1
	443432	A1056863	Hs.339871	ESTs	3.46	7.0
70	425709	AA383076	Hs.159274	outer dense fibre of sperm tails 1	23.21	7.0
	426670	AA383047	Hs.310210	ESTs	6.92	7.0
	408613	AW242088	Hs.253967	ESTs	5.77	6.8
	452235	AL039743	Hs.28514	testes development-related NYD-SP21	9.23	6.7
	434133	A1855275	Hs.236635	ESTs, Weakly similar to ATHUB actin beta	7.46	6.7
	427294	AA412594	Hs.126902	ESTs	3.44	6.7
75	427262	AA448509	Hs.128652	ESTs	5.66	6.6
	428851	AA459835	Hs.120573	hypothetical protein DKFZp434K1172	9.01	6.5
	406378			NM_021247*:Homo sapiens prolamine 3 (PRM	3.96	6.4
	425865	AA393491	Hs.183740	ESTs	9.15	6.4
	428865	NM_017481	Hs.189184	ubiquitin 3	11.07	6.4
80	439379	AA835002	Hs.125611	ESTs	5.06	6.3
	427620	BE467881	Hs.97489	ESTs, Weakly similar to B28096 fln-1 pr	9.29	6.2
	458940	BE149824	Hs.132888	KIAA1674	3.11	6.2
	426620	AW450252		ESTs	12.27	6.2
	429516	A1653299	Hs.99354	ESTs, Weakly similar to hyperpolarizatio	9.15	6.1

	426736	AA431615	Hs.130722	ESTs	3.58	6.1
	427843	AC006822	Hs.180943	hypothetical protein R30953_1	6.34	6.1
	426639	AI799059	Hs.112807	ESTs	6.93	6.0
5	438637	BE500941	Hs.126730	ESTs, Weakly similar to KIAA1214 protein	3.04	6.0
	433795	AI216683	Hs.122599	ESTs, Weakly similar to ALU7_HUMAN ALU S	10.45	5.9
	441232	AI656050	Hs.7086	hypothetical protein MGC12435	4.27	5.9
	433943	AA992805	Hs.44865	lymphoid enhancer-binding factor 1	6.87	5.8
	426955	AA393669	Hs.238094	ESTs	4.75	5.8
10	428918	AL038867	Hs.2324	protamine 2	38.40	5.8
	427851	AA846543	Hs.98257	ESTs	15.87	5.8
	428208	AA442327	Hs.104854	ESTs	6.34	5.7
	422207	AI828862	Hs.10964	ESTs	6.43	5.7
	431153	AW972342	Hs.77823	hypothetical protein FLJ21343	9.24	5.7
15	419350	AC005328		Homo sapiens chromosome 19, cosmid R2668	14.94	5.6
	427107	AA885566	Hs.180346	ESTs	6.25	5.6
	429461	AI188219	Hs.39311	ESTs, Weakly similar to HSJ2_HUMAN DNAJ	3.92	5.6
	432512	NM_003284	Hs.3017	transition protein 1 (during Xistons to	22.03	5.6
	434451	AW445179	Hs.121438	ESTs	7.89	5.5
20	420348	AL137385	Hs.97140	Homo sapiens mRNA; cDNA DKFZp434M1125 (f	11.26	5.5
	427214	AA442240	Hs.178213	ESTs	8.41	5.5
	458658	AI301117	Hs.122055	ESTs	4.35	5.5
	457034	AA398061	Hs.295587	Homo sapiens chromosome 21 segment HS21C	11.29	5.4
	423120	AW160551	Hs.124021	soggy-1 gene	8.88	5.4
25	438983	AF085584	Hs.20029	proacrosin binding protein sp32 precursor	22.69	5.4
	426619	AI357194	Hs.119284	ESTs	7.07	5.4
	440822	AI554887		Homo sapiens clone 19187 placenta expres	3.60	5.4
	416205	AA176396	Hs.169624	ESTs	10.26	5.4
	426712	AW173177	Hs.197755	hypothetical protein MGC5356	8.17	5.3
30	427840	AI216654	Hs.98251	ESTs	6.44	5.3
	439314	AA382413	Hs.178144	ESTs	8.35	5.3
	428943	BE551631	Hs.20969	ESTs	6.31	5.2
	409209	AA460180	Hs.73217	ESTs	7.85	5.2
	441710	AI187883	Hs.127510	ESTs, Weakly similar to ENC1_HUMAN ECTOD	7.73	5.1
35	420571	AA442366	Hs.98952	Human DNA sequence from clone RP1-29G22	9.39	5.1
	428563	AA431816	Hs.98650	ESTs	14.94	5.1
	433994	AL042483	Hs.336499	ESTs	6.84	5.0
	441856	AI674774	Hs.128014	ESTs	3.74	5.0
	427789	AA412428	Hs.48642	hypothetical protein FLJ23093	4.29	5.0
40	418967	NM_001725	Hs.89535	bactericidal/permeability-increasing pro	4.14	4.9
	430232	AA469940	Hs.105324	ESTs, Moderately similar to FRHUH ferrit	10.66	4.9
	421850	AW274576	Hs.121021	ESTs	12.27	4.9
	449438	AA880329	Hs.279307	hypothetical protein DKFZp434I2117	4.50	4.9
	426699	AA383337	Hs.121269	ESTs	5.67	4.9
45	426627	AF012359	Hs.195685	ESTs	20.66	4.9
	427285	AA401664	Hs.97784	ESTs	4.72	4.8
	423693	AL133633	Hs.131779	Homo sapiens mRNA; cDNA DKFZp434E2118 (f	6.03	4.8
	457019	AA421844	Hs.12830	hypothetical protein	3.87	4.8
	405264			NM_030813: Homo sapiens suppressor of po	4.48	4.8
50	450506	AI668605	Hs.60380	ESTs, Moderately similar to ALU6_HUMAN A	3.76	4.8
	421378	L77564	Hs.103978	serine/threonine kinase 22B (spermogene	7.35	4.8
	431215	AA496078	Hs.121554	Human DNA sequence from clone RP11-218C1	8.66	4.7
	427423	BE267041	Hs.177925	exonuclease NEF-sp	19.27	4.7
	438756	AW081754	Hs.303923	hypothetical protein DKFZp434L1717	12.05	4.7
55	424197	AF096834	Hs.142989	germ cell specific Y-box binding protein	17.70	4.7
	423284	AC005784	Hs.126486	Homo sapiens chromosome 19, cosmid R3134	7.50	4.7
	432117	AL036195	Hs.2909	protamine 1	55.33	4.7
	424426	AI478416	Hs.132888	KIAA1674	5.41	4.6
	437387	AI198874	Hs.28847	AD026 protein	5.04	4.6
60	420718	NM_002301	Hs.59881	lactate dehydrogenase C	9.18	4.6
	420768	AI468780	Hs.292503	ESTs, Weakly similar to T47142 hypotheti	5.70	4.6
	423577	M86808	Hs.131361	pyruvate dehydrogenase (liponate) alpha	10.93	4.5
	436661	AI125270	Hs.128069	ESTs, Weakly similar to T19142 hypotheti	3.82	4.5
	427749	BE045979	Hs.98095	Homo sapiens cDNA: FLJ23052 fis, clone L	6.45	4.5
65	441830	AA383104	Hs.42954	hypothetical protein DKFZp564D0372	11.29	4.5
	427877	AW138725	Hs.178067	ESTs	4.09	4.5
	426623	AA382826	Hs.132793	ESTs	26.62	4.5
	429865	AL040379	Hs.99551	Homo sapiens cDNA FLJ11789 fis, clone HE	13.25	4.5
	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	3.88	4.4
70	417592	AA204664	Hs.182437	ESTs, Weakly similar to I54383 chromosom	3.46	4.4
	421938	AA405951		gb:zu66c01.r1 80ares_testis_NHT Homo sap	4.69	4.4
	424144	AA454033	Hs.41644	AKAP-associated sperm protein	19.15	4.4
	426710	BE041517	Hs.143893	ESTs	5.57	4.4
	428710	AI850919	Hs.126780	ESTs, Weakly similar to T12519 hypotheti	11.86	4.4
75	438641	AW138484	Hs.190653	ESTs	6.19	4.4
	420614	AL110281	Hs.99364	putative transmembrane protein	6.86	4.4
	422705	NM_006686	Hs.119287	actin-like 7B	9.73	4.4
	421805	AL042716	Hs.130947	hypothetical protein DKFZp434N1415	5.89	4.4
	448963	AA459796	Hs.331247	Homo sapiens, clone IMAGE:3610712, mRNA,	6.77	4.3
80	426738	AA421097	Hs.291902	ESTs	3.49	4.3
	440403	AW665135	Hs.130531	ESTs	6.97	4.3
	456085	AI184560	Hs.130362	ESTs, Weakly similar to A47582 B-cell gr	6.30	4.3
	439594	AI245026	Hs.111099	hypothetical protein MGC10974	7.85	4.3
	428909	AI190714	Hs.98945	ESTs	7.78	4.3

5	426735	T78716	Hs.120446	ESTs	5.10	4.3
	438653	AW188039	Hs.131813	ESTs	5.29	4.3
	443038	AI968058	Hs.209206	ESTs, Weakly similar to S38782 actin bai	7.29	4.2
	428677	AI657119	Hs.120036	troponin I, cardiac	10.73	4.2
	424220	AK000869	Hs.143251	hypothetical protein	9.13	4.2
	426299	H93373	Hs.168222	acrosomal vesicle protein 1	4.87	4.2
	428871	AA913840	Hs.98903	ESTs	3.76	4.2
	410163	AF151977	Hs.59260	NTT5 protein	7.29	4.2
10	433133	AB027249	Hs.104741	PDZ-binding kinase; T-cell originated pr	5.29	4.2
	427757	AI142295	Hs.129794	ESTs	3.57	4.1
	426721	AA383588	Hs.131816	ESTs, Weakly similar to T29012 hypotheti	11.13	4.1
	401692			C16000122*gi5689527[db][BAA83047.1] (A	6.37	4.1
	403783			NM_031956.Homo sapiens NYD-SP14 protein	3.74	4.0
15	421611	AA459841	Hs.97309	ESTs	11.51	4.0
	404271			ENSP00000244792*-Phosphoglycerate kinase	4.02	4.0
	441800	AW027571	Hs.7973	hypothetical protein DKFZp434G156; KIAA1	8.86	4.0
	423000	AF049615	Hs.122959	Huntingtin Interacting protein M	3.60	4.0
	423118	AL035460	Hs.124009	Human DNA sequence from clone RPS-860F19	4.84	4.0
20	420419	AA397798	Hs.11614	HSPC085 protein	4.07	3.9
	435897	AF289223	Hs.128322	I-complex 11 (a murine top homolog)	23.29	3.9
	428516	R38137	Hs.156469	ESTs, Moderately similar to KIAA0940 pro	5.28	3.9
	427179	AA400690	Hs.97543	ESTs	6.18	3.9
	426609	AL040604	Hs.99344	hypothetical protein PRTD-NY3	10.07	3.9
25	452579	AA131657	Hs.23830	ESTs	5.24	3.9
	441443	BE466999	Hs.129293	ESTs	4.60	3.9
	427709	AI631811	Hs.180403	STRIN protein	3.82	3.9
	435484	AA682756	Hs.88051	ESTs	5.10	3.9
	426555	AA389291	Hs.130767	Homo sapiens cDNA: FLJ23653 fls, clone 1.	4.61	3.8
30	436302	AL355841	Hs.99330	hypothetical protein FLJ23588	7.14	3.8
	421620	AA446183	Hs.91885	ESTs, Weakly similar to I55214 salivary	5.20	3.8
	427086	AA436131	Hs.188781	ESTs	5.76	3.8
	420475	AW408407	Hs.187018	ESTs	3.99	3.8
	441357	AI240184	Hs.343487	ESTs	4.63	3.8
35	438643	AA757628	Hs.10941	ESTs, Weakly similar to IPP1_HUMAN PROTE	8.04	3.8
	441806	AI024442	Hs.346385	ESTs	5.48	3.8
	413209	AW083791	Hs.21263	suppressor of potassium transport defect	9.02	3.8
	414544	AA149285	Hs.115659	hypothetical protein MGC5521	10.15	3.8
	427251	AI026844	Hs.98843	ESTs, Highly similar to GRA2_HUMAN GLYC	7.69	3.8
40	437982	N93465	Hs.121764	ESTs, Weakly similar to testicular tekli	3.46	3.7
	442589	BE409869		protein kinase, cAMP-dependent, regulato	4.50	3.7
	425841	BE262961	Hs.99052	ESTs	8.26	3.7
	410350	AA446395	Hs.62595	chromosome 9 open reading frame 9	7.64	3.7
	440487	AI203685	Hs.135763	ESTs	5.90	3.7
45	419455	AW172570	Hs.14600	ESTs	4.23	3.7
	436588	AA759233		ESTs	5.04	3.7
	421610	AA393188	Hs.90034	hypothetical protein FLJ21916	5.53	3.7
	441982	AI216902	Hs.48802	ESTs	4.79	3.6
	427288	AI139000	Hs.97792	hypothetical protein DKFZp434i099	5.17	3.6
50	414439	W45387	Hs.100007	regulatory factor X, 2 (influences HLA c	4.43	3.6
	401798			Target Exon	4.83	3.6
	433395	AF039442	Hs.160881	Homo sapiens colon cancer antigen NY-CO-	3.17	3.6
	438054	AI476330	Hs.234934	ESTs	3.56	3.6
	426658	AA387912	Hs.115366	Human DNA sequence from clone RP4-803K15	7.26	3.6
55	431985	AA536130		Novel human gene mapping to chromosome 20	6.13	3.6
	427872	AA835058	Hs.9622	Human DNA sequence from clone RP1-261G23	4.04	3.6
	437886	AA813689	Hs.123436	ESTs, Weakly similar to KIAA1205 protein	4.69	3.6
	420431	AB007131		Homo sapiens cDNA FLJ12825 fls, clone NT	4.24	3.5
	409467	Z22780	Hs.307358	cylicin, basic protein of sperm head cyt	5.13	3.5
60	422770	AL117544	Hs.120021	DKFZP434I092 protein	8.02	3.5
	437399	AI808626	Hs.121188	ESTs, Weakly similar to T28922 hypotheti	5.03	3.5
	428448	AA625766	Hs.98609	ESTs, Weakly similar to A Chain A, Coagu	4.30	3.5
	426705	AL042749	Hs.97714	ESTs	10.45	3.5
	427312	AA400657	Hs.136283	ESTs	4.47	3.5
65	423329	AF054910	Hs.127111	laktn 2 (testicular)	4.40	3.5
	439290	AI638094	Hs.236896	ESTs	3.29	3.4
	451481	AA300228	Hs.295866	hypothetical protein DKFZp434N1923	6.18	3.4
	420500	AC005261	Hs.98338	serine/threonine kinase 13 (neuronal PL1-	6.24	3.4
	441168	AI198850	Hs.131654	DMRT-like family B with proline-rich C-t	10.39	3.4
70	420462	X57655	Hs.98243	serine protease inhibitor, Kazal type, 2	20.38	3.4
	425985	AI208684	Hs.163960	Homo sapiens heat shock transcription fa	5.02	3.4
	444968	AW828509	Hs.148653	ESTs	5.10	3.4
	429210	AA448011	Hs.131918	ESTs	4.22	3.4
	442970	R28215	Hs.143878	Homo sapiens mRNA for FLJ00024 protein,	4.20	3.4
75	422782	AL133054	Hs.120369	hypothetical protein DKFZp434I2215	4.72	3.4
	436601	AA969884		ESTs	4.84	3.4
	421209	AJ010230	Hs.102576	ret finger protein-like 1 antisense	7.83	3.4
	415705	U06632	Hs.966	collin	6.30	3.4
	435587	AF215924	Hs.97899	putative allantolcase	3.48	3.3
80	427572	AA417291	Hs.97978	hypothetical protein MGC4766 similar to	3.54	3.3
	427541	AI798983	Hs.82921	solute carrier family 35 (CMP-staic aci	10.33	3.3
	429404	NM_005738	Hs.201672	ADP-ribosylation factor-like 4	3.57	3.3
	415014	AW954064	Hs.24951	ESTs	4.03	3.3
	420547	AF155140	Hs.98738	gonadotrophin-regulated testicular RNA ha	10.76	3.3

5	412092	H43229	Hs.125201	ESTs, Weakly similar to I38022 hypotheli	5.27	3.3
	441579	AW468847	Hs.127194	ESTs	7.13	3.3
	420619	AF130256	Hs.99430	testis zinc finger protein	5.19	3.3
	425388	AB014595	Hs.155976	cullin 4B	3.07	3.3
	426638	NM_012337	Hs.158450	nasopharyngeal epithelium specific prote	3.52	3.3
10	429938	BE295804	Hs.226377	phosphate cytidyltransferase 2, ethanol	3.03	3.3
	453017	R84301	Hs.31387	DKFZP564J0123 protein	3.30	3.3
	424466	AL040420	Hs.148250	Homo sapiens mRNA; cDNA DKFZp434N1535 (f	4.81	3.3
	442084	HB1173	Hs.34596	ESTs	4.78	3.3
	423196	AK001866	Hs.125139	hypothetical protein FLJ11004	4.63	3.3
15	434183	AW104257	Hs.123426	ESTs, Weakly similar to SN1L_HUMAN PROBA	5.73	3.3
	428093	AW594506	Hs.104830	ESTs	6.95	3.3
	433982	AA724720	Hs.112941	ESTs	5.11	3.2
	428921	AL096749	Hs.225433	Homo sapiens mRNA; cDNA DKFZp434G153 (fr	4.04	3.2
	408415	AW418788		ESTs, Weakly similar to S43569 R01H10.6	3.49	3.2
20	407722	BE252241	Hs.38041	pyridoxal (pyridoxine, vitamin B6) kinas	6.77	3.2
	402857			Target Exon	3.19	3.2
	416667	AK000526	Hs.79457	hypothetical protein FLJ20519	3.69	3.2
	436114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	14.29	3.2
	427748	AA421041		ESTs	4.57	3.2
25	422794	AJ011733	Hs.120857	synaplogrin 4	4.23	3.2
	417488	AL046052	Hs.321046	hypothetical protein FLJ11743	3.57	3.2
	440115	R41808		ESTs, Weakly similar to B Chain B, Solut	4.67	3.2
	437143	AW204056	Hs.8917	ESTs	4.16	3.2
	417473	M55268	Hs.82201	casein kinase 2, alpha prima polypeptide	4.02	3.2
30	426594	AA884317	Hs.97130	ESTs	3.45	3.2
	428733	AA346824	Hs.191996	Homo sapiens organic cation transporter	6.29	3.2
	440884	AJ382142	Hs.132104	ESTs	8.48	3.2
	427141	AW628007	Hs.87643	testis-specific protein TSP-NY	5.60	3.2
	431534	AL137531	Hs.258890	Homo sapiens mRNA; cDNA DKFZp434F0919 (f	5.10	3.2
35	438670	AI275603	Hs.123428	ESTs	4.08	3.2
	412443	AW951103	Hs.130767	Homo sapiens cDNA: FLJ23553 fls, clone L	4.26	3.2
	452251	R37132	Hs.65009	ESTs	4.01	3.1
	444141	AW629475	Hs.8977	ESTs, Weakly similar to RED1_HUMAN DOUBL	4.89	3.1
	428254	AK000542	Hs.183362	hypothetical protein FLJ20535	5.23	3.1
40	421621	AL045589	Hs.180197	ESTs	7.09	3.1
	451017	BE391847	Hs.181173	hypothetical protein MGC10771	3.57	3.1
	457138	AW140059	Hs.98579	ESTs	13.17	3.1
	428524	AA429772		ESTs	4.40	3.1
	428726	AA432195	Hs.96694	ESTs	6.47	3.1
45	431310	AW327889	Hs.252433	Homo sapiens cDNA FLJ13794 fls, clone TH	4.07	3.1
	428076	AA420979	Hs.234895	ESTs, Weakly similar to Lysozyme [H.sapi	5.97	3.1
	427532	AA442152	Hs.104744	hypothetical protein DKFZp434J0617	3.45	3.1
	424450	AL137526	Hs.147472	dyncin intermediate chain 2	6.01	3.1
	433963	AI218808	Hs.187778	ESTs	5.68	3.1
50	424181	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	3.20	3.1
	440933	AI208217		ESTs	3.44	3.1
	441854	AA215990	Hs.99841	ESTs, Weakly similar to dJ1108D11.1 [H.s	4.03	3.1
	423313	NM_014269	Hs.128838	a disintegrin and metalloproteinase doma	6.36	3.1
	428630	AA431270	Hs.140646	ESTs	3.59	3.1
55	448813	AF169802	Hs.22142	cytochrome b5 reductase b5R2	5.63	3.0
	434720	AJ208541	Hs.189180	ESTs, Weakly similar to cytochrome c-lik	6.04	3.0
	436328	AJ291145	Hs.122042	Human DNA sequence from clone RP4-576H24	7.10	3.0
	429293	AI757879	Hs.99214	ESTs	5.69	3.0
	427255	AA400082	Hs.343593	ESTs, Weakly similar to TD54_HUMAN TUMOR	5.37	3.0
60	440713	AA904448	Hs.126368	ESTs	6.28	3.0
	418499	AI627392	Hs.302023	hypothetical protein FKSG25	7.88	3.0
	423216	NM_015896	Hs.167380	BLU protein	6.68	3.0
	444844	AW070634	Hs.144794	ESTs	5.00	3.0
	430252	AI638774	Hs.105328	testes development-related NYD-SP20	21.75	3.0
65	427829	AI188225		ESTs	7.36	3.0
	426879	AI889340	Hs.115437	hypothetical protein MGC3048	7.24	3.0
	427362	AA625582	Hs.97762	EST	4.38	3.0
	441973	T80072	Hs.10688	ESTs, Weakly similar to HRIHFB2157 [H.sa	4.06	2.9
	428989	AF104250	Hs.194712	pint (Drosophila)-like 1	4.45	2.9
70	438735	M76676		ESTs	3.81	2.9
	432238	AL133057	Hs.274135	Homo sapiens mRNA; cDNA DKFZp434K1815 (f	11.37	2.9
	427585	AA609861	Hs.190592	ESTs, Moderately similar to WASP-family	6.26	2.9
	427306	AI476743	Hs.229275	ESTs	3.00	2.9
	418725	AL117637	Hs.306094	DKFZP434I225 protein	7.13	2.9
75	456748	AW137749	Hs.125902	ubiquitin specific protease 2	3.48	2.9
	443162	T49951	Hs.9029	DKFZP434G032 protein	3.60	2.9
	433836	AA610065	Hs.179548	ESTs	3.33	2.9
	439680	AW245741	Hs.58461	ESTs, Weakly similar to A35659 knappa-	3.22	2.9
	437426	AW136558	Hs.125246	ESTs	4.49	2.9
80	405528			. C2002547:g[14507721]e[1NP_003310.1] tit	6.03	2.9
	442977	AW291731	Hs.144090	ESTs	4.23	2.9
	433330	AW207084	Hs.132816	hypothetical protein MGC14601	13.24	2.8
	424275	AW673173	Hs.144505	DKFZP556F0548 protein	5.60	2.8
	428657	AA770016	Hs.121192	ESTs	3.64	2.8
	410202	AB023213	Hs.60177	KIAA0996 protein	3.00	2.8
	428080	AI198658	Hs.98330	ESTs	4.09	2.8
	427252	AA400089	Hs.97757	hypothetical protein FLJ13031	4.34	2.8

	458255	AW140126	Hs.132357	ESTs	3.23	2.8
	433612	AF078164	Hs.61188	Homo sapiens Ku70-binding protein (KUB3)	3.95	2.8
	440582	AA993337	Hs.129082	ESTs	5.29	2.8
5	435566	AI457958	Hs.80464	hepatitis B virus x-interacting protein	3.28	2.8
	433771	AI028794	Hs.112684	ESTs	3.36	2.8
	447924	AI817226	Hs.313413	ESTs, Weakly similar to T23110 hypotheti	5.30	2.8
	426703	AI221893	Hs.121549	ESTs	3.93	2.8
	430251	AA609245	Hs.181451	ESTs	4.04	2.8
10	427184	AI969351	Hs.180471	ESTs	6.78	2.8
	439909	AW450062	Hs.187134	ESTs, Moderately similar to AF263742 1 g	3.65	2.8
	448885	AW003686	Hs.30325	ESTs, Highly similar to AF200923 1 test	3.34	2.7
	450340	AA442322	Hs.60288	ESTs	5.39	2.7
	428100	AW665592	Hs.190413	ESTs	5.32	2.7
15	449333	AI203021		ESTs	4.35	2.7
	429861	AI989571	Hs.99510	ESTs	3.28	2.7
	426622	AL044400	Hs.25371	ESTs, Weakly similar to A37232 mucin, tr	5.38	2.7
	427256	AL042436	Hs.97723	ESTs	4.08	2.7
	408407	AF214680	Hs.44685	C3HC4-like zinc finger protein	3.27	2.7
20	403328			Target Exon	4.26	2.7
	436264	AA707457	Hs.120014	ESTs	3.58	2.7
	427104	AA398187	Hs.104682	ESTs, Weakly similar to mitochondrial ci	3.68	2.7
	428640	AI200931	Hs.98104	ESTs	4.80	2.7
	428789	AW296167	Hs.91930	ESTs	4.23	2.7
25	435274	AA887547	Hs.160905	ESTs	4.25	2.7
	426612	AA922067	Hs.184185	ESTs	7.17	2.7
	435110	N42688	Hs.81001	F-box only protein 25	4.85	2.7
	433792	AA778861		ESTs	4.06	2.7
30	423278	AL117627	Hs.126289	Homo sapiens mRNA; cDNA DKFZp434B115 (fr	3.04	2.7
	427284	AA400298	Hs.144696	ESTs	5.81	2.6
	423375	Z94277	Hs.127689	type 1 protein phosphatase inhibitor	3.38	2.6
	422362	Z46967	Hs.115460	calicin	4.72	2.6
	439993	T18864	Hs.144924	serine/threonine protein kinase SSTK	5.03	2.6
	409364	AI480252	Hs.137368	ESTs	7.22	2.6
35	419224	NM_012189	Hs.314452	fibrous sheathin II	13.88	2.6
	428915	AI041278	Hs.87908	Snf2-related CBP activator protein	4.73	2.6
	427181	AI183653	Hs.27888	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.21	2.6
	442122	AI932330		ESTs	3.07	2.6
40	424812	AF059252	Hs.153299	DCM-3 (C. elegans) homolog Z	3.80	2.6
	430856	AI183529	Hs.2706	glutathione peroxidase 4 (phospholipid h	3.19	2.6
	427234	AA398867	Hs.104875	ESTs	3.43	2.6
	423005	AL080148	Hs.123004	DKFZP434B204 protein	3.53	2.6
	428214	AA936282	Hs.120397	ESTs	4.14	2.6
	452613	AA461599	Hs.23459	ESTs	7.78	2.6
45	410380	AL133068	Hs.62880	novel protein similar to mouse MOV10	3.45	2.6
	452637	AW247390	Hs.77735	hypothetical protein FLJ11618	3.43	2.6
	401712			Target Exon	4.61	2.6
	429186	BE503443	Hs.112095	hypothetical protein DKFZp434F1819	5.90	2.6
50	438124	AA778810	Hs.122045	ESTs	3.43	2.6
	422937	U03270	Hs.122511	centrin, EF-hand protein, 1	3.60	2.6
	410279	BE271977	Hs.61809	hypothetical protein FLJ14117	4.36	2.6
	428625	W87565	Hs.18568	ESTs	5.29	2.6
	433439	AA431176	Hs.133230	ribosomal protein S15	3.50	2.6
	433760	AW592321		ESTs	3.26	2.6
55	431219	AI190773	Hs.127204	ESTs, Weakly similar to similar to CR16,	5.10	2.5
	411773	NM_006799	Hs.72026	protease, serine, 21 (testisin)	8.07	2.5
	453468	W00712	Hs.32590	DKFZP566F084 protein	3.56	2.5
	445158	AI992108	Hs.127206	ESTs	3.80	2.5
	440860	R10482	Hs.132876	ESTs	4.26	2.5
60	452420	BE664871	Hs.29463	centrin, EF-hand protein, 3 (COC31 yeast	3.95	2.5
	433281	N48573	Hs.146037	hypothetical protein DKFZp434C135	5.68	2.5
	429869	AI269514	Hs.129802	ESTs	3.49	2.5
	433949	AI674766	Hs.112877	ESTs	5.15	2.5
	427688	AA298760	Hs.180181	hypothetical protein FLJ14904	10.46	2.5
65	414708	AA393379	Hs.97415	ESTs, Weakly similar to T33068 hypotheti	3.87	2.5
	408485	AW274294	Hs.144092	ESTs, Weakly similar to A Chain A, Sacch	8.10	2.4
	412889	AA290712	Hs.62407	CXC chemokine ligand 16	5.64	2.4
	426956	AA393673		ESTs, Weakly similar to ALU5_HUMAN ALU S	4.68	2.4
	429152	AA447209	Hs.99099	Homo sapiens NYD-SP28 mRNA, complete cds	4.34	2.4
70	426247	U92982	Hs.98834	ESTs	5.40	2.4
	427589	T19219	Hs.97978	hypothetical protein MGC4766 similar to	3.40	2.4
	429099	BE439952	Hs.196177	phosphorylase kinase, gamma 2 (testis)	5.85	2.4
	453353	U33055	Hs.32959	G protein-coupled receptor kinase 2 (Dro	4.82	2.4
	413372	H55532		tubulin, alpha 2	9.32	2.4
75	411737	AW160339	Hs.71791	hypothetical protein	5.26	2.4
	453868	NM_014433	Hs.35984	rhomboid tumor deletion region protein 1	3.05	2.4
	427098	AA398181	Hs.97602	ESTs	3.21	2.4
	427185	AA428708	Hs.99336	ESTs, Weakly similar to T15446 hypotheti	4.27	2.4
	426808	AA364109	Hs.177950	ESTs	7.80	2.4
80	444790	AB030506	Hs.11955	B9 protein	3.32	2.4
	426718	AA383556	Hs.126413	ESTs	4.20	2.4
	411441	AL042355	Hs.70202	WD repeat domain 10	6.14	2.4
	450862	AI983354	Hs.7740	oxysterol binding protein-like 1	4.97	2.3
	427054	AA421240	Hs.97570	ESTs	3.10	2.3

5	438633	AI653327	Hs.123501	ESTs	3.46	2.3
	427199	AW015836	Hs.292919	ESTs	4.31	2.3
	440182	AA868919	Hs.250110	ESTs	3.03	2.3
	435517	AA928626	Hs.130177	ESTs	3.64	2.3
	440309	BE044261	Hs.149774	ESTs	3.52	2.3
	420338	AA825595	Hs.88269	Homo sapiens, clone MGC-17339, mRNA, com	4.23	2.3
	433829	AI190715	Hs.102021	ESTs	6.08	2.3
	429485	AW197086	Hs.99338	ESTs	3.14	2.3
10	423058	AW964568	Hs.111591	ESTs	3.36	2.3
	433822	AI218609	Hs.112772	ESTs	3.83	2.3
	442268	BE278064	Hs.8179	hypothetical protein, clone 2746033	3.00	2.3
	434298	AA860090	Hs.116290	ESTs	3.71	2.3
	440720	AW662776	Hs.336943	Human DNA sequence from clone RP11-60H7	3.08	2.3
15	427554	AW246678	Hs.179615	hypothetical protein FLJ10058	3.39	2.3
	414251	AL042306	Hs.97689	VASA protein	11.25	2.3
	430254	AI809520		ESTs	3.27	2.3
	437418	AI478954	Hs.59459	ESTs	3.43	2.2
	437522	AA983844	Hs.121383	ESTs	4.15	2.2
20	422808	AA449014	Hs.121025	chromosome 11 open reading frame 5	3.09	2.2
	436695	AA725655	Hs.120480	ESTs	5.26	2.2
	422247	U18244	Hs.113602	solute carrier family 1 (high affinity a	6.78	2.2
	421625	AA405386	Hs.178004	ESTs	3.22	2.2
	434807	AA364183	Hs.323443	hypothetical protein FLJ11806	5.51	2.2
25	428174	AA913321	Hs.126778	ESTs	3.09	2.2
	409735	AL035295	Hs.56175	H.sapiens gene from PAC 106H8, similar t	3.11	2.2
	444467	AI150368		ESTs	3.81	2.2
	433832	AA918018	Hs.172516	ESTs	6.94	2.2
	440036	AW593295	Hs.210956	ESTs	5.87	2.2
30	415240	AA161411	Hs.58668	chromosome 21 open reading frame 57	3.66	2.2
	432538	BE258332	Hs.278362	male-enhanced antigen	3.58	2.1
	440882	AI205777	Hs.129538	ESTs	3.83	2.1
	436605	AI187742		ESTs	3.41	2.1
	422990	AF035620	Hs.122764	BRCA1 associated protein	5.66	2.1
35	432174	AW590264	Hs.132806	ESTs	3.05	2.1
	409267	NM_012453	Hs.52515	transducin [beta]-like 2	5.46	2.1
	423021	AL036111	Hs.292767	ESTs	3.87	2.1
	439012	BE383814	Hs.6455	RuvB (E coli homolog)-like 2	5.25	2.1
40	433812	AA725026	Hs.97165	ESTs, Weakly similar to T31611 hypothet	3.62	2.1
	456924	AI631510	Hs.196956	ESTs, Highly similar to match to EST AA3	4.38	2.1
	437249	AA432202	Hs.103147	hypothetical protein FLJ21347	3.38	2.1
	426038	AA368101	Hs.99052	ESTs	3.03	2.1
	427065	AA397903	Hs.236635	ghz18912.r1 Soares_testis_NHT Homo sap	3.23	2.1
45	428824	W23624	Hs.173059	ESTs	3.07	2.1
	428224	X54017	Hs.183088	acrosin	3.18	2.1
	436954	AA740151	Hs.130425	ESTs	3.20	2.1
	444470	AA412195	Hs.13740	ESTs	4.27	2.1
	457579	AB030816	Hs.38761	HRAS-like suppressor	5.30	2.1
	427686	AA417083	Hs.104789	ESTs	3.49	2.1
50	439273	AW139099	Hs.269701	ESTs	3.83	2.1
	434318	AW207552	Hs.116328	ESTs, Weakly similar to A39554 transcrip	4.01	2.1
	427015	AA397520		ESTs	4.28	2.1
	421598	AW830842	Hs.106061	RD RNA-binding protein	3.30	2.1
55	427235	AA398959	Hs.148271	ESTs	3.07	2.1
	434520	AA205273	Hs.177011	hypothetical protein	3.19	2.0
	456051	T86626	Hs.78239	hypothetical protein FLJ20808	3.11	2.0
	418322	AA284166	Hs.84113	cyclin-dependent kinase inhibitor 3 (CDK	8.41	2.0
	451807	W52854		hypothetical protein FLJ23293 similar to	3.52	2.0
	448984	AW751955	Hs.22753	hypothetical protein FLJ22318	4.73	2.0
60	420484	W32953	Hs.98289	VRK3 for vaccinia related kinase 3	3.86	2.0
	414181	AK000476	Hs.75798	hypothetical protein	3.33	2.0
	424558	AF036847	Hs.150490	FK506-binding protein 6 (36kD)	7.70	2.0

TABLE 548

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
428618	2568_1	BC017898 BI826643 BG715794 BG722697 BI460787 BG773459 H52859 AI852853 AI990773 AW655193 AW340601 AA913806 AI337099 BE045942 AW572790 AW515852 H15004 AA909115 BI485310 BI482024 BI581578 BI463075 BG722527 R86003 BG623286 H15003 BI562131 BG435272
428599	10110_1	BE736800 BM471423 AL557221 BG763302 BF742196 BF991016 BG200112 BF920027 BG576409 BG332214 BI830557 AI827504 AW183574 AI805171 AI126491 AA448257 AI090641 AW183329 AA994873 AI203683 BE041513 AA382280 AA382261 AL554887 BE273483
426930	1310779_1	AI809889 AA393442 AI150574 AI200886 AI221692 AA608977 AA813213
434317	599587_1	AI209094 AI377740 AW117382 AW182289 AI674095 AW188019 AA897352 AA931314 AA923336 AW665317 AA629314 AA776691 AA908846 AA974625 AA884357 AI808590
428620	142987_1	AL042392 AI147451 AA758821 AW450252 AA399310 AI656343 AI836688 AW515660 AI190733 AI025812 AA723645 AA709253 AA725709 AA398244 AA382463 AI139637
419350	13086_1	AI218809 BC014609 BG724383 AI024359 AA904573 AI138595 AA858685 AI768931 BI828436 BG717350 BG719800 AW182303 AA448181 BI826870 BI827131 BI830254 BI824155 BI831745 T19190 BI830415
440822	532606_1	BG207582 BG192113 AA977616 AW274024 AI554897 AI221379 AA969158 AA905867 AI873494 AI015039
421938	863689_1	AA412363 AA300575 BG773248 AA412243 AA405951

442589	33097_2	NM_004157 X14968 BG480486 BE409869 BG723898 BG476313 AU121626 BE386516 AI999297 AW172340 AA899658 R23436 AJ015037 BE250558 BF590945 AW385993 BF583000 AA070235 AL556082 M78388 AW504473 AW370139 BG913697 BE899096 BG827945 BE741233 AI015465 AW370169 BE297350 AA093249 AI122828 AA909991 AA759233
5	436688 2470836_1	AL591713 BF197809 AI985094 AW448916 AI243277 AI449630 AL449629
	431986 76926_1	AW241405 AW205071 AI671586 AI652354 AI638465 AW590359 AW662771 AW594067 BE502532 AI218894 BE466416 BF056295 AI247366
	420431 29290_1	AI990484 AI917746 AW665925 AI216456 AW182169 AA969884 AA723888 AI018419
	436601 10131_1	BI602176 BI603138 BI459895 BI756030 AW418788 AA883999 AA724858 AI480311 AW196355 AI004813 AI661117 BE814363 AW589856
	408416 4581_6	AA448124 AA447962 BI461165 AA405629
10	427748 1372622_1	AI208966 AA421041 AA815377 AA411964
	440115 34_3	BF980396 R51074 BF979863 AI539370 BM128735 AA993397 AI611039 AW593985 R41808
	428524 1382184_1	AI208080 AA442862 AA429772
	440933 960517_1	AI125404 AW593312 AI247364 AI208217 AA910021 AI015307
15	427829 1373537_1	AI190292 AI188225 AA416673 AA416596 AA952888 AA872172 AA906874
	438735 10316_1	M76676 NM_022571 BG772522 BF516449 AI537485 AW517245 BF762536 AA634446 AW196331 AI203035 BG722281
	449333 36378_1	AK056320 AL522040 BI793043 AW071691 AI433882 AA855414 AA702684 BI792794 H96879 R52351 AA211126 AA442875 N25725 AA442563 N3446 N25222 Z41110 N26507 N73447 N24077 N20492 AW275550 H99619 AL518306 AL522041 AW959849 AL518307 AA725907 AI865113
20	433792 2204621_1	AI309906 F10184 BM451081 BE257595 BG721625 BI828509 BG700470 F12568 Z45396 BI829288 AA354618 AA364851 AA421448 T74231
	442122 2684549_1	R52350 AA482415 AI203021 T88948 AI565842
	433760 584982_1	AI024286 AA769898 AA778661 AA868972 AA609524
	426956 667337_1	AI932330 AI190707 AI376782 AA976847
25	413372 32896_1	AA609179 AW592321 AA758282 AI214437 AW072537 AA781937
		BI831486 AW190479 AI472793 AA460217 AA459937 BF082576 AA393673 AA398702
		NM_006001 L11645 AI205804 AI207994 AI187362 AA709190 BI462421 BG772170 BG722772 AA436991 BG771655 BI553260 BF126025
		BF125857 BI462670 BG724164 BI562424 BG721662 BI559662 BG722455 BI595415 BG717561 BG722136 BG773507 BG720572 C03867 AI016802
		AL042663 AA770436 AA435720 T19365 AA626698 AA759057 AI208021 BF507844 AI208058 AA412719 AA426374 AI208775 AA977217 AA758055
		F34585 AA180062
30	430254 13102_1	9G700885 AA868017 AW341719 AA971332 AI688794 Z20462 AI808145 AW665263 AA884952 AA906136
	444467 1008400_1	AW663704 AI150368 AI216464
	436605 1008207_1	AI125340 AI125684 AI377949 AI125470 AI218351 AW665355 AI243952 AW663454 AI240603 AI187742 AA884214 AA723933
	427016 683123_1	AA857437 AI968733 AI968938 AA992784 AA397520 AW236244
	451807 17758_2	BM479185 AL552795 AL577722 BF038886 BM127617 BF510346 AW450652 AA865478 AW449519 BM127314 AI806539 AW449522 AA993634
		AI827626 AA904788

TABLE 54C

Key: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Key	Ref	Strand	Nt_position
401979	2828778	Minus	75893-75851,76977-77112
406409	9256364	Minus	141101-141256
401741	2982169	Plus	195686-196823,200241-200381
406378	9256142	Minus	125408-126800
405284	7329374	Plus	28556-28584
401692	3540172	Plus	26385-26510
403783	8081824	Plus	128412-128635
404271	9828129	Minus	56392-57645
401788	6730720	Plus	22831-23448
402857	9801539	Plus	13402-14133
405528	9531957	Minus	22418-22687
403328	8468086	Minus	120428-120703
401712	6682593	Minus	76410-76527,76692-76829,78737-78866,8024

60

TABLE 55A:

Key: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of non-seminomatous mixed germ cell testicular cancer compared to normal adult testicular tissues

Key	ExAccn	UnigenelD	Unigene Title	R1
416680	AW245540	Hs.79516	brain abundant, membrane attached signal	48.80
423961	D13668	Hs.196348	pericostin(OSF-2os)	43.30
412948	BE243313	Hs.334851	UIM and SH3 protein 1	42.60
428928	BE409838	Hs.194657	cadherin 1, type 1, E-cadherin (epithel)	36.80
424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	29.80
414438	AI879277	Hs.76136	thioredoxin	29.40
406658	AI920865	Hs.77961	major histocompatibility complex, class	29.25
446899	NM_005397	Hs.16426	podocalyxin-like	28.70
411573	AB029000	Hs.70823	KIAA1077 protein	28.40
432730	AI065520	Hs.131358	ESTs	28.00
418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	28.00
444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothel	27.90
446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	26.80
447526	AL048753	Hs.303549	small inducible cytokine A2 (monocyte ch	25.00
418174	L20688	Hs.83656	Rho GDP dissociation inhibitor (GDI) bet	24.15

5	406866	AW515336	Hs.29797	ribosomal protein L10	23.66
	414682	AL021154	Hs.76884	inhibitor of DNA binding 3, dominant neg	23.60
	440440	Z28925	Hs.7188	sema domain, immunoglobulin domain (Ig),	23.60
	417139	M69043	Hs.81328	nuclear factor of kappa light polypeptide	22.35
	417426	NM_002291	Hs.82124	laminin, beta 1	21.60
10	407862	BE548267	Hs.337986	Homo sapiens cDNA FLJ10934 fis, clone OV	21.55
	439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	21.50
	413767	AI352558		tyrosine 3-monooxygenase/tryptophan 5-mo	21.50
	406669	AI493591	Hs.78146	platelet/endothelial cell adhesion molec	20.90
	412636	NM_004415		desmoplakin (DPI, DPII)	20.90
15	414092	Z14244	Hs.75752	cytochrome c oxidase subunit VIb	20.30
	414587	NM_004862	Hs.76507	LPS-induced TNF-alpha factor	19.46
	412915	AW057727	Hs.74823	NM_004541:Homo sapiens NADH dehydrogenas	19.30
	406648	AA563730	Hs.277477	major histocompatibility complex, class	19.10
	412247	AF022375	Hs.73793	vascular endothelial growth factor	17.45
20	446108	AL036596	Hs.42322	A kinase (PRKA) anchor protein 2	17.40
	424800	AL035588	Hs.153203	MyoD family inhibitor	17.20
	413063	AL035737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	16.90
	415314	N88802	Hs.5422	glycoprotein M6B	16.80
	406666	M16714	Hs.89643	major histocompatibility complex, class	16.75
25	426286	AW367283		zinc finger protein 6 (CMPX1)	16.25
	406820	AI223958	Hs.108124	ribosomal protein S4, X-linked	16.00
	444562	AA186715	Hs.336429	RIKEN cDNA 9130422N19 gene	15.85
	417088	M54915	Hs.81170	plm-1 oncogene	15.60
	449338	H73444	Hs.394	adrenomedullin	15.61
30	444784	D12485	Hs.11951	ectonucleotide pyrophosphatase/phosphodi	15.33
	414420	AA043424	Hs.76095	immediate early response 3	15.30
	425543	R23313	Hs.334965	ribosomal protein L10a	15.10
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	15.00
	420754	W79431	Hs.346911	ribosomal protein L22	14.92
35	410397	AF217517	Hs.63042	DKFZp564J157 protein	14.86
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	14.70
	415899	X78992	Hs.78909	butyrate response factor 2 (EGF-response	14.60
	406786	AW161678	Hs.111334	femlin, tight polypeptide	14.57
	422105	AI929700	Hs.111660	endosulfina alpha	14.57
40	422714	AS018335	Hs.119387	KIAA0792 gene product	14.25
	444051	N48373	Hs.10247	activated leucocyte cell adhesion molecu	14.05
	426996	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	14.00
	445863	R12234	Hs.13396	Homo sapiens clone 25028 mRNA sequence	14.00
	429614	AI371172	Hs.211539	hypothetical protein MGC4248	13.95
45	410185	BE294068	Hs.737	immediate early protein	13.85
	409038	T97490	Hs.60002	small inducible cytokine subfamily A (Cy	13.60
	410611	AW954134	Hs.20924	KIAA1628 protein	13.60
	448588	AI970276	Hs.156905	KIAA1676	13.40
	421406	AF179897	Hs.104105	Meis (mouse) homolog 2	13.10
50	420962	NM_005804	Hs.100602	MAD (mothers against decapentaplegic, Dr	13.00
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	13.00
	452322	BE566343	Hs.28988	glutaredoxin (thioltransferase)	13.00
	454413	AI653672	Hs.40092	PNAS-123	12.90
	415221	W07418	Hs.78225	annexin A1	12.89
55	425535	AB007937	Hs.168287	KIAA0468 gene product	12.48
	450000	AI952797	Hs.10888	hypothetical protein FLJ21709	12.45
	418151	AA864238	Hs.83583	actin related protein 2/3 complex, subun	12.40
	414799	AI752416	Hs.77326	insulin-like growth factor binding prote	12.19
	412025	AI827451	Hs.24143	Wiskott-Aldrich syndrome protein Interac	12.12
60	445055	BE512856	Hs.109051	SH3 domain binding glutamic acid-rich pr	12.07
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	11.90
	408437	AW957744	Hs.278469	lacrimal proline rich protein	11.80
	430542	AI557486	Hs.119122	ribosomal protein L13a	11.51
	424670	W61215	Hs.116651	epithelial V-like antigen 1	11.50
65	432409	AA805638	Hs.130732	KIAA1575 protein	11.50
	425945	AW410669	Hs.164280	solute carrier family 25 (mitochondrial	11.44
	425996	W67330		hypothetical protein AL110115	11.40
	449981	AW265634	Hs.133100	ESTs	11.40
	435522	N84214	Hs.9774	synovial sarcoma translocation gene on c	11.25
70	407179	AA206465		thymosin, beta 4, X chromosome	11.21
	412823	R28898	Hs.74170	metallothionein 1E (functional)	11.10
	429978	AA249027		ribosomal protein S6	11.10
	450377	AB033091		KIAA1265 protein	11.10
	418609	AB028624	Hs.85539	ATP synthase, H transporting, mitochondr	11.10
75	440869	NM_014297	Hs.7486	protein expressed in thyroid	11.00
	417144	AA382104	Hs.81337	lectin, galactoside-binding, soluble, 9	11.00
	451106	BE382701	Hs.25960	N-MYC oncogene	10.93
	426552	BE297660	Hs.170328	moesin	10.91
	433423	BE407127	Hs.8997	heat shock 70kD protein 1A	10.90
80	442622	NM_000435	Hs.8546	Notch (Drosophila) homolog 3	10.80
	407951	W77762	Hs.79015	antigen identified by monoclonal antibod	10.80
	449944	AF290512	Hs.58215	Homo sapiens, Similar to rhodotin, clone	10.75
	423673	BE003064	Hs.1695	matrix metalloproteinase 12 (macrophage	10.70
	435056	AW023337	Hs.5422	glycoprotein M6B	10.70
	406743	AA911568	Hs.279860	tumor protein, translationally-controlled	10.70
	422627	BE336857	Hs.118787	transforming growth factor, beta-induced	10.65
	420676	AI434780	Hs.4248	vav 2 oncogene	10.60

	444060	AA340277		Homo sapiens cDNA FLJ20167 fis, clone CO	10.60
	420028	AB014680	Hs.8786	carbohydrate (N-acetylglucosamine-6-O) s	10.50
	436075	BE090176	Hs.179902	transporter-like protein	10.30
5	450139	AK001838		serum/glucocorticoid regulated kinase	10.30
	427691	AW194426	Hs.20726	ESTs	10.26
	424201	L33075	Hs.1742	HQ motif containing GTPase activating pr	10.15
	448412	AJ219083	Hs.42532	ESTs, Moderately similar to ALU8_HUMAN A	10.10
	440528	BE313555	Hs.7252	KIAA1224 protein	10.06
10	423184	NM_004428	Hs.1624	ephrin-A1	10.05
	450847	NM_003155	Hs.25590	stanniocalcin 1	9.90
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	9.90
	438876	AI124756	Hs.5337	isocitrate dehydrogenase 2 (NADP), mito	9.90
	421395	D80084	Hs.1023	pyruvate dehydrogenase (liponamide) alpha	9.89
15	435918	AF263538	Hs.86232	growth differentiation factor 3	9.89
	411251	R19774	Hs.22835	HHGP protein	9.80
	406791	AJ220684	Hs.347939	hemoglobin, alpha 2	9.75
	441187	AW195237	Hs.7734	hypothetical protein FLJ22174	9.75
	425580	L11144	Hs.1907	galanin	9.60
20	420225	AW243046	Hs.282076	Homo sapiens mRNA for KIAA1650 protein,	9.60
	413813	M98956	Hs.75561	larotocarcinoma-derived growth factor 1	9.60
	434280	BE005398		gb:CM1-BN0116-150400-189-002 BN0116 Homo	9.60
	417944	AJ077186	Hs.82985	collagen, type V, alpha 2	9.53
	409663	AA133590	Hs.250857	calcium/calmodulin-dependent protein kin	9.51
25	428864	AK001666	Hs.185095	similar to SALL1 (sal (Drosophila))-like	9.42
	416926	H03109	Hs.263395	HT018 protein	9.41
	456236	AF045229	Hs.82280	regulator of G-protein signalling 10	9.40
	428066	AI634046	Hs.157313	ESTs	9.40
	441455	AJ271671	Hs.7854	zinc/iron regulated transporter-like	9.39
30	410325	AB023154	Hs.62284	KIAA0937 protein	9.30
	415189	L34657	Hs.78146	platelet/endothelial cell adhesion molec	9.30
	454038	X06374	Hs.37040	platelet-derived growth factor alpha pol	9.29
	452568	AA805634	Hs.300870	Homo sapiens mRNA; cDNA DKFZp567M072 (tr	9.24
	447211	AL161981	Hs.17787	KIAA1554 protein	9.22
35	422068	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	9.20
	418299	AA279530	Hs.83968	Integrin, beta 2 (antigen CD18 (p85), ly	8.93
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	8.90
	429490	AI971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	8.90
	422241	Y00052	Hs.170121	protein tyrosine phosphatase, receptor t	8.90
40	449335	AW150717	Hs.345728	STAT Induced STAT inhibitor 1	8.84
	413806	AW958264	Hs.103832	similar to yeast Upt3, variant B	8.80
	447471	AF039843	Hs.18676	sprouty (Drosophila) homolog 2	8.70
	428215	AW963419	Hs.155223	stanniocalcin 2	8.70
	446827	AI973016	Hs.15725	hypothetical protein SBB48	8.60
45	431639	AK000680	Hs.266175	phosphoprotein associated with GEMs	8.60
	433412	AV653729	Hs.8185	CGI-44 protein; sulfide dehydrogenase li	8.60
	410023	AB017169	Hs.57929	sliT (Drosophila) homolog 3	8.50
	445245	AB032973	Hs.12461	LCHN protein	8.50
	448776	BE302454	Hs.30057	MRS2 (S. cerevisiae)-like, magnesium hom	8.40
50	453856	AA804789	Hs.19447	PDZ-LIM protein mystique	8.35
	410143	AA188169		KIAA1191 protein	8.35
	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	8.30
	433208	AW002834	Hs.24095	ESTs	8.30
	423753	Y11312	Hs.132463	phosphoinositide-3-kinase, class 2, beta	8.25
55	432559	AW452948	Hs.257031	ESTs	8.20
	450581	AF081513	Hs.25195	TGF-beta 4	8.10
	450157	AW961578	Hs.60178	ESTs	8.10
	444795	AI193356	Hs.160316	ESTs	8.10
	400288	X06258	Hs.149609	Integrin, alpha 5 (fibronectin receptor,	8.05
60	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	8.00
	420059	AF161486	Hs.94769	RAB23, member RAS oncogene family	8.00
	419970	AW612022		ESTs	8.00
	411975	AI916058	Hs.144583	ESTs	7.95
	446525	AW967069	Hs.211556	hypothetical protein MGC5487	7.90
65	451831	NM_001674	Hs.460	activating transcription factor 3	7.90
	437103	AW139408	Hs.152940	ESTs	7.90
	432636	AA340864	Hs.270562	claudin 7	7.87
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	7.84
70	418682	H13139	Hs.92282	paked-like homeodomain transcription fa	7.80
	407137	T97307		gb:53n05.s1 Soares fetal liver spleen	7.80
	450147	AW373713	Hs.146324	CGI-145 protein	7.75
	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	7.70
	449571	AW016812	Hs.200266	ESTs	7.70
	429355	AW973253	Hs.292689	ESTs	7.70
75	446488	AB037782	Hs.15119	KIAA1361 protein	7.70
	414774	X02419	Hs.77274	plasminogen activator, urokinase	7.69
	422424	AI186431	Hs.296638	prostate differentiation factor	7.67
	428818	AI131291	Hs.102308	potassium inwardly-rectifying channel, s	7.65
	416078	AL034349	Hs.79005	protein tyrosine phosphatase, receptor t	7.65
80	451812	X81889	Hs.152151	plakophilin 4	7.65
	410315	AI638871	Hs.17625	Homo sapiens cDNA: FLJ22524 fis, clone H	7.60
	452674	AK001061	Hs.30925	hypothetical protein FLJ10199	7.60
	422746	NM_004484	Hs.119651	glypican 3	7.60
	414020	NM_002884	Hs.75703	small inducible cytokine A4 (homologous	7.57

5	447874	BE270640	Hs.19192	cyclin-dependent kinase 2	7.57
	426889	BE245550	Hs.171825	basic helix-loop-helix domain containing	7.55
	444933	NM_018245	Hs.12150	retinal short-chain dehydrogenase/reduct	7.53
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	7.50
	425246	A085561	Hs.155321	serum response factor (c-fos serum respo	7.50
	419223	X60111	Hs.1244	CD9 antigen (p24)	7.47
	406776	T16206	Hs.237164	ESTs, Highly similar to LDHH_HUMAN L-LAC	7.44
	401466			vesicle-associated membrane protein 4	7.43
10	435080	A1831760	Hs.155111	hypothetical protein FLJ14428	7.40
	413686	A169213	Hs.71404	ESTs	7.40
	408805	AF025374	Hs.46465	T-cell, immune regulator 1	7.40
	408568	AW015759	Hs.235709	Homo sapiens mRNA; cDNA DKFZp667B0711 (f	7.30
	444838	AV551680	Hs.208558	ESTs	7.30
15	409208	Y00093		integrin, alpha X (antigen CD11C (p150),	7.28
	427820	BE222494	Hs.180919	inhibitor of DNA binding 2, dominant neg	7.20
	452924	AW580939	Hs.97199	complement component C1q receptor	7.15
	436398	H87136	Hs.5174	ribosomal protein S17	7.15
	443195	BE148235	Hs.193063	Homo sapiens cDNA FLJ14201 fis, clone NT	7.10
20	437442	T85104	Hs.222779	ESTs, Moderately similar to similar to N	7.10
	447735	AA775268	Hs.5127	Homo sapiens cDNA: FLJ23020 fis, clone L	7.10
	401192			Target Exon	7.08
	424503	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	7.08
	402474			NM_004079: Homo sapiens cathepsin S (CTSS	7.00
25	449567	A1990790	Hs.188614	ESTs	7.00
	448019	AW947164	Hs.195641	ESTs, Moderately similar to t38022 hypot	7.00
	450506	NM_004480	Hs.418	fibroblast activation protein, alpha	7.00
	430068	AA464564		gb:zx80f10.s1 Soares ovary tumor NbHOT H	7.00
30	431427	AK004001	Hs.252748	Homo sapiens cDNA FLJ20394 fis, clone KA	6.90
	426440	BE382756	Hs.169902	solute carrier family 2 (facilitated glu	6.87
	442492	AA528489	Hs.234518	ribosomal protein L23	6.84
	417365	D50883	Hs.82028	transforming growth factor, beta recepto	6.80
	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-lin	6.80
	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	6.80
35	436684	NM_001290	Hs.4980	LIM domain binding 2	6.80
	442685	AB033017	Hs.8594	KIAA1191 protein	6.79
	413542	BE295928	Hs.75424	inhibitor of DNA binding 1, dominant neg	6.77
	411789	AF245505	Hs.72157	Adipon	6.76
	441665	AW563575	Hs.303125	p53-induced protein PIGPC1	6.75
40	440268	BE270030	Hs.338959	Homo sapiens, clone IMAGE:3677185, mRNA	6.74
	444207	A1565004		cathepsin D (lysosomal aspartyl) protease	6.72
	408912	AB011084	Hs.48924	KIAA0512 gene product: ALEX2	6.70
	429600	X78565	Hs.289114	hexabrachion (tenascin C, cytotoxicin)	6.70
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	6.70
45	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	6.70
	430332	R51790	Hs.239483	Human clone 23933 mRNA sequence	6.70
	413497	BE177661		gb:RC1-HT0598-020300-011-h02 HT0598 Homo	6.70
	433271	BE621697	Hs.14317	nucleolar protein family A, member 3 (H/	6.66
	443351	AW016783	Hs.30799	Homo sapiens cDNA FLJ13471 fis, clone PL	6.65
50	406858	A1865720	Hs.29797	ribosomal protein L10	6.65
	435748	AA689756	Hs.117335	ESTs	6.63
	423024	AA593731	Hs.325823	ESTs, Moderately similar to ALU5_HUMAN A	6.62
	422451	AA310753	Hs.42491	ESTs, Weakly similar to S65857 alpha-1C-	6.62
	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	6.61
55	434584	D57341	Hs.188361	Homo sapiens cDNA FLJ12607 fis, clone NT	6.60
	442379	NM_004613	Hs.8285	transglutaminase 2 (C polypeptide, prote	6.55
	424528	AW073971	Hs.238954	ESTs, Weakly similar to KIAA1204 protein	6.50
	450294	H42587	Hs.238730	hypothetical protein MGC10823	6.45
	417336	R70429	Hs.81988	disabled (Drosophila) homolog 2 (mitogen	6.45
60	418707	U97502	Hs.67497	butyrophilin, subfamily 3, member A2	6.43
	402145			Target Exon	6.43
	414662	AL036058	Hs.76807	major histocompatibility complex, class	6.42
	436860	H12751	Hs.5327	PRO1914 protein	6.40
	438962	BE046694		gb:hn41c11.x1 NCL CGAP_RDF2 Homo sapiens	6.40
65	435837	AA830893	Hs.119769	ESTs	6.40
	412645	AW444433	Hs.136061	Homo sapiens, Similar to hypothetical pr	6.40
	446173	BE565849	Hs.14158	copine III	6.39
	425875	AU077333	Hs.160483	erythrocyte membrane protein band 7.2 (s	6.36
	412093	BE242691	Hs.14947	ESTs	6.34
70	446921	AB012113	Hs.16530	small inducible cytokine subfamily A (Cy	6.30
	443523	AK001575	Hs.9536	hypothetical protein FLJ10713	6.30
	428311	NM_005651	Hs.183671	tryptophan 2,3-dioxygenase	6.30
	447519	U46258	Hs.339665	ESTs	6.30
	445817	NM_003642	Hs.13340	histone acetyltransferase 1	6.30
75	434423	NM_006769	Hs.3844	LIM domain only 4	6.30
	434524	AA635931	Hs.249716	ESTs	6.30
	441970	AW959918	Hs.73737	ESTs	6.30
	433675	AW977653	Hs.75319	ribonucleotide reductase M2 polypeptide	6.30
	437374	AL359571	Hs.44054	nuclein (GSK3B interacting protein)	6.25
80	437134	AA349844	Hs.42915	ARP2 (actin-related protein 2, yeast) ho	6.23
	407284	A1539227	Hs.214039	hypothetical protein FLJ23566	6.20
	426158	NM_001982	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	6.20
	447029	AL137281	Hs.17110	Homo sapiens mRNA; cDNA DKFZp434C2016 (f	6.20
	417315	AL080042	Hs.180450	ribosomal protein S24	6.20

	418840	AI821614	Hs.185831	ESTs	6.20
	410668	BE379794	Hs.159651	hypothetical protein	6.16
	425762	BE244076	Hs.159578	AT-hook transcription factor AKNA	6.13
5	413840	AI301558		RNA binding motif protein, X chromosome	6.13
	409493	AA386192	Hs.193482	Homo sapiens cDNA FLJ11903 fis, clone HE	6.12
	450944	AA554989		sudD (suppressor of bimD6, Aspergillus n	6.10
	415825	Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3-kinase B	6.10
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	6.10
10	429109	AL008637	Hs.196352	neutrophil cytosolic factor 4 (40kD)	6.10
	418460	M26315	Hs.85258	CD8 antigen, alpha polypeptide (p32)	6.10
	408996	AI979168	Hs.344096	glycoprotein (transmembrane) nmb	6.10
	432666	AW204069		ESTs, Weakly similar to unnamed protein	6.09
	435812	AA700439	Hs.188490	ESTs	6.06
15	432805	X94630	Hs.3107	CD97 antigen	6.06
	441283	AA927570	Hs.131704	ESTs	6.06
	417632	R20865	Hs.5422	glycoprotein M6B	6.00
	435905	AW997484	Hs.5003	KIAA0456 protein	6.00
	425593	AA278921	Hs.1908	proteoglycan 1, secretory granule	5.99
20	429083	Y09397	Hs.227817	BCL2-related protein A1	5.95
	410698	AI817130	Hs.9195	Homo sapiens cDNA FLJ13698 fis, clone PL	5.95
	425291	AA354572		gb:EST62857 Jurkat T-cells V Homo sapien	5.95
	449971	AA807346	Hs.288581	Homo sapiens cDNA FLJ14296 fis, clone PL	5.93
	451052	AA281504	Hs.24444	Homo sapiens cDNA: FLJ22165 fis, clone H	5.90
25	447217	BE465754	Hs.17778	neuropilin 2	5.90
	417228	AL134324	Hs.7312	ESTs	5.86
	443963	AA878183	Hs.17448	Homo sapiens cDNA FLJ13618 fis, clone PL	5.86
	452382	N38902	Hs.211539	hypothetical protein MGC4248	5.84
	427747	AW411425	Hs.180555	serine/threonine kinase 12	5.84
30	414483	R25513	Hs.10683	ESTs	5.82
	428570	AA430321	Hs.293945	ESTs	5.81
	443194	AI954968		matrix Gla protein	5.80
	429582	AI569058	Hs.22247	ESTs	5.80
	414405	AI362533		KIAA0306 protein	5.80
35	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	5.80
	437739	AW579216	Hs.264610	ESTs, Moderately similar to lbd1 (H.sapi	5.80
	417018	M16038	Hs.80887	v-yes-1 Yamaguchi sarcoma viral related	5.80
	442821	BE391929	Hs.8752	transmembrane protein 4	5.77
	434511	R28982	Hs.18106	ESTs	5.76
40	408745	AW511970	Hs.279860	tumor protein, translationally-controlled	5.70
	453187	AI161383	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	5.70
	453115	AW772041	Hs.18439	ESTs, Moderately similar to JC5238 galac	5.70
	406857	AA613726	Hs.29797	ribosomal protein L10	5.69
	418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	5.63
45	444273	AI903474	Hs.230	fibromodulin	5.65
	441623	AA316805		desmoglein 2	5.63
	418300	AI433074	Hs.86682	Homo sapiens cDNA: FLJ21578 fis, clone G	5.63
	440099	AL080058	Hs.6909	DKFZP564G202 protein	5.60
50	434096	AW862958	Hs.75825	pleomorphic adenoma gene-like 1	5.60
	417621	AV654694	Hs.82316	Interferon-induced, hepatitis C-associat	5.60
	422610	AF153820	Hs.1547	potassium inwardly-rectifying channel, s	5.60
	438278	BE408248	Hs.57988	hypothetical protein FLJ22357 similar to	5.58
	430451	AA836472	Hs.297939	cathepsin B	5.57
55	406699	L08505	Hs.182979	ribosomal protein L12	5.53
	458965	AA010319	Hs.60389	ESTs	5.50
	430592	AJ224864	Hs.9688	leukocyte membrane antigen(LRC1)	5.50
	433655	AL036559	Hs.3463	ribosomal protein S23	5.50
	428471	X57348	Hs.184510	stratfin	5.42
60	408822	AW500715	Hs.57079	Homo sapiens cDNA FLJ13267 fis, clone OV	5.40
	417849	AW291587	Hs.82733	nidogen 2	5.40
	408969	AW361666	Hs.49500	KIAA0746 protein	5.40
	428467	AK002121	Hs.184465	hypothetical protein FLJ11259	5.40
	439971	W32474	Hs.301748	RAP2A, member of RAS oncogene family	5.40
	449924	W30681	Hs.146233	Homo sapiens cDNA: FLJ22130 fis, clone H	5.40
65	406819	AA908472		gbcxg82a10.s1 NCL_CGAP_Cv8 Homo sapiens	5.39
	416655	AW988813	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	5.36
	451589	AA424791	Hs.5734	meningioma expressed antigen 5 (hyaluron	5.34
	409327	L41162	Hs.53563	collagen, type IX, alpha 3	5.34
	427968	AI857607	Hs.181301	cathepsin S	5.32
70	428307	AU076592	Hs.198951	jun B proto-oncogene	5.30
	424950	AA602917	Hs.156974	ESTs	5.30
	410619	BE512730	Hs.65114	keratin 18	5.30
	424408	AI754813	Hs.146429	collagen, type V, alpha 1	6.27
	425430	BE185921	Hs.98073	ESTs, Moderately similar to Z195_HUMAN Z	5.27
75	411165	NM_000169	Hs.59089	galactosidase, alpha	5.26
	406701	AA780613	Hs.62954	ferritin, heavy polypeptide 1	5.26
	435531	BE254088	Hs.29647	uncharacterized hematopoietic stem/proge	5.24
	418905	BE539574		actinin, alpha 4	5.23
	449303	AK001495	Hs.23467	hypothetical protein FLJ10633	5.22
80	440703	AL137663	Hs.7378	Homo sapiens mRNA; cDNA DKFZp434G227 (fr	5.20
	430314	AA369801	Hs.239138	pre-B-cell colony-enhancing factor	5.20
	444930	BE185536	Hs.301183	molecule possessing ankyrin repeats indu	5.20
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	5.20
	407254	AW129401	Hs.181165	eukaryotic translation elongation factor	5.20

	409604	AW444448	Hs.49124	ESTs	5.20
	432581	AU076465	Hs.278441	KIAA0015 gene product	5.16
	430556	AW967807	Hs.13797	ESTs	5.16
5	431315	AW972227	Hs.163986	Homo sapiens cDNA: FLJ22765 fis, clone K	5.16
	425190	AW028302	Hs.155079	protein phosphatase 2, regulatory subunit	5.15
	454227	AW963697	Hs.44743	KIAA1435 protein	5.15
	429357	AB007867	Hs.278311	plexin B1	5.12
	452191	AU076408	Hs.28309	UDP-glucose dehydrogenase	5.11
10	419073	AW372170	Hs.183918	Homo sapiens cDNA FLJ12797 fis, clone NT	5.11
	442295	AJ827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	5.10
	443030	R68048	Hs.9238	hypothetical protein FLJ23518	5.10
	421878	AA299652	Hs.111495	Homo sapiens cDNA FLJ11643 fis, clone HE	5.10
	424875	AJ87945	Hs.199310	ESTs	5.10
15	427641	AJ270591	Hs.146116	ESTs	5.10
	442806	AW294522	Hs.149991	ESTs	5.10
	442495	AJ184717		ESTs	5.10
	439941	AJ392640	Hs.18272	amino acid transporter system A1	5.10
	444981	AW855398	Hs.12210	hypothetical protein FLJ13732 similar to	5.09
20	452472	AW957300	Hs.294142	ESTs, Weakly similar to C55663 oligodend	5.07
	418117	AJ922013	Hs.83496	linker for activation of T cells	5.06
	431824	AW972842		gb:EST384937 MAGE msequences, MAGL Homo	5.06
	417558	AF045229	Hs.82280	regulator of G-protein signalling 10	5.06
	410570	AJ133086	Hs.64593	ATP synthase, H transporting, mitochondr	5.03
25	431805	NM_014053	Hs.270594	FLVCR protein	5.00
	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	5.00
	428494	AA234339	Hs.184634	hypothetical protein FLJ20005	5.00
	419641	BE170548	Hs.118190	Homo sapiens cDNA: FLJ21081 fis, clone C	5.00
	443834	H73972	Hs.134460	ESTs	5.00
30	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	5.00
	444621	AA298065	Hs.11465	glutathione-S-transferase like; glutathi	4.97
	422200	AA080895	Hs.347969	cytochrome c oxidase subunit IV	4.95
	416003	X98001	Hs.78948	Rab geranylgeranyltransferase, beta subu	4.94
	425428	AL110261	Hs.157211	DKFZP586B0621 protein	4.94
35	452063	R53185	Hs.32366	ESTs, Weakly similar to TWIST_HUMAN TWIST	4.93
	414821	M63835	Hs.77424	Fc fragment of IgG, high affinity Ia, re	4.93
	429558	AJ391454	Hs.207251	nucleolar autoantigen (55kD) similar to	4.92
	432588	X92715	Hs.3057	zinc finger protein 74 (Cof52)	4.92
	433162	AJ025842		ESTs	4.92
40	406797	AJ432224		ribosomal protein L6	4.91
	412347	AW970026	Hs.73818	ubiquinol-cytochrome c reductase hinge p	4.90
	422392	NM_005908	Hs.115945	mannosidase, beta A, lysosomal	4.90
	447197	R36075		gb:zh88601.s1 Soares placenta Nb2HP Homo	4.90
	447832	AJ433357		ESTs	4.90
45	420932	AW374605	Hs.11607	ESTs, Weakly similar to T21697 hypotheti	4.90
	413593	AA206248		gb:zq78c12.r1 Stratagene hNT neuron (937	4.90
	451658	AW195351	Hs.250520	ESTs, Moderately similar to I38022 hypot	4.90
	441224	AU076964	Hs.7753	calumenin	4.90
	408067	BE244580	Hs.342307	hypothetical protein FLJ10330	4.90
50	424871	AA479005	Hs.154036	tumor suppressing subtransferable candid	4.90
	417308	H60720	Hs.81892	KIAA0101 gene product	4.90
	438763	AJ583207	Hs.99029	CCAAAT/enhancer binding protein (C/EBP),	4.89
	418113	AJ272141	Hs.83484	SRY (sex determining region Y)-box 4	4.89
	414191	AW250089	Hs.75807	PDZ and LIM domain 1 (alfin)	4.88
55	421748	NM_014718	Hs.107809	KIAA0726 gene product	4.87
	427486	AA974433		fibroblast growth factor 4 (heparin secr	4.86
	424263	M77640	Hs.1757	L1 cell adhesion molecule (hydrocephalus	4.82
	409867	AA157857	Hs.182265	keratin 19	4.81
60	449378	AW664026	Hs.59892	ESTs	4.81
	427202	BE272922	Hs.173936	Interleukin 10 receptor, beta	4.80
	418945	BE246762	Hs.89499	arachidonate 5-lipoxygenase	4.80
	448906	AW372914	Hs.86149	phosphoinositide 3-phosphate-binding prot	4.80
	426711	AA383471	Hs.343800	conserved gene amplified in osteosarcoma	4.80
	433681	AJ004377	Hs.200360	Homo sapiens cDNA FLJ13027 fis, clone NT	4.79
65	441321	H17182	Hs.7771	B-cell associated protein	4.75
	448896	AL157484	Hs.22483	Homo sapiens mRNA; cDNA DKFZp762M127 (fr	4.75
	447232	AW499834	Hs.327	Interleukin 10 receptor, alpha	4.73
	449317	AW293413	Hs.132906	19A24 protein	4.73
	436372	AW972301	Hs.310266	ESTs	4.71
70	422082	AA016188	Hs.111244	hypothetical protein	4.70
	432465	D56165	Hs.275163	non-metastatic cells 2, protein (NM23B)	4.70
	417924	AU077231	Hs.82932	cyclin D1 (PRAD1; parathyroid adenomas	4.70
	446659	AJ353361	Hs.226376	ESTs	4.70
	414829	AA321668	Hs.77436	pleckstrin	4.70
75	418036	Z37976	Hs.83337	latent transforming growth factor beta b	4.70
	417677	NM_016055	Hs.82389	CGI-118 protein	4.70
	443559	AJ076765	Hs.269899	ESTs, Moderately similar to ALU8_HUMAN A	4.70
	423766	AA303799	Hs.300141	ribosomal protein L39	4.70
	432407	AA221036	Hs.13273	gb:z03f12.r1 Stratagene NT2 neuronal pr	4.69
80	453485	BE620712	Hs.33026	hypothetical protein PP2447	4.67
	452973	H88409	Hs.40527	ESTs	4.67
	427816	AA159248	Hs.180909	peroxiredoxin 1	4.67
	406794	AJ890243		ribosomal protein L6	4.66
	449475	AJ348027	Hs.108557	hypothetical protein PP1057	4.65

	427157	U51166	Hs.173824	thymine-DNA glycosylase	4.64
	425410	AA310974	Hs.156828	Homo sapiens cDNA FLJ10522 fis, clone NT	4.62
	407874	AI766311	Hs.289047	Homo sapiens cDNA FLJ14059 fis, clone HE	4.61
5	417535	AA203669	Hs.191482	ESTs	4.61
	421818	AW992976	Hs.50098	NM_002469:Homo sapiens NADH dehydrogenas	4.61
	408491	AI088063	Hs.7682	ESTs	4.60
	426398	AI249368	Hs.98558	ESTs	4.60
	410295	AA741357		ndogen (enactin)	4.60
10	407198	H91679		gb:U04a07.s1 Soares fetal liver spleen	4.60
	440327	R12581	Hs.191146	ESTs	4.60
	417353	AA375752	Hs.348140	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	4.60
	426141	C05686	Hs.293972	ESTs	4.60
	412922	M60721	Hs.74870	H2.0 (Drosophila)-like homeo box 1	4.59
15	434449	AW953484	Hs.3849	hypothetical protein FLJ22041 similar to	4.58
	416987	D86957	Hs.80712	KIAA0202 protein	4.57
	418863	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	4.57
	416581	H66276	Hs.108288	ESTs	4.56
	440983	M20681	Hs.7594	solute carrier family 2 (facilitated glu	4.56
20	450988	BE618571	Hs.429	ATP synthase, H transporting, mitochondr	4.56
	413663	BE247585	Hs.75462	BTG family, member 2	4.55
	410342	R31350	Hs.743	Fc fragment of IgE, high affinity 1, rec	4.54
	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kn	4.53
	453330	AI268081	Hs.342389	peptidylprolyl isomerase A (cyclophilin	4.52
25	417750	AI267720	Hs.260523	synovial sarcoma, translocated to X chro	4.51
	440774	AI420611	Hs.153934	ESTs	4.51
	422693	BE300073	Hs.279860	tumor protein, translationally-controlle	4.51
	411125	AA151647	Hs.68877	cytochrome b-245, alpha polypeptide	4.51
	449267	AI638640	Hs.220624	ESTs	4.51
30	432605	NM_002104	Hs.3065	granzyme K (serine protease, granzyme 3;	4.50
	432706	NM_013230	Hs.286124	CD24 antigen (small cell lung carcinoma	4.50
	436823	AW748865	Hs.117077	ESTs, Weakly similar to I38022 hypotheti	4.50
	437469	AW753112	Hs.15514	hypothetical protein MGC3260	4.50
	413703	BE158360		gb:PM1-HT0383-131299-001-h08 HT0383 Homo	4.50
35	415526	N76535	Hs.265591	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.50
	406623	X69392	Hs.91379	ribosomal protein L26	4.49
	456642	AW451623	Hs.109752	putative c-Myc-responsive	4.47
	406653	AA574074	Hs.77981	major histocompatibility complex, class	4.47
	408307	AI761786	Hs.204674	ESTs	4.46
40	428297	AA236291	Hs.183583	serine (or cysteine) proteinase inhibito	4.46
	447296	AW243614	Hs.18063	Homo sapiens cDNA FLJ10768 fis, clone NT	4.45
	416801	X98834	Hs.79971	sal (Drosophila)-like 2	4.45
	406870	AA075144		gb:zm96f06.s1 Stratagene ovarian cancer	4.45
	446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	4.44
45	416297	AA157834	Hs.79172	solute carrier family 25 (mitochondrial	4.44
	428773	BE256238	Hs.193163	bridging integrator 1	4.43
	427640	AF058293	Hs.180015	D-dopachrome tautomerase	4.43
	437223	C15105	Hs.330716	Homo sapiens cDNA FLJ14368 fis, clone HE	4.43
	412265	AA101325	Hs.88154	hypothetical protein FLJ12457	4.43
50	442232	AI357813	Hs.337460	ESTs, Weakly similar to A47582 B-cell gr	4.42
	441612	AI802629	Hs.113660	Homo sapiens cDNA FLJ11631 fis, clone HE	4.41
	424858	AI568170	Hs.96886	ESTs	4.41
	408380	AF123050	Hs.44532	diubiquitin	4.40
	411960	R77776	Hs.18103	ESTs	4.40
55	428782	X12830	Hs.193400	Interleukin 8 receptor	4.40
	408380	AI806090	Hs.44344	hypothetical protein FLJ20534	4.40
	456629	AW691985		histone deacetylase 3	4.40
	414416	AW409985	Hs.76084	hypothetical protein MGC2721	4.40
	422499	AI268666	Hs.19631	ESTs, Weakly similar to I38022 hypotheti	4.39
60	414219	W20010	Hs.75823	ALL1-fused gene from chromosome 1q	4.39
	427779	AA905997	Hs.180780	TERA protein	4.38
	422340	AW296219	Hs.115325	RAB7, member RAS oncogene family-like 1	4.37
	413276	Z24725	Hs.75280	mitogen inducible 2	4.36
	452651	AI218918	Hs.30200	KIAA0654 protein	4.35
65	453467	AI535997	Hs.30089	ESTs	4.35
	435981	BE293127	Hs.283722	GTT1 protein	4.35
	415691	AW963978	Hs.24723	ESTs	4.34
	435958	AW161481	Hs.111577	Integral membrane protein 3	4.34
	420099	D80011	Hs.95140	KIAA0189 gene product	4.33
70	412522	R48881	Hs.102991	hypothetical protein FLJ13958	4.33
	457073	AA233210	Hs.179943	ribosomal protein L11	4.31
	427337	Z46223	Hs.176663	Fc fragment of IgG, low affinity IIb, r	4.31
	420732	AA789133	Hs.63525	ESTs	4.30
	432731	R31178	Hs.287820	fibronectin 1	4.30
75	437275	AW976035	Hs.282395	ESTs, Weakly similar to A47582 B-cell gr	4.30
	408784	AW971350	Hs.63386	ESTs	4.30
	441982	AW972542	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone H	4.30
	418926	AW900992	Hs.93796	DKFZP586D2223 protein	4.30
	429058	AF138863	Hs.35254	hypothetical protein FLB6421	4.30
80	434963	AW974957	Hs.288719	Homo sapiens cDNA FLJ12142 fis, clone MA	4.30
	413677	AW503116	Hs.301819	zinc finger protein 146	4.29
	428970	BE276891	Hs.194691	retinoic acid induced 3	4.28
	406896	AI610447	Hs.48778	nban protein	4.26
	433550	AA989061	Hs.177376	ESTs	4.26

	406230		Target Exon	4.25
	435555	AW105663	Hs.6947 HSPC069 protein	4.25
	448717	R67419	Hs.21851 Homo sapiens cDNA FLJ12900 fis, clone NT	4.24
5	437386	W52452	ribosomal protein L10	4.24
	416759	AK000978	Hs.79741 hypothetical protein FLJ10116	4.23
	447341	AF106941	Hs.18142 arestin, beta 2	4.22
	410423	AW402432	Hs.63489 protein tyrosine phosphatase, non-recept	4.22
	409453	AI885516	Hs.95612 ESTs	4.22
10	428463	ABD11110	Hs.184367 GTPase activating protein-like	4.22
	444681	AJ243937	Hs.288316 chromosome 6 open reading frame 9	4.21
	416072	AL110370	Hs.79000 growth associated protein 43	4.20
	450937	R49131	Hs.26267 ATP-dependant Interferon response protei	4.20
	447595	AW379130	Hs.18953 phosphodiesterase 9A	4.20
15	418452	BE379749	Hs.85201 C-type (calcium dependent, carbohydrate-	4.20
	430594	AK000790	Hs.246885 hypothetical protein FLJ20783	4.20
	425259	ALD49280	Hs.155397 Homo sapiens mRNA; cDNA DKFZp566K143 (fr	4.20
	431560	BE244135	Hs.260238 hypothetical protein FLJ10842	4.20
	439403	BE265745	ESTs, Weakly similar to ALUC_HUMAN [H]	4.20
20	409245	AA361037	ESTs, Weakly similar to ALUC_HUMAN [H]	4.18
	437296	AA350994	Hs.20281 tRNA isopentenylpyrophosphate transferas	4.17
	406877	AA226392	Hs.179943 KIAA1700	4.17
	419552	AL157485	Hs.91973 ribosomal protein L11	4.17
	406661	X66975	Hs.172550 hypothetical protein	4.15
25	452432	AW206008	Hs.283378 polypyrimidine tract binding protein (he	4.15
	448782	AL050295	Hs.283378 Homo sapiens cDNA: FLJ21778 fis, clone H	4.14
	407110	AA018042	Hs.252085 KIAA0758 protein	4.14
	422960	AW890487	Hs.252085 Prader-Willi/Angelman syndrome-5	4.14
	432841	M83425	Hs.62 cadherin 13, H-cadherin (heart)	4.13
30	415657	AA856115	Hs.127797 protein tyrosine phosphatase, non-recept	4.12
	420298	AI199510	Hs.267912 Homo sapiens cDNA FLJ11381 fis, clone HE	4.11
	419726	U50330	Hs.1274 ESTs, Weakly similar to ALU7_HUMAN ALU S	4.11
	426075	AW513691	Hs.270149 bone morphogenetic protein 1	4.11
	430255	AK000703	Hs.323822 ESTs, Weakly similar to 2109260A B cell	4.10
35	418699	BE539639	Hs.173030 Homo sapiens mRNA for KIAA1551 protein,	4.10
	443035	Z45822	Hs.8906 ESTs, Weakly similar to ALU8_HUMAN ALU S	4.10
	457415	AK000010	Hs.258798 Homo sapiens clone 24889 mRNA sequence	4.10
	412220	BE350058	Hs.36787 hypothetical protein FLJ20003	4.10
	427509	M82505	Hs.2161 chromodomain helicase DNA binding protei	4.10
40	444633	AF111713	Hs.286218 complement component 5 receptor 1 (C5a1	4.10
	441384	AA447849	Hs.286680 junctional adhesion molecule 1	4.10
	431958	X63629	Hs.2877 Homo sapiens cDNA: FLJ22182 fis, clone H	4.09
	422310	AA318822	Hs.98370 cadherin 3, type 1, P-cadherin (placenta	4.09
	439815	AA206079	Hs.6693 cytochrome P450, subfamily IIS, polypept	4.08
45	417930	H81136	Hs.334604 hypothetical protein FLJ20420	4.07
	418458	AA332941	Hs.85226 Homo sapiens mRNA for KIAA1870 protein,	4.06
	424484	R68537	Hs.47982 lipase A, lysosomal acid, cholesterol es	4.06
	417035	AA192455	Hs.22988 ESTs	4.06
	412627	BE391959	Hs.74276 Homo sapiens clone IMAGE:451939, mRNA se	4.06
50	414890	BE281095	Hs.77573 chloride intracellular channel 1	4.06
	452248	AA093668	Hs.28578 uridine phosphorylase	4.05
	450687	AA011518	Hs.271778 muscleblind (Drosophila)-like	4.05
	444224	AV648599	Hs.199438 ESTs, Weakly similar to I36022 hypotreti	4.05
	451351	AW056261	Hs.321435 ESTs	4.05
55	407792	AI077715	Hs.39384 ESTs, Weakly similar to ALU1_HUMAN ALU S	4.04
	439864	AI720078	Hs.291997 putative secreted ligand homologous to f	4.04
	408745	AW936356	Hs.300925 ESTs, Weakly similar to A475B2 B-cell gr	4.04
	409132	AJ224538	Hs.50732 ESTs, Weakly similar to A46010 X-linked	4.03
	410597	W16518	Hs.279518 protein kinase, AMP-activated, beta 2 no	4.01
60	409485	S80990	Hs.252136 amyloid beta (A4) precursor-like protein	4.01
	426398	BE266390	Hs.169718 ficolin (collagen/fibrinogen domain-cont	4.01
	417777	AJ823763	Hs.7065 calponin 2	4.01
	446979	AI654443	Hs.197683 ESTs, Weakly similar to I78885 sarineth	4.01
	418000	R82342	Hs.79856 ESTs	4.00
65	426547	AA243464	Hs.294101 ESTs, Weakly similar to S65657 alpha-1C-	4.00
	436394	AA531187	Hs.126705 pre-B-cell leukemia transcription factor	4.00
	409956	AW103364	Hs.727 ESTs	4.00
	414602	AW630088	Hs.78550 Inhibin, beta A (activin A, activin AB a	4.00
	446013	AJ360167	Hs.152774 Homo sapiens mRNA; cDNA DKFZp564B1264 (f	4.00
70	452404	AW450675	Hs.212709 ESTs	4.00
	444736	AA533491	Hs.23317 ESTs	4.00
	438590	AA811465	Hs.123375 hypothetical protein FLJ14681	4.00
	451838	AW005856	Hs.193969 ESTs	4.00
	449832	AA694264	Hs.60049 ESTs	4.00

TABLE 55B

Key: Unique Eos probaset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Key CAT Number Accession

413787	7612_1	BC003047 S80794 NM_003405 X78138 AY007132 L08439 AW340648 AW131665 A1062748 A1470204 B1711078 BF350700 B1496963 A1087141 AA720684 AA862331 AA605146 BM313650 A1089749 A1359738 N69107 AW995424 A1086917 A1063995 AW340217 N99662 A1829449 A1089839 A1608761 A1342365 A1199076 AA908944 A1248943 A1160053 A1191245 A1218477 A1077943 AA864930 A1310394 AA872977 A1279782 W61343 AA565955 W46596 AA126874 AA223241 AA491574 R48413 AA491520 B0505114 A1465689 BE464590 AW664539 H67049 A1534332 C21397 A1085941 AW028427 BG939820 A1697089 A1039008 A125315 A1655561 AW150042 L20422 X57345 B1458375 A1142852 B1666601 BE888276 A1119302 B1603754 BG705953 B1598754 BE296713 BG002538 BF951911 N29226 BE909424 AV698274 AV683116 AV708195 AA127790 A124697 D54224 F08031 AA340253 BF923383 BM467808 B1546644 BG777200 BG705941 BG468577 A10127209 AW403970 B1597630 B1458091 AV689560 B1693267 BG506219 B1837163 B1667275 AA343750 BE783112 BF671405 BF954720 H67636 H69456 AA484894 B1699271 BF998207 N15147 BF945817 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BG949393 BE714441 AW996245 BE711801 A1294090 BE064323 BE719390 BE940148 BG991212 BF375714 BF349522 BG986267 T48793 B1013292 BE001925 AW365156 AW365154 AW605653 BF763109 BE931637 BE713879 BF354008 BF678726 H90899 AW365145 W36382 A1984847 BE880923 BG390191 AW470082 AW014585 A1423255 B1714731 BG054694 AW780248 N31683 AW664132 AW467353 A1583152 AA617918 BF447795 A1088367 AA807328 AW576970 A1741153 A1755003 A1474016 A1422030 A1348114 AW997085 BM271753 A1363147 BM311311 A1146640 A1246771 AW512619 A1359020 BG054897 A1292234 A1215830 A1283836 C06205 AW503423 AW272880 N33205 AW873021 AA070724 A1753886 AW192487 A1087151 AA658909 A1348308 A1335577 AA825442 AW440066 AW131357 AW513210 A1082314 A1085455 BE551404 AA780704 AW008596 A1795954 AA917471 A100531 AA668626 N272207 A1306482 AW440562 A1084687 AA347280 AA053536 BF471739 A1241682 AA931543 AA484310 AA812486 A1032216 AA685779 A1916338 A1350590 BF198106 A133377 A1300638 BF872828 A1282741 A1351487 AW105544 AA973627 AW517914 AA715424 AA508454 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BE940512 BE940608 H28028 BF913868 AI301558 D79095 AI762695 AA311547 AI673002 N67358 AA885913 AI288084 N67347 Z40311 T94918 AW1722693 AW170339 AW975566 AA452774 AA504759 AA370643 T79706 AA721503 BF658887 BG829217 AI343373 AW236167 BE568091 BF747959 BF241262 BE940663 AA35278 R05794 AW027091 AI660259 AI268890 T94871 AW162884 N67183 AW149083 H42473 AI678254 R26706 AI419684 R24905 AW386558 AW363261 N31299 H63489 AW195475 AA452592 BE844216 T91205 H64955 BF858811 AW962778 AW388295 BF857615 BF856552 BF856548 BF857611 AW886752 BG626557 AW965540 R76280 AA335845 BF370246 BE835794 AA725102 AW152576 BF065494 AI743398 BE464853 AI391675 AI453078 BE017670 AI803141 AI417070 AA489486 BE836818 AW050475 BE835628 AI015220 AW300496 AA343881 H98062 AA554989 N32774 AA012825 BF989549 AI576463 W80527 AW576215 N32300 AA50065 AW137525 AI290944 T16431 T50379 AA830657 N78847 T51070 AW505288 AI46370 AA100986 AA824552 BE835780 AA770859 BF370223 H03890 R76557 AA558585 AA565499 AI360576 AW204069 AA991648 AA864939 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AI336371 AI989381 AI131425 AI147483 AI311537 AW338638 AI141649 AA709414 AI187177 AA780884 AI333805 AA045312 AI623918 AI349421
 W63763 W70299 AA557276 AA299007 N98212 W74064 N24823 T64892 AA054724 W73059 AI869152 N93462 N71889 AI537432 R71628
 AA303089 AI498550 T60941 AV706417 AW067848 AI150577 AW338118 AI336313 AA826256 AI139518 AA662948 AA902723 AI970175 W68682
 AI089380 AI148372 H99951 AW183001 AI270317 AA532767 AA044727 AA931652 R82469 AA150261 W67788 H67495 R80715 AW149812 N78914
 AI862034 W61122 AW023118 W69375 T88917 T47984 N21531 R35646 AA055544 H15534 AA668295 AA090586 AA044764 BF994641 R79547
 N21313 BF674610 H02874 AW975323 R16904 AA328030 AA054671 R79546 BF832310 AI249109
 BG015794 BE158357 BE158353 BE158358 BE158360 BE158352 BE158351 BE158355
 AA075144
 AW891955 AW604749 BE080572 R15559 BE177623 AW883520 AW945343 AI246157 T07082 AW805679 W96278 AA135796 W32615 AW995418
 AW801688 BE003837 AW801621 AW385721 AW385742 AW385714 AW604757 W87409 AW604738 AW385757 AW580796 AW601247 BE003239
 BE003183 AA847112 AW580975 AW604760 AW385727 BE164590 BE003090 AW362791 AW604759 AW666589 AW604768 N44337 AI378548
 AW890438 AA077172 AI288683 AA229639 AA091945 AW945454 AA063629 AA702504 AW661938 AW894816 AW580841 AA094372 T06399
 AW885686 BE244086 BE005035 AW861913 AA551773 AW858460 AW370926 AW754352 AW889695 AW384408 AI907428 BE067491 AW861939
 AA248197 AW381373 AW177325 AW806879 AA935217 BE067498 BE083742 BE067470 AW894935 BE082529 AI246811 BE179917 BE002200
 AW607506 AW392889 AW894560 AW381360 AI904206 AW863533 C00609 AW381372 BE082530 AW898120 BE075323 AW392799 AW801420
 AI695314 BE083790 AW858968 AW945650 BE177153 AW970506 BE350419 AI906919 AW360794 AI906917 AW685979 AW794240 AW945566
 AI688683 AI688694 AW009660 AW601421 AW360793 BE066524 BE083901 AW369847 AW381871 AW935435 AW606758 AW806778 AW838449
 BE180466 AW858501 BE180464 AI371163 AA778231 AI174991 BE011720 AW877776 AW877800 AW877795 T19900 AW866365 AW898099
 BE011715 BE167842 BE011718 BE011724 AW363639 AW878658 AW878662 AW894887 BE082356 AW898121 AW804286 AW610312 AI904717
 AW610318 AW896909 AW610286 AW801923 AW880003 AI762171 AW062582 AW368713 AW062593 AW176663 AW842064 AW842069
 AW842095 AI243049 AW902074 AW062592 AW176664 AW751692 BE087703 AI907439 BE009686 BE172115 BE077030 AW608556 AW835577
 AI909628 BE077029 AW176241 BE077552 BE160370 BE160288 AW835566 AW606765 AW606770 AW835578 AW606758 AW806778 AI907484
 BE172821 AW605768 AW999517 AW844165 BE171738 AW751683 AW810493 BE177484 BE177487 AA090510 AW844117 BE173367 AW999678
 AI124870 BE163472 AW841823 AW379762 AW893297 AI290296 BE089132 AA810287 AW176676 AW07662 BE172639 AW893232 AA329629
 BE089008 BE178350 BE178214 BE063291 AW820236 AW999653 BE089486 BE173126 BE171775 BE185787 AA558280 AI174840 AW999112
 BE218391 BE172734 BE178021 BE172738 BE173324 AW603494 AL036722 R38192 R60905 H53721 H41052 AL037917 R37795 AW998872
 AA767189 AW042722 H50699 AA768399 AA767764 AI087888 H44202 BE222792 N90597 W81396 N90615 AI935353 BE501168 F10945
 AW118215 AI970480 AI627641 AW236081 AA574090 AI627652 AI661913 AI759993 N69591 N69276 BE467722 AW392780 BE172467 H92861
 AI524921 F02989 Z39328 F02705 F01414 T88678 AI215165 H87220 AW374781
 BM476606 BI545004 BI834836 BG112453 BI199049 BG112759 AA149846 H97925 AA306121 AA313204 W52451 AJ734997 AA931168 AA429766
 N47913 AA584321 BF940241 AI083648 AI089410 AI347705 AI343661 AI186232 AI689031 N98464 AI820039 AI459034 AV652512 AA822990
 BE857200 AA932998 AA740573 AI826264 AA855683 AI344650 AI027349 AI056087 AA442777 AA603724 AA873347 AI056717 AI092185 AI032895
 AA535689 BF806025 BF806061 BF805885 BF746099 BF746097 AI309259 AI597603 BF806066 AK090653 AI129205 AI248410 H72993 AW615341
 BF805990 BF805982 AA933819 T34373 T35604 H56242 AA548145 T35607 BF806691 N94015 AV703438 BG774276 H82341 R76371
 AK056682 AF086220 AI375066 AA284293 W32566 AW797961 AA960897 AA504145
 AF030234 BC017465 BG008526 AW505550 BM460141 N47324 AA361037 AA321632 N45606 AV752798 AV657116 AA298632 AU137857
 AW467027 AI742080 AI624350 H58206 AA478518 AW439997 AW393555 AW393523 AI559753 AI808732 R66856 H01374 BI257389 BI259830
 AW808845 BM466252 AW956813 BE768647 AV658853 BM055248 BF372070 BF372055 BF372061 AA347852 AA905863 BG505078 AV654024
 BF093291 AW021929 H22650 AA459715 BG496341 BE697763 BI254209 BG498543 H42946 BI099780 BI086741 H87896 H87599 BF691752
 BE768511 BG940948 W37195 BF372041 BE883796 BF372082 BF367329 BF909744 AW966003 AV714014 BI492868 BI495144 AA921845
 AI693426 AI652147 AI435448 N47325 AI434429 AA573137 AI183429 AI829962 AI332526 BF513937 AI189561 AI221962 AI378034 AW118897
 AW655247 AW340077 N41605 AA478519 AA463875 AI858260 AA463379 AI292305 BE045947 AA971089 AI125820 BG940947 AI080245
 AA884954 AI125702 AI382834 AA931835 AI358631 AW439905 AI027633 AI399648 AI014533 AA347851 AA738261 N67374 N69081 AI768667
 AA948472 AI182114 AA293133 AI186725 AA889214 AI222635 BI495143 N29505 N48912 AA769041 AI492769 D66771 AA095911 BE222062
 D56772 AW372285 BM054985 D12485 BG534562 AW003511 H87486 H42880 AW190293 BF594697 BF377611 H22043 BI255749 BI482848
 H16217 H21980 H22651 H88179 H87354 H44062 H25185 H44128
 AB018301 AL050295 BF513128 AW385080 AI551708 AI352542 AI829703 AI819388 AW629019 AW073189 AW273857 AW118788 AI453845
 AI452494 AA886341 AI057144 AA904647 AI423547 AW263913 AI094774 AI434419 AI039548 AI002491 AI240412 Z25099 AA995178 AW050649
 AW026140 AI796309 AI584012 BE165686 AI787991 AI309041 AA724059 AI695284 AI245085 T63971 Z40627 BE166681 BG570071 BF921915
 BI562702 BG506502 AV658058 R48378 AA121543 AI096938 AA618131 H40993 R48277 AI352281 BG540263 BG538901 N95226 AI3566752
 AI221152 Z28777 R16574 AW966449 AA044116 AW797518 BI010405 AA044288 AI093508 BE140169 T64039 BG433106 AW130367 AW130361
 N73937 AA127680 AW044037 AI086437 AA384077 BF941499 T93784 BG003285
 BF090249 AW954847 AW890487 AI305236 D60845 D60537 AA825429 W36294 AW890410 AW088235 BF740240 AA448709 AI350279 AA879119
 AA319510 BE702077 BE699015 BE702046 AW901293 T99319 D81708 BF475488 D60383 D81751 BE699260

TABLE 55C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
401466	6682292	Plus	28745-29023
401192	9719502	Minus	69559-70101
402474	7547176	Minus	53528-53628, 55755-55920, 57530-57757
402145	8018280	Plus	113088-114800
406230	4760409	Plus	71716-72515

TABLE 56A:

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenelD: Unigenes number
 Unigenes Title: Unigenes gene title
 R1: Ratio of seminomatous testicular cancer compared to normal adult testicular tissues

Pkey	ExAccn	UnigenelD	Unigenes Title	R1
414438	AI879277	Hs.76136	thioredoxin	47.30

	424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	44.80
	438091	AW373062		nuclear receptor subfamily 1, group 1, m	40.10
	412948	BE243313	Hs.334851	LIM and SH3 protein 1	34.90
5	417088	M54915	Hs.81170	p1m-1 oncogene	31.10
	430542	A1557486	Hs.119122	ribosomal protein L13a	29.60
	412915	AW087727	Hs.74823	NM_004541:Homo sapiens NADH dehydrogenas	29.10
	418174	L20688	Hs.83656	Rho GDP dissociation inhibitor (GDI) bet	28.15
	406820	A1223958	Hs.108124	ribosomal protein S4, X-linked	28.13
10	433800	A1034361	Hs.135150	lung type-I cell membrane-associated gly	28.10
	406658	A1920965	Hs.77961	major histocompatibility complex, class	27.85
	416680	AW245540	Hs.79516	brain abundant, membrane attached signal	27.70
	446525	AW967069	Hs.211556	hypothetical protein MGC5487	27.20
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	26.30
15	422578	AF239666	Hs.1545	caudal type homeo box transcription fact	25.80
	429978	AA249027		ribosomal protein S6	25.40
	418870	AF147204	Hs.89414	chemokine (C-X-C motif), receptor 4 (fus	24.60
	440207	A1371978	Hs.128326	ESTs	24.50
	425543	R23313	Hs.334895	ribosomal protein L10a	24.30
20	442682	BE379584		dephosphorylation of phosphoglycerate-protei	24.10
	444562	AA186715	Hs.336429	RIKEN cDNA 9130422N19 gene	24.05
	413063	AL036737	Hs.75184	chitinase 3-like 1 (cartilage glycoprote	24.00
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	22.90
	420367	AA259090	Hs.257028	ESTs	22.90
25	406956	AW515336	Hs.29797	ribosomal protein L10	22.77
	417139	M69043	Hs.81328	nuclear factor of kappa light polypeptid	22.75
	412636	NM_004415		desmoplakin (DPI, DPII)	22.40
	420678	AI434780	Hs.4248	vav 2 oncogene	22.10
	440869	NM_014297	Hs.7486	protein expressed in thyroid	21.40
30	446827	AI973016	Hs.15725	hypothetical protein SBBI48	21.20
	410315	AI638871	Hs.17625	Homo sapiens cDNA: FLJ22524 fis, clone H	21.10
	420754	W79431	Hs.346911	ribosomal protein L22	20.98
	435538	AB011540	Hs.4930	low density lipoprotein receptor-related	20.90
	440440	Z28925	Hs.7188	semu domain, immunoglobulin domain (Ig),	20.80
35	428490	AI971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	20.40
	425769	U72513	Hs.159486	Human RPL13-2 pseudogene mRNA, complete	19.60
	422714	AB018335	Hs.119387	KIAA0792 gene product	19.15
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	19.00
	413787	AL352558		tyrosine 3-monooxygenase/tryptophan 5-mo	18.50
40	452874	AK001061	Hs.30925	hypothetical protein FLJ10199	18.50
	430266	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	18.00
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	17.90
	448588	AI970276	Hs.156905	KIAA1678	17.70
	444784	D12485	Hs.11951	ectonucleotide pyrophosphatase/phosphodi	17.50
45	428782	X12630	Hs.193400	interleukin 6 receptor	17.40
	414092	Z14244	Hs.75752	cytochrome c oxidase subunit VIIb	17.20
	425945	AW410669	Hs.164280	solute carrier family 25 (mitochondrial	17.15
	420759	T11832	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	17.10
	440528	BE313555	Hs.7252	KIAA1224 protein	17.06
50	410143	AA188169		KIAA1191 protein	17.05
	421181	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	16.90
	426083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	16.70
	429183	AB014604	Hs.197955	KIAA0704 protein	16.70
	450937	R49131	Hs.26267	ATP-dependent interferon response protel	16.60
55	449571	AW016812	Hs.200266	ESTs	16.50
	432730	AI066520	Hs.131358	ESTs	16.20
	428295	AW367283		zinc finger protein 6 (CMPX1)	16.15
	439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	15.90
	420028	AB014680	Hs.8788	carbohydrate (N-acetylglucosamine-6-O) s	16.80
60	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	15.80
	456236	AF045229	Hs.82280	regulator of G-protein signalling 10	15.70
	429469	M64590	Hs.27	glycine dehydrogenase (decarboxylating;	15.50
	428928	BE408838	Hs.194657	cadherin 1, type 1, E-cadherin (epithell	14.90
	452322	BE565343	Hs.28988	glutaredoxin (thioltransferase)	14.90
	406656	M16714	Hs.89643	major histocompatibility complex, class	14.85
65	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	14.71
	450377	AB033091		KIAA1265 protein	14.70
	426998	W57330		hypothetical protein AL110115	14.60
	430332	R51790	Hs.239483	Human clone 23933 mRNA sequence	14.60
70	427691	AW184426	Hs.20728	ESTs	14.42
	429614	AI371172	Hs.211539	hypothetical protein MGC4248	14.35
	451106	BE382701	Hs.26980	N-MYC oncogene	14.21
	422241	Y00052	Hs.170121	protein tyrosine phosphatase, receptor t	14.13
	436860	H12751	Hs.5327	PRO1914 protein	13.90
75	446899	NM_005397	Hs.16426	podocalyxin-like	13.90
	450000	AI952797	Hs.10888	hypothetical protein FLJ21709	13.75
	408380	AF123050	Hs.44532	diubiquitin	13.70
	447526	AL048753	Hs.303649	small inducible cytokine A2 (monocyte ch	13.40
	427521	AW973352		ESTs	13.30
80	410598	AI817130	Hs.9185	Homo sapiens cDNA FLJ13698 fs, clone PL	13.25
	428664	AK001666	Hs.189085	similar to SALL1 (sal (Drosophila)-like	13.23
	408822	AW500715	Hs.57079	Homo sapiens cDNA FLJ13267 fs, clone OV	13.23
	425289	AW139342	Hs.155530	interferon, gamma-inducible protein 16	12.70
	426552	BE297860	Hs.170328	moesin	12.69

5	415857	AA866115	Hs.127797	Homo sapiens cDNA FLJ11381 fis, clone HE	12.55
	436398	H87136	Hs.6174	ribosomal protein S17	12.50
	418151	AA864238	Hs.83583	actin related protein 2/3 complex, subun	12.30
	453020	AL162039	Hs.31422	Homo sapiens mRNA: cDNA DKFZp434M229 (fr	12.30
	410275	U85558	Hs.61796	transcription factor AP-2 gamma (activat	12.28
	414587	NM_004862	Hs.76507	LPS-induced TNF-alpha factor	12.25
	425875	AU077333	Hs.160483	erythrocyte membrane protein band 7.2 (s	12.25
	416938	BE383507	Hs.78921	A kinase (PRKA) anchor protein 1	12.20
10	419384	AA490866	Hs.39429	ESTs	12.20
	410186	BE294088	Hs.737	Immediate early protein	12.15
	407862	BE548267	Hs.337986	Homo sapiens cDNA FLJ10934 fis, clone OV	12.05
	433793	AW975959	Hs.107513	ESTs, Moderately similar to KIAA1058 pro	12.00
	406743	AA911568	Hs.279860	tumor protein, translationally-controlled	11.90
15	406989	AW361666	Hs.49500	KIAA0746 protein	11.80
	430268	AK000737	Hs.237480	hypothetical protein FLJ20730	11.80
	447735	AA775268	Hs.6127	Homo sapiens cDNA: FLJ23020 fis, clone L	11.80
	410325	AB023154	Hs.62264	KIAA0937 protein	11.70
	445817	NM_003542	Hs.13340	histone acetyltransferase 1	11.70
20	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p85), ly	11.61
	445863	R12234	Hs.13386	Homo sapiens clone 25028 mRNA sequence	11.60
	454413	AI653672	Hs.40092	PNAS-123	11.60
	418460	M26315	Hs.85258	CDB antigen, alpha polypeptide (p32)	11.40
	428065	AI634046	Hs.157313	ESTs	11.40
25	432805	X94630	Hs.3107	CD97 antigen	11.36
	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	11.35
	444060	AA340277		Homo sapiens cDNA FLJ20167 fis, clone CO	11.30
	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-in	11.30
	405963	AA133590	Hs.250857	calcium/calmodulin-dependent protein kin	11.11
30	402474			NM_004079:Homo sapiens cathepsin S (CTSS	11.00
	407112	AA070801	Hs.51615	ESTs, Weakly similar to ALU7_HUMAN ALU S	11.00
	406786	AW161678	Hs.111334	ferritin, light polypeptide	10.95
	428227	AA321849	Hs.2248	small inducible cytokine subfamily B (Cy	10.90
	444656	AI277924	Hs.145199	ESTs	10.90
35	453856	AA804789	Hs.19447	PDZ-LIM protein mystique	10.85
	440774	AI420611	Hs.153934	ESTs	10.82
	408669	AI493581	Hs.78146	platelet/endothelial cell adhesion molec	10.80
	431699	AK000680	Hs.266175	phosphoprotein associated with GEMs	10.80
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	10.80
40	418509	AB028824	Hs.85539	ATP synthase, H transporting, mitochondr	10.70
	437374	AL359571	Hs.44054	nuclein (GSK3B interacting protein)	10.65
	415899	X78992	Hs.78909	butyrate response factor 2 (EGF-response	10.60
	450719	AI098837	Hs.21349	ESTs, Weakly similar to R88B_HUMAN RAS-R	10.43
	424800	AL035588	Hs.153203	MyoD family inhibitor	10.40
45	446682	AW205632	Hs.211198	ESTs	10.40
	447211	AL161981	Hs.17767	KIAA1554 protein	10.31
	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	10.30
	422105	AI929700	Hs.111680	endosulfine alpha	10.21
	417144	AA382104	Hs.81337	lactin, galactoside-binding, soluble, 9	10.20
50	422068	AI807519	Hs.104520	Homo sapiens cDNA FLJ13694 fis, clone PL	10.20
	452651	AI218918	Hs.30209	KIAA0854 protein	10.15
	418707	U97502	Hs.87497	butyrophilin, subfamily 3, member A2	10.11
	426996	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	10.10
	427761	AA412205	Hs.140986	ESTs	10.10
55	443623	AK001575	Hs.9536	hypothetical protein FLJ10713	9.90
	402145			Target Exon	9.82
	413686	AI469213	Hs.71404	ESTs	9.80
	446488	AB037782	Hs.15119	KIAA1361 protein	9.80
	449246	AW411209	Hs.23363	hypothetical protein FLJ10983	9.80
60	424321	W74048	Hs.1765	lymphocyte-specific protein tyrosine kin	9.80
	407179	AA206485		thymosin, beta 4, X chromosome	9.72
	413497	BE177661		gb:RC1-HT0598-020300-011-h02 HT0598 Homo	9.70
	430068	AA464964		gb:z80f10.s1 Soares ovary tumor NbHOT H	9.70
	446795	AI797713	Hs.156471	ESTs	9.70
65	435522	N64214	Hs.9774	synovial sarcoma translocation gene on c	9.65
	451864	N20370	Hs.69547	ESTs	9.65
	419490	NM_006144	Hs.80708	granzyme A (granzyme 1, cytotoxic T-lymp	9.60
	419904	AA974411	Hs.18672	ESTs	9.60
	427711	M31659	Hs.180408	solute carrier family 25 (mitochondrial	9.60
70	409208	Y00093		Integrin, alpha X (antigen CD11C (p150),	9.52
	424950	AA802917	Hs.156974	ESTs	9.50
	447534	AW953935	Hs.288656	ESTs	9.50
	419223	X60111	Hs.1244	CD9 antigen (p24)	9.41
	423573	BE003054	Hs.1695	matrix metalloproteinase 12 (macrophage	9.40
75	422960	AW890487		cadherin 13, H-cadherin (heart)	9.33
	412025	AI827451	Hs.24143	Wiskott-Aldrich syndrome protein interac	9.32
	408784	AW971350	Hs.63386	ESTs	9.30
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease JH.sapi	9.30
	432409	AA806538	Hs.130732	KIAA1575 protein	9.30
80	440273	AI805392	Hs.325335	Homo sapiens cDNA: FLJ23523 fis, clone L	9.30
	407110	AA018042	Hs.252085	Prader-Willi/Angelman syndrome-5	9.22
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	9.20
	434280	BE006398		gb:CM1-BND116-150400-189-h02 BND116 Homo	9.20
	434524	AA635931	Hs.249716	ESTs	9.20

	450294	H42587	Hs.238730	hypothetical protein MGC10823	9.20
	407254	AW129401	Hs.181165	eukaryotic translation elongation factor	9.10
	434442	AA737415		ESTs	9.10
5	440268	BE270030	Hs.336959	Homo sapiens, clone IMAGE3677185, mRNA	9.03
	447519	U46258	Hs.339665	ESTs	9.00
	433156	R59206	Hs.17519	Homo sapiens cDNA: FLJ22539 fis, clone H	8.98
	410730	AW368860		DnaJ (Hsp40) homolog, subfamily B, membe	8.90
	436823	AW749865	Hs.117077	ESTs, Weakly similar to I38022 hypotheti	8.90
	442806	AW294522	Hs.149991	ESTs	8.90
10	433271	BE621697	Hs.14317	nucleolar protein family A, member 3 (H	8.89
	445577	N40696	Hs.137064	cytoplasmic polyadenylation element bind	8.81
	406437	AW957744	Hs.278469	lacritmal proline rich protein	8.80
	420962	NM_005904	Hs.100602	MAD (mothers against decapentaplegic, Dr	8.80
15	431187	AW971146	Hs.293187	ESTs	8.80
	421098	AI697901	Hs.192425	ESTs	8.70
	424528	AW073971	Hs.238954	ESTs, Weakly similar to KIAA1204 protein	8.70
	446108	AL036596	Hs.42322	A kinase (PKA) anchor protein 2	8.70
	401091			decay accelerating factor for complement	8.62
20	433412	AV653729	Hs.8185	CGI-44 protein; sulfide dehydrogenase li	8.60
	438089	W05391		nuclear receptor subfamily 1, group I, m	8.60
	431958	X63529	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	8.60
	452568	AA805634	Hs.300870	Homo sapiens mRNA; cDNA DKFZp547W072 (fr	8.59
	414191	AW250089	Hs.75607	PDZ and LIM domain 1 (elfin)	8.56
25	411979	X85134	Hs.72984	retinoblastoma-binding protein 5	8.50
	414829	AA321568	Hs.77436	pleckstrin	8.50
	430162	AW450843	Hs.346348	ESTs	8.50
	448412	AI219083	Hs.42532	ESTs, Moderately similar to ALU8_HUMAN A	8.50
	423753	Y11312	Hs.132453	phosphoinositide-3-kinase, class 2, beta	8.45
30	407833	AW955632	Hs.56666	ESTs, Weakly similar to S19560 proline-r	8.43
	416975	NM_004131	Hs.1051	granzyme B (granzyme 2, cytotoxic T-lymp	8.40
	433208	AW002834	Hs.24095	ESTs	8.40
	428970	BE276891	Hs.194691	retinoic acid induced 3	8.38
	425284	AF155568		NS1-associated protein 1	8.33
35	437108	AA434054	Hs.80624	hypothetical protein MGC2560	8.33
	408360	AI806090	Hs.44344	hypothetical protein FLJ20534	8.30
	426827	AW067805	Hs.172665	methylene-tetrahydrofolate dehydrogenase	8.30
	453716	AA037675	Hs.152675	ESTs	8.30
40	418840	AI821614	Hs.185831	ESTs	8.20
	434649	AA738254	Hs.165390	ESTs, Highly similar to A40350 transcrip	8.20
	449556	AA002008	Hs.188833	ESTs	8.20
	425535	AB007937	Hs.158287	KIAA0468 gene product	8.17
	409493	AA386192	Hs.193482	Homo sapiens cDNA FLJ11903 fis, clone HE	8.13
	432559	AW452848	Hs.257631	ESTs	8.10
45	436797	AA731491	Hs.334477	hypothetical protein MGC14879	8.10
	420099	D80011	Hs.95140	KIAA0189 gene product	8.01
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	8.00
	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	8.00
	434423	NM_006769	Hs.3844	LIM domain only 4	8.00
50	437886	BE284111	Hs.31314	retinoblastoma-binding protein 7	8.00
	418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	7.92
	433655	AL036559	Hs.3463	ribosomal protein S23	7.89
	435968	AW161481	Hs.111577	integral membrane protein 3	7.89
	434511	R28982	Hs.18106	ESTs	7.88
55	423523	AW299828	Hs.193580	ESTs	7.86
	409327	L41182	Hs.53563	collagen, type IX, alpha 3	7.84
	411950	R77776	Hs.18103	ESTs	7.80
	434159	AW135214	Hs.191828	ESTs	7.80
	447500	AI381900	Hs.159212	ESTs	7.80
60	406699	L06505	Hs.182979	ribosomal protein L12	7.75
	422603	BE242587	Hs.118651	hematopoietically expressed homeobox	7.68
	428759	AI590401	Hs.21213	ESTs	7.66
	406776	T16206	Hs.237164	ESTs, Highly similar to LDHHL_HUMAN L-LAC	7.62
	422589	AW858865		gltcRC3-CT0297-290100-013-d03 CT0297 Homo	7.60
65	444795	AI193356	Hs.160316	ESTs	7.60
	406663	U24683		immunoglobulin heavy constant mu	7.59
	442821	BE391929	Hs.8752	transmembrane protein 4	7.56
	412347	AW970026	Hs.73818	ubiquitin-cytochrome c reductase hinge p	7.52
	407252	AA659037	Hs.163780	ESTs	7.50
70	414405	AI362533		KIAA0306 protein	7.50
	427395	AW298741	Hs.97861	ESTs, Moderately similar to I38022 hypot	7.50
	429999	AI761902	Hs.99597	ESTs	7.50
	441436	AW137772	Hs.185980	ESTs	7.50
	447644	AW861622	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	7.50
75	420943	AI718702	Hs.279930	major histocompatibility complex, class	7.46
	447674	BE270640	Hs.19192	cyclin-dependent kinase 2	7.43
	413420	AW410235	Hs.75348	proteasome (prosome, macropain) activato	7.42
	422451	AA310753	Hs.42491	ESTs, Weakly similar to S65657 alpha-1C-	7.41
	437134	AA349944	Hs.42915	ARP2 (actin-related protein 2, yeast) ho	7.40
80	408912	AB011084	Hs.48924	KIAA0512 gene product, ALEX2	7.40
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	7.40
	431427	AK000401	Hs.252748	Homo sapiens cDNA FLJ20394 fis, clone KA	7.40
	437469	AW753112	Hs.15514	hypothetical protein MGC3280	7.40
	432598	AI341227	Hs.157106	ESTs	7.38

	447484	AA464839	Hs.292566	hypothetical protein FLJ14697	7.34
	441612	AI802629	Hs.113660	Homo sapiens cDNA FLJ11631 fis, clone HE	7.30
	408067	BE244580	Hs.342307	hypothetical protein FLJ10330	7.30
	434963	AW974957	Hs.288719	Homo sapiens cDNA FLJ12142 fis, clone MA	7.30
5	437103	AW139408	Hs.152940	ESTs	7.30
	442495	AI184717		ESTs	7.30
	445929	AK896680	Hs.323401	dpy-30-like protein	7.30
	446013	AI360167	Hs.152774	ESTs	7.30
10	436075	BE090176	Hs.179902	transporter-like protein	7.20
	450139	AK001838		serum/glucocorticoid regulated kinase	7.20
	423905	AW578960	Hs.135150	lung type-I cell membrane-associated gly	7.17
	406819	AA908472		gb:op82a10.s1 NCL_CGAP_Ov8 Homo sapiens	7.16
	407719	AW863866	Hs.44021	Homo sapiens mRNA for FLJ00065 protein,	7.12
	425593	AA278921	Hs.1908	proteoglycan 1, secretory granule	7.10
15	413886	AW958264	Hs.103832	similar to yeast Upk3, variant B	7.10
	422616	BE300330	Hs.118725	selenophosphate synthetase 2	7.10
	424677	U08414		zinc finger protein 137 (clone pHZ-30)	7.10
	427254	AL121523	Hs.97774	ESTs	7.10
	427307	AF117947	Hs.174796	PDZ domain-containing guanine nucleotide	7.10
20	438980	AW502384		gb:UL-HF-BR0p-aka-12-0-ULr1 NIH_MGC_5	7.10
	451129	BE072881		gb:RC2-BT0548-200300-012-e09 BT0548 Homo	7.10
	441878	AI801859	Hs.127982	ESTs	7.09
	443247	BE614387	Hs.333893	c-Myc target JPO1	7.04
25	412645	AW444433	Hs.136061	Homo sapiens, Similar to hypothetical pr	7.00
	417315	AI080042	Hs.180450	ribosomal protein S24	7.00
	429058	AF138863	Hs.35254	hypothetical protein FLB6421	7.00
	429281	AA830856	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	7.00
	445245	AB032973	Hs.12481	LCHN protein	7.00
30	414812	X72755	Hs.77367	monokine induced by gamma interferon	7.00
	445055	BE512856	Hs.109051	SH3 domain binding glutamic acid-rich pr	6.97
	410397	AF217517	Hs.63042	DKFZp564J157 protein	6.96
	418686	AW959433	Hs.326290	hypothetical protein FLJ12581	6.96
	449924	W30681	Hs.146233	Homo sapiens cDNA: FLJ22130 fis, clone H	6.95
35	418134	AA397769	Hs.86617	ESTs	6.90
	424768	AA353895	Hs.152983	HUS1 (S. pombe) checkpoint homolog	6.90
	443303	U67319	Hs.9216	caspase 7, apoptosis-related cysteine pr	6.90
	411852	AA528140	Hs.107515	ESTs, Weakly similar to T00329 hypothet	6.88
	451838	AW005866	Hs.193969	ESTs	6.88
40	425367	BE271188	Hs.155975	protein tyrosine phosphatase, receptor t	6.87
	453485	BE620712	Hs.33026	hypothetical protein PP2447	6.85
	401466			vesicle-associated membrane protein 4	6.84
	457073	AA233210	Hs.179943	ribosomal protein L11	6.83
	412093	BE242691	Hs.14947	ESTs	6.83
45	442492	AA528489	Hs.234518	ribosomal protein L23	6.83
	449971	AA807346	Hs.288581	Homo sapiens cDNA FLJ14298 fis, clone PL	6.83
	431773	BE409442	Hs.268557	pleckstrin homology-like domain, family	6.82
	416401	N80139	Hs.268916	ESTs	6.80
	426501	AW043782	Hs.293616	ESTs	6.80
50	435080	AI831760	Hs.155111	hypothetical protein FLJ14428	6.80
	436876	AI124756	Hs.5337	isocitrate dehydrogenase 2 (NADP), mitoc	6.80
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	6.80
	432666	AW204069		ESTs, Weakly similar to unnamed protein	6.79
	424201	L33075	Hs.1742	IQ motif containing GTPase activating pr	6.77
55	425277	NM_001241	Hs.155478	cyclin T2	6.72
	425246	AI085581	Hs.155321	serum response factor (c-fos serum respo	6.70
	428728	NM_016525	Hs.191381	hypothetical protein	6.70
	430289	W28673	Hs.106747	serine carboxypeptidase 1 precursor prot	6.70
	433735	AA608955	Hs.109653	ESTs	6.70
60	430556	AW967807	Hs.13797	ESTs	6.69
	417535	AA203569	Hs.191482	ESTs	6.69
	418117	AI922013	Hs.83495	linker for activation of T cells	6.67
	417558	AF045229	Hs.82280	regulator of G-protein signaling 10	6.65
	424541	AW392551	Hs.180559	ESTs, Weakly similar to A56194 thromboxa	6.62
65	447341	AF106941	Hs.18142	arrestin, beta 2	6.61
	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	6.60
	442460	NM_014135	Hs.8345	PR00641 protein	6.60
	428818	AI131291	Hs.102308	potassium inwardly-rectifying channel, s	6.59
	453932	AW006303	Hs.329296	ESTs, Weakly similar to (define not ava	6.57
70	415221	W07418	Hs.78225	annexin A1	6.56
	450256	AA286887	Hs.24724	MFH-amplified sequences with leucine-ric	6.54
	441384	AA447849	Hs.288660	Homo sapiens cDNA: FLJ22182 fis, clone H	6.51
	421684	BE281591	Hs.105768	hypothetical protein FLJ10511	6.50
	441224	AU076964	Hs.7753	calumenin	6.50
75	443749	R38828	Hs.143463	ESTs	6.50
	448094	H24387	Hs.32061	ESTs, Weakly similar to 138022 hypothet	6.50
	416801	X98834	Hs.79971	sal (Drosophila)-like 2	6.40
	418259	AA215404		ESTs	6.40
	421633	AF121860	Hs.106260	sorting nexin 10	6.40
80	435937	AA830893	Hs.119769	ESTs	6.40
	445612	N94126	Hs.12969	hypothetical protein	6.40
	451553	W18193		ESTs, Moderately similar to HERC2 (H.sap	6.40
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	6.40
	422693	BE300073	Hs.279860	tumor protein, translationally-controlled	6.39

5	434817	AA082118	Hs.102737	goliath protein	6.38
	414476	AA301867	Hs.76224	EGF-containing fibulin-like extracellula	6.35
	425410	AA310874	Hs.156828	Homo sapiens cDNA FLJ10522 fis, clone NT	6.34
	431840	AA534908	Hs.2860	POU domain, class 5, transcription facto	6.33
	435812	AA700439	Hs.188490	ESTs	6.31
	401113			solute carrier family 22 (organic cation	6.30
	408418	AW963897	Hs.44743	KIAA1435 protein	6.30
	412220	BE360058	Hs.36787	chromodomain helicase DNA binding protei	6.30
10	426780	BE242284	Hs.172199	adenylate cyclase 7	6.30
	427202	BE272922	Hs.173936	interleukin 10 receptor, beta	6.30
	434699	AA643687	Hs.149425	Homo sapiens cDNA FLJ11980 fis, clone HE	6.30
	447887	AA114050	Hs.19949	caspase 8, apoptosis-related cysteine pr	6.30
	449576	AW014631	Hs.225068	ESTs	6.30
15	449333	NM_016245	Hs.12150	retinal short-chain dehydrogenase/reduct	6.30
	432841	M93425	Hs.62	protein tyrosine phosphatase, non-recept	6.27
	411975	A1916058	Hs.144583	ESTs	6.26
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	6.25
	433162	A1025842		ESTs	6.23
	449322	A1638616	Hs.196566	ESTs	6.22
20	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	6.20
	440327	R12581	Hs.191146	ESTs	6.20
	442832	AW206560	Hs.253569	ESTs	6.20
	456382	AW973003	Hs.179909	hypothetical protein FLJ22995	6.20
25	427968	A1857607	Hs.181301	cathepsin S	6.18
	414682	AL036058	Hs.78807	major histocompatibility complex, class	6.16
	418113	A1272141	Hs.83484	SRY (sex determining region Y)-box 4	6.16
	406870	AA075144		gb:zm86f06.s1 Stratagene ovarian cancer	6.15
	416003	X98001	Hs.78948	Rab geranylgeranyltransferase, beta subu	6.15
30	445493	A1915771		metallothionein 1E (functional)	6.15
	424687	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	6.14
	427477	AW973119	Hs.178391	ribosomal protein L44	6.14
	422499	A1268666	Hs.19631	ESTs, Weakly similar to I38022 hypot	6.13
	443441	AW291196	Hs.92195	ESTs	6.12
35	413677	AW503116	Hs.301819	zinc finger protein 146	6.11
	406797	A1432224		ribosomal protein L6	6.10
	406857	AA613726	Hs.29797	ribosomal protein L10	6.10
	410387	A1277357	Hs.47094	ESTs	6.10
	410503	AW975746	Hs.188662	KIAA1702 protein	6.10
40	441962	AW972642	Hs.289008	Homo sapiens cDNA: FLJ21814 fis, clone H	6.10
	425762	BE244076	Hs.158578	AT-hook transcription factor AKNA	6.08
	406877	AA226392	Hs.179943	ribosomal protein L11	6.07
	407784	AW139585	Hs.12708	ESTs	6.05
	416297	AA157634	Hs.79172	solute carrier family 25 (mitochondrial	6.05
45	446272	BE268912	Hs.14601	hematopoietic cell-specific Lyn substrat	6.01
	412949	A1471639	Hs.71913	ESTs	6.00
	420059	AF161486	Hs.94769	RAB23, member RAS oncogene family	6.00
	435756	AM18466	Hs.33665	ESTs	6.00
	451658	AW195351	Hs.250520	ESTs, Moderately similar to I38022 hypot	6.00
50	441623	AA315805		desmoglein 2	5.98
	416926	H03109	Hs.263395	HTD18 protein	5.96
	425190	AW028302	Hs.155079	protein phosphatase 2, regulatory subun	5.95
	441244	BE612935	Hs.184052	PP1201 protein	5.95
	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	5.95
55	430504	H52761		Homo sapiens, clone MGC:12617, mRNA, com	5.94
	422310	AA316822	Hs.98370	cytochrome P450, subfamily IIS, polypept	5.92
	406605	AF025374	Hs.48465	T-cell, immune regulator 1	5.91
	433891	AA613792		gb:mo97h03.s1 NC1_CGAP_Pz2 Homo sapiens	5.90
	406542			C19000728*gi12585552[sp]Q9Y2Q1[Z257_HU	5.90
60	406858	A1865720	Hs.29797	ribosomal protein L10	5.90
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	5.90
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	5.90
	439451	AF086270	Hs.278554	heterochromatin-like protein 1	5.90
	455263	AW981702		Homo sapiens cDNA FLJ14028 fis, clone HE	5.90
65	441321	H17182	Hs.7771	B-cell associated protein	5.88
	429083	Y08397	Hs.227817	BCL2-related protein A1	5.87
	406806	AW088535		ribosomal protein, large, P0	5.87
	416987	D88957	Hs.80712	KIAA0202 protein	5.86
	450988	BE618571	Hs.429	ATP synthase, H transporting, mitochondr	5.83
70	428773	BE256238	Hs.193163	bridging integrator 1	5.83
	406794	A1890243		ribosomal protein L6	5.82
	457752	A1821270	Hs.285843	Homo sapiens cDNA FLJ14384 fis, clone HE	5.82
	435511	AA683336	Hs.189046	ESTs	5.81
	451589	AA424791	Hs.5734	meningioma expressed antigen 5 (hyaluron	5.80
75	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	5.80
	412528	A1123478	Hs.32112	ESTs	5.80
	424875	A1187945	Hs.199310	ESTs	5.80
	426981	AL044675	Hs.173081	KIAA0530 protein	5.80
	447711	AM59554	Hs.161286	ESTs	5.80
80	449961	AW265634	Hs.133100	ESTs	5.80
	415759	AK000978	Hs.79741	hypothetical protein FLJ10116	5.80
	415082	AA160000	Hs.137396	ESTs, Weakly similar to JC5236 galactosy	5.79
	422773	AB028862	Hs.301552	KIAA1039 protein	5.78
	441455	AJ271671	Hs.7854	zinc/iron regulated transporter-like	5.78

5	414774	X02419	Hs.77274	plasminogen activator, urokinase	5.77
	449317	AW293413	Hs.132906	19A24 protein	5.75
	425787	AA363867	Hs.155029	ESTs	5.73
	414890	BE281085	Hs.77573	uridine phosphorylase	5.72
	426354	NM_004010	Hs.169470	dystrophin (muscular dystrophy, Duchenne)	5.71
10	435861	BE293127	Hs.283722	GTT1 protein	5.71
	419378	R24922	Hs.90078	nucleotide-sugar transporter similar to	5.70
	431155	AW971213		gb:EST383301 MAGE resequences, MAGL Homo	5.70
	437457	AA757900	Hs.270823	ESTs, Weakly similar to S65657 alpha-1C-	5.70
	446659	A1353361	Hs.226376	ESTs	5.70
15	457250	AA811987	Hs.125779	ESTs	5.70
	414150	AA136026		gb:zn88d07.r1 Stratagene lung carcinoma	5.68
	439924	A1885897	Hs.125293	ESTs	5.67
	452472	AW957300	Hs.294142	ESTs, Weakly similar to C55663 oligodend	5.66
	451812	X81889	Hs.152151	plakophilin 4	5.65
20	432588	X92715	Hs.3057	zinc finger protein 74 (Cos52)	5.63
	440119	AA865455	Hs.125331	ESTs, Moderately similar to unknown [H.s	5.63
	424326	NM_014479	Hs.145298	ADAM-like disintegrin protease, decysin	5.60
	431770	BE221880	Hs.268555	5'-3' exonuclease 2	5.60
	436511	AA721252	Hs.291502	ESTs	5.60
25	446630	AW364793	Hs.15740	Homo sapiens mRNA; cDNA DKFZp434E033 (fr	5.60
	406623	X69392	Hs.81379	ribosomal protein L26	5.60
	452382	N38902	Hs.211539	hypothetical protein MGC4248	5.57
	416047	BE438894	Hs.78991	DNA segment, numerous copies, expressed	5.56
	437296	AA350994	Hs.20281	KIAA1700	5.56
30	453985	N44545	Hs.251855	ESTs	5.56
	443351	AW016783	Hs.30799	Homo sapiens cDNA FLJ13471 fis, clone PL	5.55
	448877	A1583696	Hs.253313	ESTs	5.53
	435748	AA689756	Hs.117335	ESTs	5.52
	420732	AA789133	Hs.53525	ESTs	5.51
35	421818	AW992976	Hs.50098	NM_002489:Homo sapiens NADH dehydrogenas	5.50
	430815	AA488953		gb:aa55e05.r1 NCL_CGAP_GCB1 Homo sapiens	5.50
	435716	A1433540		gb:1689j05.x1 NCL_CGAP_Kid11 Homo sapien	5.50
	437442	T85104	Hs.222779	ESTs, Moderately similar to similar to N	5.50
	449625	NM_014253		odt (odd Ozten-m, Drosophila) homolog 1	5.50
40	456497	AW957956	Hs.123648	ESTs, Weakly similar to AF108460 1 ubinu	5.50
	451287	AK002158	Hs.26194	likely homolog of mouse immunity-associ	5.50
	433701	AW445023	Hs.15155	ESTs	5.49
	427640	AF058293	Hs.180015	D-dopachrome tautomerase	5.47
	420552	AK000492	Hs.98806	hypothetical protein	5.45
45	449338	H73444	Hs.394	adrenomedullin	5.42
	427176	AW381568	Hs.40334	ESTs	5.42
	409945	AW015935	Hs.122642	ESTs	5.40
	421568	W85858	Hs.99804	ESTs	5.40
	423961	D13666	Hs.136348	perlestin(OSF-2os)	5.40
50	440719	AA150869	Hs.25267	ATP-dependant Interferon response protei	5.40
	443035	Z45822	Hs.8908	Homo sapiens clone 24889 mRNA sequence	5.40
	458659	AW749895	Hs.332520	Homo sapiens mRNA; cDNA DKFZp434A1014 (f	5.40
	424415	NM_001975	Hs.146580	enolase 2, (gamma, neuronal)	5.40
	420137	AA306478	Hs.95327	CD3D antigen, delta polypeptide (TIT3 co	5.39
55	422163	AF027208	Hs.112360	prominin (mouse)-like 1	5.38
	439815	AA206079	Hs.6683	hypothetical protein FLJ20420	5.37
	452432	AW206008	Hs.283378	Homo sapiens cDNA: FLJ21778 fis, clone H	5.37
	457465	AW301344	Hs.122908	DNA replication factor	5.37
	412935	BE267045	Hs.75064	tubulin-specific chaperone c	5.36
60	409485	S80990	Hs.252136	ficolin (collagen/vibronin domain-cont	5.35
	430283	BE391688		RAB7, member RAS oncogene family	5.33
	406814	AA642947	Hs.119122	ribosomal protein L13a	5.33
	409019	AW385412		myosin regulatory light chain 2, smooth	5.30
	410561	BE540255	Hs.6994	Homo sapiens cDNA: FLJ22044 fis, clone H	5.30
65	412623	E26898	Hs.74170	metallothionein 1E (functional)	5.30
	417450	AA314435	Hs.17519	Homo sapiens cDNA: FLJ22539 fis, clone H	5.30
	418702	BE268368	Hs.86945	ESTs, Weakly similar to A46010 X-linked	5.30
	419926	AW800992	Hs.93796	DKFZP586D2223 protein	5.30
	422900	AA641201	Hs.222051	ESTs	5.30
70	423494	AW504365	Hs.24143	Wiskott-Aldrich syndrome protein Interac	5.30
	427667	AK001279	Hs.180171	Homo sapiens cDNA FLJ10417 fis, clone NT	5.30
	427774	AA276583	Hs.180737	Homo sapiens clone 23654 and 23905 mRNA	5.30
	430177	AW969233	Hs.302745	MSTP028 protein	5.30
	430835	A1240006	Hs.192326	ESTs	5.30
75	433009	AA761668		gb:rz24c08.s1 NCL_CGAP_GCB1 Homo sapiens	5.30
	438776	AL360140	Hs.176005	Homo sapiens mRNA full length insert cDN	5.30
	447082	T85314	Hs.54629	thioredoxin-like	5.30
	415995	NM_004573		phospholipase C, beta 2	5.29
	424578	AK001973	Hs.150890	hypothetical protein	5.27
80	441303	AW293081	Hs.241801	ESTs	5.27
	427818	AA158248	Hs.180909	peroxiredoxin 1	5.27
	443963	AA878183	Hs.17448	Homo sapiens cDNA FLJ13818 fis, clone PL	5.26
	450273	AW298454	Hs.24743	hypothetical protein FLJ20171	5.24
	444708	AW971049	Hs.11774	protein (peptidyl-prolyl) cis/trans isome	5.23
	415121	D60871	Hs.34955	Homo sapiens cDNA FLJ13485 fis, clone PL	5.21
	458079	A1796870	Hs.54277	DNA segment on chromosome X (unique) 992	5.21
	405085			NM_006662*:Homo sapiens Sn2-related CBP	5.20

5	413401	AI361861	Hs.118659	ESTs	5.20
	418459	R85436	Hs.268814	ESTs	5.20
	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	5.20
	426496	D31765	Hs.170114	KIAA0061 protein	5.20
	431749	AL049263	Hs.306292	Homo sapiens mRNA; cDNA DKFZp554F133 (fr	5.20
10	434372	AA631373		gbcnp86c01.s1 NCL_CGAP_Try1 Homo sapiens	5.20
	436812	AW298067		gb:U1-H-BWD-ajp-g-08-D-U1.s1 NCL_CGAP_Su	5.20
	441390	AI692550	Hs.131175	ESTs	5.20
	449419	R34910	Hs.119172	ESTs	5.20
	453127	AI696671	Hs.294110	ESTs	5.20
15	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	5.20
	417750	AI267720	Hs.260523	synovial sarcoma, translocated to X chro	5.19
	451614	AA847992	Hs.137003	ESTs	5.18
	410423	AW402432	Hs.63489	protein tyrosine phosphatase, non-recept	5.16
	405799	AA908548		gbcog83g12.s1 NCL_CGAP_Ov8 Homo sapiens	5.16
20	413963	R84282	Hs.75643	nuclear factor (erythroid-derived 2), 45	5.15
	422293	X94453	Hs.114366	pyrroline-5-carboxylate synthetase (glut	5.14
	432465	D56165	Hs.275163	non-metastatic cells 2, protein (NM23B)	5.12
	414768	AW376989	Hs.259855	elongation factor-2 kinase	5.12
	447232	AW499834	Hs.327	interleukin 10 receptor, alpha	5.12
25	430478	NM_014349	Hs.241535	apolipoprotein L, 3	5.11
	420151	AA255931	Hs.106704	ESTs	5.11
	434274	AA628539	Hs.116252	ESTs, Moderately similar to ALU1_HUMAN A	5.10
	419317	AA236282	Hs.172318	ESTs	5.10
	424699	AW206227	Hs.287727	hypothetical protein FLJ23132	5.10
30	428403	AI393040	Hs.326159	leucine rich repeat (in FLJ) Interactin	5.10
	430968	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	5.10
	431709	AF220185	Hs.267923	uncharacterized hypothalamus protein HT0	5.10
	436137	AI056769	Hs.133612	ESTs	5.10
	440948	AW188311	Hs.128619	ESTs	5.10
35	448497	BEB13269	Hs.21893	hypothetical protein DKFZp761N0624	5.09
	416655	AW988613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	5.09
	417228	AL134324	Hs.7312	ESTs	5.09
	424868	AI568170	Hs.98886	ESTs	5.08
	418905	BE539674		actinin, alpha 4	5.08
40	427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fs, clone L	5.07
	442618	R56222	Hs.28514	ESTs	5.06
	445715	AB012958	Hs.13137	UV radiation resistance associated gene	5.06
	406813	AW276131		ribosomal protein L13a	5.06
	454128	AL031259	Hs.41639	programmed cell death 2	5.05
45	440709	AW797724	Hs.130350	ESTs	5.05
	436372	AW972301	Hs.310286	ESTs	5.05
	446173	BE565849	Hs.14158	copine III	5.04
	453330	AI265081	Hs.342389	peptidylprolyl isomerase A (cyclophilin	5.03
	418876	AA740616		gb:ny97f11.s1 NCL_CGAP_GC81 Homo sapiens	5.00
50	408405	AK001332	Hs.44672	hypothetical protein FLJ10470	5.00
	410570	AI133095	Hs.84593	ATP synthase, H transporting, mitochondr	5.00
	410800	BE280421	Hs.94499	ESTs	5.00
	431451	AA761378	Hs.192013	ESTs	5.00
	432879	AW815932	Hs.173734	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.00
55	435655	AW106563	Hs.6947	HSPC069 protein	5.00
	435919	AI052189	Hs.114104	ESTs	5.00
	436394	AA531187	Hs.126705	ESTs	5.00
	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fs, clone PL	5.00
	442232	AI357813	Hs.337460	ESTs, Weakly similar to A47582 B-cell gr	5.00
60	442685	AB033017	Hs.8594	KIAA1191 protein	5.00
	444454	BE018316	Hs.11183	sorting nexin 2	5.00
	444670	HS8373	Hs.332938	hypothetical protein MGC5370	5.00
	447197	R36075		gbcyh88b01.s1 Soares placenta Nb2HP Homo	5.00
	450113	AI683098	Hs.200868	ESTs, Moderately similar to ALU7_HUMAN A	5.00
65	450511	R07423	Hs.85092	thyroid hormone receptor Interactor 11	5.00
	450887	AA011518	Hs.271778	ESTs, Weakly similar to B8022 hypothetical	5.00
	452056	AW959065	Hs.101150	Homo sapiens, clone IMAGE:4054156, mRNA,	5.00
	457068	X69391		ribosomal protein L6	5.00
	406793	AW264291	Hs.5662	guanine nucleotide binding protein (G pr	4.97
70	439864	AI720078	Hs.291937	ESTs, Weakly similar to A47582 B-cell gr	4.96
	420298	AI199510	Hs.267912	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.94
	440638	AI376551		gb:te64e10.x1 Soares_NFL_T_GBC_S1 Homo s	4.92
	400261			Eos Control	4.91
	414420	AA043424	Hs.76095	Immediate early response 3	4.90
75	415799	AA653718	Hs.225841	DKFZP434D193 protein	4.90
	434866	AF151103	Hs.112259	T cell receptor gamma locus	4.90
	449057	AB037784	Hs.22941	KIAA1363 protein	4.90
	448625	AW970786	Hs.178470	hypothetical protein FLJ22662	4.90
	451598	N28102	Hs.118078	ESTs	4.88
80	409686	AK000002	Hs.55879	Homo sapiens mRNA; cDNA DKFZp434L0827 (f	4.88
	410597	W16518	Hs.279518	amyloid beta (A4) precursor-like protein	4.88
	446291	BE397753	Hs.14623	interferon, gamma-inducible protein 30	4.86
	447150	AI439011	Hs.86386	myeloid cell leukemia sequence 1 (BCL2-r	4.85
	418453	AA332941	Hs.85226	lipase A, lysosomal acid, cholesterol es	4.85
	422627	BE336857	Hs.118787	transforming growth factor, beta-induced	4.84
	437186	AA336305	Hs.5472	hypothetical protein FLJ20173	4.84
	415825	Y18024	Hs.78877	inositol 1,4,5-trisphosphate 3-kinase B	4.84

	406781	AA639388		gb:ncq88b06.s1 NCI_CGAP_Co9 Homo sapiens	4.83
	449810	AB008681	He.23994	activin A receptor, type IIB	4.82
	410323	A1241708	He.296322	Homo sapiens cDNA: FLJ22844 fis, clone K	4.81
	444662	BE513613	He.11538	actin related protein 2/3 complex, subun	4.81
5	422340	AW296219	He.115325	RAB7, member RAS oncogene family-like 1	4.81
	400424	AJ276316	He.287374	zinc finger protein 304	4.80
	411573	AB029000	He.70823	KIAA1077 protein	4.80
	421045	BE144608	He.55533	ESTs	4.80
10	426235	AA353113	He.112497	Homo sapiens cDNA: FLJ22743 fis, clone H	4.80
	430387	AW372884	He.240770	nuclear cap binding protein subunit 2, 2	4.80
	438590	AA811465	He.123375	ESTs	4.80
	442071	BE048433	He.276043	ESTs	4.80
	449567	AI990790	He.188614	ESTs	4.80
15	453213	AA062650	He.6217	Homo sapiens cDNA FLJ12521 fis, clone NT	4.80
	440129	AA865818		ESTs, Weakly similar to S71886 Ste20-lik	4.78
	437802	AI475995	He.122910	ESTs	4.77
	409461	AA382169	He.54483	N-myc (and STAT) interactor	4.77
	421932	W51778	He.323949	kangal 1 (suppression of tumorigenitidy	4.74
20	428453	AB011110	He.164367	GTPase activating protein-like	4.74
	413441	AI929374	He.75367	Src-like-adaptor	4.74
	446560	AK001567	He.311002	Homo sapiens cDNA FLJ10705 fis, clone NT	4.73
	435641	AA687361	He.221318	ESTs	4.71
	410557	AA085803	He.192997	ESTs, Moderately similar to I78885 serin	4.70
25	412766	BE544475	He.54347	ESTs	4.70
	415526	N76536	He.265591	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.70
	418973	AA233056	He.191518	ESTs	4.70
	421433	AI829192	He.22380	ESTs	4.70
	432925	AA878324	He.254750	ESTs	4.70
30	438869	AF076009		gb:Homo sapiens full length Insert cDNA	4.70
	442233	AW967149	He.28439	ESTs, Weakly similar to I38022 hypotheti	4.70
	447196	D61523	He.283435	ESTs	4.70
	448552	AW973653	He.20104	hypothetical protein FLJ00062	4.70
	444681	AJ243937	He.288316	chromosome 6 open reading frame 9	4.66
35	414598	AI094221	He.135150	lung type-I cell membrane-associated gly	4.66
	447817	BE620775	He.4866	Homo sapiens cDNA FLJ14387 fis, clone HE	4.65
	416062	AA724811	He.334791	Homo sapiens cDNA FLJ14609 fis, clone NT	4.65
	406881	X66975	He.172550	polypyrimidine tract binding protein (he	4.64
	424582	AF026849	He.150922	BGS1 (yeast homolog)-like	4.64
40	411165	NM_000169	He.69089	galactosidase, alpha	4.63
	439905	AW997484	He.5003	KIAA0456 protein	4.63
	445776	NM_001310	He.13313	cAMP responsive element binding protein-	4.62
	424730	NM_003358	He.23703	ESTs, Moderately similar to CEGT_HUMAN C	4.62
	414747	U30872	He.77204	centromere protein F (350/400kD, mitosh	4.62
45	410668	BE379794	He.159651	hypothetical protein	4.61
	406774	AW518383	He.177592	ribosomal protein, large, P1	4.60
	406648	AA563730	He.277477	major histocompatibility complex, class	4.60
	407961	W77762	He.79815	antigen identified by monoclonal antibod	4.60
	415682	A347128	He.191870	ESTs	4.60
50	417621	AV654694	He.82316	interferon-induced, hepatitis C-associated	4.60
	419970	AW612022		ESTs	4.60
	420012	AW957965	He.99014	Homo sapiens, clone IMAGE3632168, mRNA	4.60
	431574	AW572659	He.261373	hypothetical protein dJ434014.3	4.60
	432586	AA568548		ESTs	4.60
55	437438	AL359620	He.14217	hypothetical protein DKFZp762P2111	4.60
	441365	AI822034	He.137097	ESTs	4.60
	444539	AI955765	He.146907	ESTs, Weakly similar to 2004389A chromos	4.60
	458965	AA010319	He.60389	ESTs	4.60
	406655	M21533	He.277477	major histocompatibility complex, class	4.60
60	414915	NM_002462	He.76391	myxovirus (influenza) resistance 1, homo	4.60
	414821	M83835	He.77424	Fc fragment of IgG, high affinity Ia, re	4.59
	423766	AA303799	He.300141	ribosomal protein L39	4.59
	451351	AW058261	He.321435	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.56
	450043	AA895899	He.24332	CGI-26 protein	4.56
65	447742	AF113925	He.19405	caspase recruitment domain 4	4.54
	433339	AF019226	He.8036	glioblastoma overexpressed	4.54
	426395	BE151985		hypothetical protein FLJ23316	4.53
	418300	AI433074	He.86682	Homo sapiens cDNA: FLJ21578 fis, clone C	4.53
	423799	AW026300	He.132906	19A24 protein	4.53
70	445093	A207197		ESTs	4.52
	428044	AA093322	He.301404	RNA binding motif protein 3	4.52
	453968	AA847843	He.62711	High mobility group (nonhistone chromoso	4.51
	414194	BE175494	He.75811	N-acetylsphingosine amidohydrolase (acid c	4.50
	427747	AW411425	He.180655	serine/threonine kinase 12	4.50
75	406745	AW511970	He.279860	tumor protein, translationally-controlled	4.50
	407013	U35637	He.83870	gb:Human nebulin mRNA, partial cds	4.50
	407198	H91679		gb:yv04a07.s1 Soares fetal liver spleen	4.50
	414546	AA353776	He.901	CD48 antigen (B-cell membrane protein)	4.50
	429587	AI675749	He.211608	nucleoporin 153kD	4.50
	436566	BE545586	He.278712	Homo sapiens cDNA FLJ11074 fis, clone PL	4.50
80	437634	AW293046	He.255158	ESTs	4.50
	438971	W32474	He.301748	RAP2A, member of RAS oncogene family	4.50
	442485	BE092285	He.29724	hypothetical protein FLJ13187	4.50
	445873	AA250970	He.251948	poly(A)-binding protein, cytoplasmic 1-I	4.50

	450497	H64159	Hs.15328	ESTs	4.50
	417497	AW402482	Hs.82212	CD53 antigen	4.50
	447667	AL117611	Hs.19150	Homo sapiens mRNA; cDNA DKFZp564A2164 (f	4.49
5	413856	D13639	Hs.75586	cyclin D2	4.49
	419556	U29615	Hs.91093	chitinase 1 (chitinoliosidase)	4.49
	429617	X89984	Hs.211563	B-cell CLL/lymphoma 7A	4.48
	427157	U51166	Hs.173824	thymine-DNA glycosylase	4.48
	446021	BE389213	Hs.286	ribosomal protein L4	4.47
10	413822	R08950	Hs.272044	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.46
	412819	T25829	Hs.24048	FK506 binding protein precursor	4.46
	448717	R67419	Hs.21851	Homo sapiens cDNA FLJ12900 fis, clone NT	4.45
	401846			NM_000988*:Homo sapiens ribosomal protei	4.44
	422303	AW410382	Hs.27556	hypothetical protein FLJ22405	4.43
	442358	BE567985	Hs.18585	ESTs, Moderately similar to ALU4_HUMAN A	4.43
15	436623	AI417073	Hs.107285	ESTs	4.42
	412146	M92444	Hs.73722	APEX nuclease (multifunctional DNA repai	4.42
	437042	AK000702	Hs.5420	hypothetical protein FLJ20695	4.42
	416754	H07145	Hs.6799	ESTs, Weakly similar to T12483 hypotheti	4.41
20	436671	AW137159	Hs.183291	ESTs	4.40
	410079	U94362	Hs.58589	glycogenin 2	4.40
	420150	AA648712	Hs.29798	KIAA1712 protein	4.40
	424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3(h	4.40
	428931	AA994979	Hs.98967	ATPase, H(+)-transporting, lysosomal, non	4.40
25	429109	AL008637	Hs.186352	neutrophil cytosolic factor 4 (40kD)	4.40
	430280	AA361258	Hs.237868	Interleukin 7 receptor	4.40
	438330	AW450572	Hs.257316	ESTs	4.40
	438962	BE046594		gbcln41c11.x1 NCLCGAP_RDF2 Homo sapiens	4.40
	444794	AI419991	Hs.145225	ESTs	4.40
30	445100	AW186205	Hs.12311	Homo sapiens clone 23570 mRNA sequence	4.40
	449659	R60031	Hs.188899	eukaryotic translation initiation factor	4.40
	449832	AA694264	Hs.60049	ESTs	4.40
	452404	AW450675	Hs.212709	ESTs	4.40
	447296	AW243614	Hs.18063	Homo sapiens cDNA FLJ10768 fis, clone NT	4.39
35	425097	NM_014247		PDZ domain containing guanine nucleotide	4.37
	441607	NM_006010	Hs.7912	neuronal cell adhesion molecule	4.37
	405742	AI468091	Hs.279860	tumor protein, translationally-controlled	4.36
	425095	AW014160	Hs.182585	KIAA1276 protein	4.34
	410342	R31350	Hs.743	Fc fragment of IgE, high affinity 1, rec	4.34
40	442333	AI650877	Hs.129302	ESTs	4.33
	424971	AA479005	Hs.154036	tumor suppressing subtransferable candid	4.32
	415912	H08859	Hs.206469	ESTs, Weakly similar to ALU6_HUMAN ALU S	4.32
	437386	W52452		ribosomal protein L10	4.31
	408558	AW015759	Hs.235709	Homo sapiens mRNA; cDNA DKFZp667B0711 (f	4.30
45	408875	NM_015434	Hs.48804	DKFZP434B168 protein	4.30
	409604	AW444448	Hs.49124	ESTs	4.30
	418866	T65754		gbcyc11c07.s1 Stratagene lung (937210) H	4.30
	419423	D26488	Hs.90315	KIAA0007 protein	4.30
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	4.30
50	422797	AB033064	Hs.236463	KIAA1238 protein	4.30
	428457	AK002121	Hs.184465	hypothetical protein FLJ11259	4.30
	432293	AK001099	Hs.274273	Homo sapiens cDNA FLJ10237 fis, clone HE	4.30
	434551	BE387182	Hs.280658	ESTs, Highly similar to A35661 DNA excis	4.30
	436138	H53323	Hs.25717	Homo sapiens cDNA: FLJ23454 fis, clone H	4.30
55	438915	AA280174	Hs.285681	Williams-Beuren syndrome chromosome regi	4.30
	449217	AA278535	Hs.23262	ribonuclease, RNase A family, k6	4.30
	452994	AW962597	Hs.31305	KIAA1547 protein	4.30
	418883	BE387036	Hs.1211	acid phosphatase 5, tartrate resistant	4.30
	437250	BE257342	Hs.94576	hypothetical protein MGC3062	4.29
60	440910	H97875	Hs.117974	ESTs	4.29
	406853	AA514553	Hs.252259	hypothetical protein FLJ23059	4.28
	432295	BE091049	Hs.343665	ribosomal protein S15a	4.28
	400244			Eos Control	4.28
	413518	BE149455	Hs.75415	beta-2-microglobulin	4.28
65	409132	AJ224538	Hs.50732	protein kinase, AMP-activated, beta 2 no	4.27
	406746	AA580995	Hs.279860	tumor protein, translationally-controlled	4.26
	400395	AF111167		v-fos FBJ murine osteosarcoma viral onco	4.26
	443229	AI057129	Hs.133396	ESTs	4.26
	450201	T97838	Hs.25722	ESTs	4.25
70	409636	AA305729	Hs.18272	amino acid transporter system A1	4.25
	422082	AA016188	Hs.111244	hypothetical protein	4.24
	444099	D87432	Hs.10315	solute carrier family 7 (cationic amino	4.24
	453902	BE502341	Hs.3402	ESTs	4.24
	415189	L34657	Hs.78146	platelet/endothelial cell adhesion molec	4.22
75	404854			Target Exon	4.21
	406653	AA574074	Hs.77961	major histocompatibility complex, class	4.20
	400440	X83957	Hs.83870	nebulin	4.20
	415049	N67334	Hs.50158	ESTs	4.20
	418304	AA215702		gbczr97g10.r1 NCLCGAP_GCB1 Homo sapiens	4.20
80	423180	AF068902	Hs.125031	choline/ethanolaminephosphotransferase	4.20
	424584	AW752714	Hs.5174	ribosomal protein S17	4.20
	429412	NM_005235	Hs.2407	POU domain, class 2, associating factor	4.20
	438141	AW946871		gbcRC2-ET0022-080500-012-d02 ET0022 Homo	4.20
	438607	AW080237	Hs.252884	ESTs	4.20

5	451952	AL120173	Hs.301663	ESTs	4.20
	455397	AW936332		gb:QV4-DT0021-281299-070-g01 DT0021 Homo	4.20
	417116	Z43916	Hs.7634	hypothetical protein FLJ12287 similar to	4.19
	453247	T80198	Hs.111806	ESTs	4.19
	430451	AA836472	Hs.297939	calthepsin B	4.19
	414283	AW960011	Hs.154993	ESTs	4.18
	452248	AA093668	Hs.28578	muscleblind (Drosophila)-like	4.18
	450746	D82673	Hs.278589	general transcription factor II, I	4.16
10	444797	AB018333	Hs.12002	KIAA0790 protein	4.18
	445718	H79791	Hs.15227	ESTs	4.15
	425783	AI026740	Hs.1948	ribosomal protein S21	4.15
	414837	U24266	Hs.77448	aldehyde dehydrogenase 4 family, member	4.15
	406710	AI708347	Hs.184014	ribosomal protein L31	4.15
15	424436	AW818428	Hs.4953	golgi autoantigen, golgin subfamily a, 3	4.14
	422343	AI628633	Hs.346823	gb:ly77d05.x1 NCJ_CGAP_Kid11 Homo sapien	4.13
	416207	NM_014745	Hs.79077	Homo sapiens, clone MGC:2908, mRNA, comp	4.13
	406724	C14071	Hs.234518	ribosomal protein L23	4.12
	449475	AJ348027	Hs.108557	hypothetical protein PP1057	4.12
20	413828	L19067		v-rel avian cellcarcinoembryofectoma viral	4.11
	416819	U77735	Hs.80205	plm-2 oncogene	4.11
	436674	AA725002	Hs.272018	low molecular mass ubiquitinone-binding pr	4.11
	405266			Target Exon	4.10
	408995	AJ978168	Hs.344096	glycoprotein (transmembrane) nmb	4.10
25	410704	BE076754		gb:CM1-BT0601-180200-121-b10 BT0601 Homo	4.10
	420651	AA281062	Hs.28493	hypothetical protein FLJ20142	4.10
	423096	AA732684	Hs.278428	progesterone induced protein	4.10
	428328	AA426080	Hs.292812	ESTs, Weakly similar to I38022 hypothetl	4.10
	429355	AW973253	Hs.292689	ESTs	4.10
30	433308	AA582718	Hs.291650	ESTs	4.10
	443559	AI076765	Hs.269899	ESTs, Moderately similar to ALU8_HUMAN A	4.10
	450650	AA648886	Hs.151999	ESTs	4.10
	453785	AJ682236	Hs.283732	ESTs, Moderately similar to ALU1_HUMAN A	4.10
	406864	AA613706	Hs.252259	ribosomal protein S3	4.10
35	410768	AF038185	Hs.55187	Homo sapiens clone Z3700 mRNA sequence	4.09
	415612	AI98267	Hs.110613	KIAA0421 protein	4.09
	434203	BE262677	Hs.283558	hypothetical protein PRO1855	4.08
	439237	AW408158	Hs.318893	ESTs, Weakly similar to A47582 B-cell gr	4.08
	441374	AA043696	Hs.7822	Homo sapiens mRNA; cDNA DKFZp564C1216 (f	4.08
40	443415	AI056523	Hs.133472	ESTs	4.08
	424338	W78816	Hs.49943	ESTs, Weakly similar to S65657 alpha-1C-	4.07
	422305	AI928242	Hs.283438	ESTs, Highly similar to AF198488 1 trans	4.07
	400233			Eos Control	4.06
	421959	AW751497	Hs.98370	cytochrome P450, subfamily IIS, polypept	4.06
45	442622	NM_000435	Hs.8546	Notch (Drosophila) homolog 3	4.06
	424795	AW102850	Hs.153177	ribosomal protein S28	4.05
	446231	NM_002163	Hs.14453	interferon consensus sequence binding pr	4.05
	452933	AW391423	Hs.288555	Homo sapiens cDNA: FLJ22425 fls, clone H	4.05
	427681	AB018263	Hs.180338	tumor necrosis factor receptor superfamily	4.05
50	409061	AI204994	Hs.7874	Homo sapiens cDNA: FLJ21435 fls, clone C	4.03
	413891	BE271020		tumor suppressor deleted in oral cancer-	4.03
	414004	AA737033	Hs.7155	ESTs, Moderately similar to Z115357A TYK	4.02
	417035	AA192455	Hs.22958	Homo sapiens clone IMAGE:451938, mRNA se	4.02
	410584	AB011112		KIAA0540 protein	4.01
55	417353	AA375752	Hs.348140	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	4.00
	423645	AI215632	Hs.147487	ESTs	4.00
	430048	T65064	Hs.73605	ESTs	4.00
	431113	AK000673	Hs.274337	hypothetical protein FLJ20666	4.00
	434170	AA628509	Hs.122329	ESTs	4.00
60	434584	D57341	Hs.188361	Homo sapiens cDNA FLJ12807 fls, clone NT	4.00
	435391	AA704588	Hs.58534	ESTs	4.00
	446768	AV660306	Hs.110286	ESTs	4.00
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	4.00
	451831	NM_001674	Hs.460	activating transcription factor 3	4.00

TABLE 56B

Pkey: Unique Eos probe/identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Pkey CAT Number Accession

438091 22448_1 AK054860 AV652198 AV652192 AV652138 AV652127 AV652194 BE935919 AV652017 AV651995 AV651548 AV646083 AV651985 AV646184
 AV646179 AW880409 AA345002 BF155189 BE968931 X56197 AL603014 AW953629 BM263546 BE550772 AA701084 AI681352 AA358889
 AW938841 BF438147 W05391 H75313 BF326185 AV646335 AV651589 AV646340 AV651992 AV646384 AV646364 AV687497 BF155183
 AV646370 AW797876 AI906821 X56196 BE833835 AA628440 BE833808 BF224205 AA709128 BE673807 AI923886 AA947032 AI276125 AI185720
 AW510698 AA987230 BE467708 AW898628 AW898644 AI146984 AW043642 AI288245 AI186932 AI635262 AI139455 AI298739 AI813954
 AI024768 BE699445 BE699444 AI707807 D52654 AI214518 AI004723 AI698085 AW087420 AI565133 AA845571 AW898622 BF110144 AW513280
 AI061126 BF352770 AI268939 AI435818 BF476318 AI024767 BE174213 AA757598 AA513019 AA902959 AI860794 AI334784 BF108411
 BM310532 AW513771 AI951391 AI337671 BF095606 BF095601 BF095468 AW890091 BF095753 AW243400 AW898607 AW898616 BF362762
 AI922204 AW898625 BE699468 BE174196 AW102923 D52715 BE699468 D52477 D55017 BF956933 BG623583 AV646254 AA463522 BI003244
 AI299190 W40186 BE174210 BF939091 BF434180 AW579001 T55662 H01811 T52522 BF945037 BF955938 D54679 D53933 R67100 BG925552

			BF999056 R83430 Z29922 TB5791 W03942 H63289 A1091537 BF086583 AA345570 H48870 H80720 T83523 B1039626 B1037700 R00353 BF155184 N98343 N78072 H01812 T55581
429978	35194_2		BE738425 BE738323 BM126944 AW629678 AW265195 A1916735 A1394255 A1573090 A1354442 AW612857 A1339558 A1919424 A1377532 A1354441 A1308821 AA772275 AW055215 A1589706 A1336532 AA806647 AV82125 H93575 AW071172 AW769904 A1863985 AW265018 AW196655 D79662 BE042393 N75017 AW014741 C75509 BE748621 H92431 AW079261 AW901780 AA329482 AW960115 B1260621 A1767625 R31663 B1918654 AW963196 C06195 A1678018
5			AK056685 BG399272 AA187835 BF821903 AV660550 AV660556 AV660502 BG564397 BE379584 BF446961 A1653056 AW973709 A1853173 BG054997 A1266043 B1064879 A1658750 A1492830 AW021142 A1722184 A1710066 A1082443 A1167921 D59940 B1492088 H74180 AW130886 A1348677 A1278577 AA761517 A1698203 AA115535 A1264790 AW205074 AA860452 AA554902 A1000715 D62102 BE544768 A1376090 D59939 AW242249 AA525421 R34211 R34328 BF248064 BF241437 BF572759 BF218832
10	412636	1438_1	M77830 NM_004415 AF139065 BG681115 BG740377 B1712964 BG000656 AA128470 B1438324 H27408 BE931630 BE167165 AW370827 AW370813 J05211 BG688865 BG740734 BG680618 BG739778 B1765807 BM353403 BM353248 AW177784 AW205789 AW951576 AWB48592 BE182164 BF149266 BE940187 B1060445 B1060444 BF350983 BE720095 BE720069 BE716154 BE082584 BE082576 BE004047 AA857316 B1039774 BE713818 BE713549 AW170253 BE160433 B1039775 AW86475 BM462504 BE931734 BF149264 AA340777 BF381183 BG621737 A1127260 AW364859 BF993352 BG223489 BE819009 BF381184 BE715956 R58704 AA852212 AW366566 B1090358 BF087707 BEB19046 BE819005 AA377127 BE073467 BE819069 BE819048 B1036306 BG990973 B1040954 BF199111 A1140155 A1951766 A1434518 AWB04674 BF762969 BE837009 BE925826 BF149265 AW995615 BE814264 B1039782 A1140407 BE144243 BE709863 BF985642 BE001923 BF933510 AW265328 BG436319 BE182166 AW365176 AW847688 BE818280 AW177933 BF873679 AW178000 BE082526 BF476886 BF086994 BF592276 BE082507 BE082514 BE082505 BF873593 AW088840 AW846778 BF804153 AW365157 BE813930 BE002030 AW365153 BE184941 BF749421 BE184920 BF83582 BE184933 BF842254 BE698470 BE931048 BF999889 BF368816 BE184924 BE159646 BE714632 BE184948 BG988845 AA131128 AA099891 W39488 C04715 BF098124 BE855341 AW799304 AL603116 BE149760 BE705967 BE705966 BE705958 AW848723 AW376699 AW376817 AW376697 AW360507 BF751115 BE695084 AWB48371 AW376782 AW848789 AW849074 AW361413 BF927725 BF094211 AW997139 BE885474 BE185187 BE156621 BE716089 BE713297 BE713298 BE179915 AW799309 BF872345 BF086576 BE705939 AW752599 BG005197 BF350086 BE715196 BE715155 BF752396 BF093817 BF831190 BF752409 BE006561 BG058922 BF094833 BF094748 BF094583 AW377699 AW607238 BE082519 AW377700 BF349467 A1190590 A1554403 A1392926 A1158477 B1467252 A1158919 A1768816 BF082516 A1439101 AA451823 A1340326 A1590975 B1791553 A1070963 A1142882 AA039975 AA946936 AA644381 BM314884 AA702424 A1471612 AW190555 A1220573 A1304772 A1270345 A1627383 AA552300 A1911702 AW166807 A1346078 W85070 A1489191 AA026864 A1830049 AW780435 A1078449 A1819984 A1858282 B1486888 A1860594 A1025932 AA026047 AA703232 AA658154 AA515500 AW192085 AA918281 T77661 A1827207 A1205263 BF082491 AW021347 A1568068 BE939862 AA088866 D12062 AA056527 AA782109 W19287 W02156 AW150038 AA022701 T87181 H44405 A1910434 BF082513 A1494069 A1270027 A1635878 AA128330 BG681425 BE706078 R20904 BG680059 BG676647 BF764409 AA026654 A1745630 B1762796 BG287391 AW798780 BE706045 BE926470 AW799118 BF087936 BE002273 AW879451 A1571075 BE067788 AV721320 A1022652 N29754 C03378 N84767 AA131077 H30146 BE714290 A1666869 A1688892 A115596 AW106614 A1887258 A1538877 BE926474 BE067737 BG319485 AA247685 AW798883 AW103521 BF989173 AW860878 BE939707 BE185750 BE714064 BE713903 BE713868 BE713763 BG960164 BE713810 AW365151 BG955489 BE005272 BF915937 AW365148 A1055927 BF992760 AW853812 BG954443 B1770853 BG679406 BG740832 BG681087 BG688430 AA455100 T87267 BE695209 BE696210 B1089483 BE006273 BE872225 AW381912 BE925515 BG677012 BG741970 AA026480 BE706999 BG677157 BE009090 BG681378 BE712291 BG961488 BG678984 B1040941 AW363270 AW384371 AW847442 B1088669 BE813665 W95048 W25458 AW177786 AA025851 BE931733 BF154837 BG949393 BE714441 AW962435 BE711601 A1284090 BE064323 BE719390 BE940148 BG991212 BF375714 BF349522 BG956267 T48793 B1013292 BE001925 AW385155 AW365154 AW806653 BF763109 BE931637 BE167181 BE713879 BF354008 BF678726 H08899 AW365145 W38362 A1499487
40	413787	7612_1	BC003047 S80794 NM_008406 X78138 AY007132 L08439 AW340648 AW131665 A1082748 A1470204 B1711078 BF350700 B1495963 A1087141 AA720684 AAB62331 AA605146 BM313650 A1089749 A1359738 N69107 AW995424 A1086917 A1083995 AW340217 N99662 A1829449 A1089839 A1608761 A1342365 A1195076 AA908944 A1248943 A1160053 A1191245 A1218477 A1077943 AA564930 A1310394 AAB72478 A1279782 W61343 AA565955 W46596 AA126874 AA223241 AA491574 R84813 AA491520 BG056114 AA489689 BE464550 AW664539 H67097 AL534332 C21397 A1085941 AW026427 BG939820 A1697089 A1039008 A1125315 A1655561 AW150042 L20422 X57345 B1458375 A1142662 B1666601 BE888276 A1119302 B1603754 BG706553 B1598754 BE256713 BG002538 BF951911 N29226 BE909424 AV689274 AV689116 AV708195 AA127798 A124697 D54224 F08031 AA340253 BF923383 BM467808 B1546644 BG777200 BG705941 BG468577 A1127209 AW403970 B1597630 B1458091 AV689560 B1668267 BG508219 B1837163 B1667275 AA343750 BE783112 BF671405 BF954720 H67636 H69456 AA484894 B1869271 BF998207 N31547 BF945817 BF947918 N80830 BG880194 AA156681 B1493502 AW273118 A1473820 AA608688 A1355337 AV712091 AA084101 BF592033 H13301 A1854305 AA505883 A1423863 AW084401 A1917740 R69868 AA033631 N79982 BE885276 A1635674 AA096126 A1700018 AV707753 A1082545 A1145681 AA629032 A1421367 AA740589 AA150830 A1248541 AA988608 AA150478 W65437 BM310234 AA262704 T28031 A1811116 BM272753 H21979 T15405 AA939406 F04963 A1882296 AW156269 AA905196 BG223568 A1831016 A1766457 A811102 AA778573 A1822133 AA775858 A1261476 AA219489 A1686035 A1672093 BE537084 AW189078 D82530 A123121 AL583492 BG350791 R65901 W65436 BE155392 B109081 BE155394 A1120538 AW166100 A1359620 A174338 N20527 W47413 AA156615 A1272249 H25293 BE614558 H68864 AW383484 H78021 H11617 R58892 H23204 N21530 R82489 AW383522 AA774536 AL534331 W94127 W46459 A1866231 AA513281 AA192468 H69844 W85627 AW383642 AW383528 AA171496 AL537424 BE814868 BF823254 R82553 A1089817 A1559406
50	410143	MH1244_8	AK000357 A1571830 AA579613 AA668790 BF939495 BF196886 A1860982 BF591561 A1809189 AW410232 BF739789 A1144332 BF438721 A107495 A1423359 N52503 BE855784 N94367 A1023931 AA563662 A1744624 A1221298 A1299523 A1299520 A1299522 AW664938 AA970424 AAB79079 AA622643 AW195955 AA470473 AW392767 A1218127 AAB73430 AA906005 AA748160 H89523 AA103882 A100252 AW664938 AA970424 AAB79079 A1581622 A1361357 AA468498 AW008684 AA903275 A1187724 A187718 AA880505 BF092771 A1066555 BE714172 BG289028 AW080390 BE001197 BF132049
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70	450377	12109_1	AB033091 AL520743 BE811813 N53332 N99716 A1581910 AA280655 BE710392 AV705100 AW293978 AW444566 AA281459 A1679751 A1873695 BG700891 B1553517 R80518 BG779771 BG534451 AA479402 AW861580 BF081430 A1857643 A1768486 AW512118 AA478302 AW770384 AW072470 A1041596 A149699 AW592685 AA976261 BE879747 BG114119 AW183811 AA909939 BF571621 BF360794 BF361375 BE925899 AL050284 BC010371 BF882270 AL042656 BF095732 AW812618 BF095731 BG212397 BF678765 B1038602 BG388664 AW675337 BG289398 BE939598 AW806570 AA527097 AW150540 A1693720 AA743384 A1915793 N48185 A1573107 AA043474 A1351615 A1958490 A1910763 R50866 A1699181 N73808 H08164
75	425996	138046_1	BM006551 AA367152 AW953705 A1631833 AW237429 AW027804 AA729039 BE503409 A1521935 BF739953 AA702982 AA557633 AA780065 A1218139 AW194264 D20120 A1082715 A1369980 BE857686 BE326711 AW953706 A1393749 A1383821 W07189 A1431768 A1796526 A1521794 A1796380 AW117545 A1749657 A1537634 N50122 AW973352 BF222929 AW016853 BF058130 A1651829 BE551767 AA558414 A1339359 BF058601 A1961162 A1341422 A1208248 A1206165 AA548736 AA768578 A1539081 AW025567 AA736837 N78575 AW694357 AA480892
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			AA969444 AI080438 AA552500 AW237538 AA481080 AI246378 AA566227 AA398921 AA207051 AA721378 BF438608 AI086295 AI886630 AA904112 AI086458 AW271985 AW078688 AA725342 BF326598 AA843572 AI082535 AA766664 AI453279 AA435673 AI619515 AA879080 AA234592 AA890223 AA765824 BI258822 AA393631 AW968840 BE940639 T83865 BE762742 AW897470 W05089 N41323 T87376 R65544 H88711 BI087136 BE177661 H06215 BE144709 BE144829 AA947566 AK074047 AI144342 AW014280 BM145128 N28267 AW206231 AA989041 H93197 AW594063 BG236296 AW235606 AW081031 AA765843 BM144372 AA889341 AI824638 AI963970 AI637671 AW196330 BG427526 BM148789 BF893644 BF881946 BF090249 AW954947 AW890487 AI305236 D60845 D60537 AA825429 W36294 AW890410 AW088235 BF740240 AA448709 AI350279 AA879119 AA319510 BE702077 BE689015 BE702046 AW901293 T99319 D81708 BF475488 D60383 D81751 BE689260 BE005398 AA628622 AA994155 AA662701 AA633929 AA737416 BG427950 AA826016 AI903441 BG939868 AW979154 AA640872 BG547134 AA457091 AW368860 W88852 R94779 AA088823 BM475665 BE644917 AW770789 AW952971 N64863 BM263259 AI224545 AI184866 N69114 AW518902 AI440169 AA809472 AV654440 AA281642 AU185230 AW337382 AI872923 AI537113 N73882 T83378 H63731 BF671784 AW897824 AI811204 AA344646 BE009112 BG899664 H91240 R60548 N41701 BM476120 BE672181 AI697653 AA98187 AI280879 AW340123 AI912727 AI081775 AI089556 AI191349 AI871604 AI631607 AI890800 AI701917 AW771624 AA663041 AI991576 AI160622 AA771763 BE089784 BE089788 AI222942 AW418516 AA329211 AI095736 BE550294 AA738345 BE218683 BE670548 BG149505 BF061776 D19821 BE005786 BE178892 BE005728 BF841237 BE005648 R27634 AW954733 AA315006 AWB56665 AL047566 AA393792 AI670731 AI037957 AW674364 AI038137 N62286 AI241379 BE501096 AW090696 AI927369 AI669226 AI369437 AI371075 AW612409 AI686711 AI183269 AA477177 AI078122 AA635190 AA790984 AA781508 D81020 BF575223 AI356183 D79312 AI375558 H61111 BG283489 BE090666 BE090664 BE090662 H26545 AI184717 AW518883 AF121173 AK001838 AU135179 AU134241 AV651702 AV650032 AV651304 AV650101 AV651263 AV651888 AV651866 AA628554 AV651355 AV651174 AV651172 AW656145 AU117599 AU135385 BG254665 AA165919 BG483981 AW809606 BG494194 AA622011 AI676156 AA687804 AI701729 AU133725 AW961387 AU144387 AU151757 AA551031 BE675412 N34769 AA713483 AI890079 AI588918 AI361889 AI209020 AA668981 AI240990 AA741144 AA490899 AI200221 AW589574 W96201 BG154182 AV655159 AA328145 N36348 AI081357 N76715 AA693346 AA742488 AI269719 AA897483 AI886459 AU155873 H04255 AW243986 AA557748 AI286227 R68891 R33453 AW388097 AA908472 U09414 NM_Q03438 AA503545 AI022449 AA043458 AA766074 AA765442 AA805052 AI028211 AW609708 AW502394 AA828822 AI982587 BE072881 AI762181 BE072946 AA568565 AA555499 AI360576 AW204069 AA991848 AA864939 BM310925 AA426110 BM310629 BF434286 AW015091 BF476996 AW118867 BE575185 AI688588 AI453594 AW590589 AI652425 AI827969 BF056946 AI802866 AI393360 AI476224 AW590639 AW136271 AI458252 AI524726 AA843768 AA782158 AI336058 AI087532 AW461563 AA459408 AA59633 AA418444 W23607 BG940150 AI493445 AW054729 AI221829 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		AA830462

TABLE 56C

Pkey:	Unique number corresponding to an Eos probe set
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) Nature 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
NL_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
402474	7547175	Minus	53526-53628,55755-55920,57530-57167
402145	8018280	Plus	113086-114800
401091	9958240	Plus	94780-94898
401466	6682292	Plus	28748-29023
401113	9966541	Minus	19419-19959
406542	7711498	Plus	117335-118473
405088	8072509	Plus	73684-73841,74081-74217,74510-74779,7492
401846	7712190	Minus	82775-82823,82912-83022
404854	7143420	Plus	14260-14537
405266	4156171	Minus	63337-63552

TABLE 57A: 703 genes upregulated in testicular cancer relative to normal body tissues

Table 57A lists about 703 genes upregulated in testicular cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probe sets on the Eos/Affymetrix Hu3 Genechip array. Gene expression data for each probe set obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of having oncogenic function or of transducing intracellular signals, or of being modifiable by small molecules, peptides, or antibodies (e.g. kinase, death-domain, 7tm, phosphatase, or ion transporter). Certain predicted protein domains are noted.

	Pkey:	Unique Eos probeset identifier number
	ExAccn:	Exemplar accession number, GenBank accession number
	UniGeneID:	UniGene number
5	Pred.Prod.Domains:	Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
	UniGene Title:	UniGene gene title
	R1	95th percentile of testicular cancer AIs divided by the 50th percentile of normal tissues AIs, where the 10th percentile of all normal tissue AIs was subtracted from both the numerator and denominator
10	Pkey; ExAccn; UniGeneID; UniGene Title; Pred.Prod.Domains; R1	
		424687; J05070; Hs.151738; matrix metalloproteinase 9 (gelatinase B, 92kD gelatinase, 92kD type IV collagenase); matrix metalloproteinase 9 (gelatinase B; 31.23
		440119; AA065455; Hs.125331; ESTs, Moderately similar to unknown (H.sapiens); ESTs, Moderately similar to unknown (H.s; 27.37
15		421241; X91817; Hs.102866; transketolase-like 1; transketolase-like 1; 26.89
		431840; AA534908; Hs.2860; POU domain, class 5, transcription factor 1; POU domain, class 5, transcription factor; 25.03
		435918; AF263536; Hs.86232; growth differentiation factor 3; growth differentiation factor 3; 19.88
		432686; AW204069; Hs.351118; ESTs, Weakly similar to unnamed protein product (H.sapiens); ESTs, Weakly similar to unnamed protein; 17.74
		419556; U29615; Hs.91093; chitinase 1 (chitinotrioseidase); chitinase 1 (chitinotrioseidase); 17.64
20		452838; U65011; Hs.30743; preferentially expressed antigen in melanoma; preferentially expressed antigen in melanoma; 17.06
		417896; AA214684; ; ESTs; ESTs; 15.96
		412266; AA101325; Hs.86154; hypothetical protein FLJ12457; hypothetical protein FLJ12457; 15.93
		425572; AB011076; Hs.158307; undifferentiated embryonic cell transcription factor 1; undifferentiated embryonic cell transcript; 15.82
		423905; AW579960; Hs.135150; lung type-I cell membrane-associated glycoprotein; lung type-I cell membrane-associated gly; 15.11
25		419741; NM_007019; Hs.93002; ubiquitin carrier protein E2-C; ubiquitin carrier protein E2-C; 15.08
		427584; BE410283; Hs.179718; v-myb avian myeloblastosis viral oncogene homolog-like 2; v-myb avian myeloblastosis viral oncogene; 14.17
		418696; AW359433; Hs.326290; hypothetical protein FLJ12581; hypothetical protein FLJ12581; 13.58
		416819; U77735; Hs.80205; pim-2 oncogene; pim-2 oncogene; 13.20
		414034; UB9277; Hs.305985; early development regulator 1 (homolog of polyhomeotic 1); early development regulator 1 (homolog o; 12.93
30		464077; AC005952; Hs.37082; insulin-like 3 (Leydig cell); insulin-like 3 (Leydig cell); 12.90
		432730; AIO66520; Hs.131358; ESTs; ESTs; 12.84
		446293; AJ420213; Hs.148722; LIM domain transcription factor LIM-1 (hLIM-1) mRNA; LIM domain transcription factor LIM-1 (h; 12.74
		423854; AB011130; Hs.127436; calcium channel, voltage-dependent, alpha 2/delta subunit 2; calcium channel, voltage-dependent, alpha; 12.46
		450581; AF081513; Hs.25195; TGF-beta 4; TGF-beta 4; 12.42
35		450719; AIO98837; Hs.21349; ESTs, Weakly similar to RBBB_HUMAN RAS-RELATED PROTEIN RAB-8B (H.sapiens); ESTs, Weakly similar to RBBB_HUMAN RAS-R; 12.26
		431462; AW583672; Hs.256311; granin-like neuroendocrine peptide precursor; granin-like neuroendocrine peptide precu; 11.96
		431354; BE046956; Hs.251673; DNA (cytosine-5)-methyltransferase 3 beta; DNA (cytosine-5)-methyltransferase 3 be; 11.91
		402199; ; Target Exon; Target Exon; 11.85
		424578; AK001973; Hs.150690; hypothetical protein; hypothetical protein; 11.81
40		416350; AF188625; Hs.189507; phospholipase A2, group IID; phospholipase A2, group IID; 11.67
		439979; AV600291; Hs.6823; hypothetical protein FLJ10430; hypothetical protein FLJ10430; 11.57
		410048; W76467; Hs.343874; proline oxidase homolog; proline oxidase homolog; 11.42
		442573; H93366; Hs.7567; branched chain aminotransferase 1, cytosolic; branched chain aminotransferase 1, cytos; 11.42
		414812; X72756; Hs.77367; monokine induced by gamma interferon; monokine induced by gamma interferon; 11.38
45		421917; AB028943; Hs.109445; KIAA1020 protein; KIAA1020 protein; 11.15
		440006; AK000517; Hs.6844; NALP2 protein; PYRIN-Containing APAF1-like; NALP2 protein; PYRIN-Containing APAF1-I; 10.92
		414683; S78298; Hs.76888; hypothetical protein MGC12702; hypothetical protein MGC12702; 10.91
		423673; BE003054; Hs.1695; matrix metalloproteinase 12 (macrophage elastase); matrix metalloproteinase 12 (macrophage; 10.74
		433800; AIO34361; Hs.135150; lung type-I cell membrane-associated glycoprotein; lung type-I cell membrane-associated gly; 10.68
50		429120; AK001673; Hs.196530; hypothetical protein FLJ10811; hypothetical protein FLJ10811; 10.48
		444371; BE540274; Hs.239; forkhead box M1; forkhead box M1; 10.46
		441553; AA281219; Hs.121296; ESTs; ESTs; 10.37
		426534; U58096; Hs.2061; testis specific protein, Y-linked; testis specific protein, Y-linked; 10.28
		441878; AIO01868; Hs.127982; ESTs; ESTs; 10.06
55		432117; AL036195; Hs.2909; protamine 1; protamine 1; 10.01
		425427; AIO52662; Hs.317432; branched chain aminotransferase 1, cytosolic; branched chain aminotransferase 1, cytos; 9.97
		416201; AA467752; Hs.195161; ESTs; ESTs; 9.97
		410929; H47233; Hs.30643; ESTs; ESTs; 9.91
		427486; AA974433; Hs.352432; fibroblast growth factor 4 (heparin secretory transforming protein 1, Kaposi sarcoma oncogene); fibroblast growth factor 4 (heparin secr; 9.81
60		427239; BE270447; Hs.356512; ubiquitin carrier protein; ubiquitin carrier protein; 9.68
		402680; ; Target Exon; Target Exon; 9.68
		409208; Y00093; Hs.172631; Integrin, alpha X (antigen CD11C (p150), alpha polypeptide); Integrin, alpha X (antigen CD11C (p150); 9.46
		443426; AF088158; Hs.9329; chromosome 20 open reading frame 1; chromosome 20 open reading frame 1; 9.42
		440207; AIO371978; Hs.128328; ESTs; ESTs; 9.41
65		433001; AF217513; Hs.279905; clone HQ0310 PRO0310p1; clone HQ0310 PRO0310p1; 9.41
		447534; AW953935; Hs.288655; ESTs; ESTs; 9.33
		442333; AIO50877; Hs.129302; ESTs; ESTs; 9.28
		421307; BE539976; Hs.103305; Homo sapiens mRNA; cDNA DKFZp434B0425 (from clone DKFZp434B0425); Homo sapiens mRNA; cDNA DKFZp434B0425 (f; 8.24
		423458; AIO24212; Hs.351113; ESTs; ESTs; 9.23
70		431958; X63629; Hs.2877; cadherin 3, type 1, P-cadherin (placental); cadherin 3, type 1, P-cadherin (placenta; 9.23
		422938; NM_001809; Hs.1594; centromere protein A (17kD); centromere protein A (17kD); 9.21
		411027; AF072099; Hs.67846; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4; leukocyte immunoglobulin-like receptor; 9.21
		425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); topoisomerase (DNA) II alpha (170kD); 9.18
		428684; AK001666; Hs.189095; similar to SALL1 (sal (Drosophila)-like; similar to SALL1 (sal (Drosophila)-like; 9.17
75		428970; BE276891; Hs.194691; retinoic acid induced 3 (RAIG1); metabotropic glutamate family GPCR; retinoic acid induced 3 (RAIG1); metabo; 9.11
		447733; AF157482; Hs.19400; MAD2 (mitotic arrest deficient, yeast, homolog)-like 2; MAD2 (mitotic arrest deficient, yeast, h; 9.11
		422310; AA316622; Hs.98370; cytochrome P450, subfamily IIS, polypeptide 1; cytochrome P450, subfamily IIS, polypept; 9.10
		449722; BE280074; Hs.23960; cyclin B1; cyclin B1; 8.86
		441580; F13386; Hs.7888; v-erb-a avian erythroblastic leukemia viral oncogene homolog-like 4 (HER4); v-erb-a avian erythroblastic leukemia vi; 8.86
80		440983; M20661; Hs.7594; solute carrier family 2 (facilitated glucose transporter), member 3; solute carrier family 2 (facilitated glu; 8.86
		408342; AJ077058; Hs.54089; BRCA1 associated RING domain 1; BRCA1 associated RING domain 1; 8.83
		420367; AA259090; Hs.257028; ESTs; ESTs; 8.82
		415947; U04045; Hs.78934; mutS (E. coli) homolog 2 (colon cancer, nonpolyposis type 1); mutS (E. coli) homolog 2 (colon cancer; 8.73
		418613; AA744529; Hs.85575; mitogen-activated protein kinase kinase kinase kinase 1; mitogen-activated protein kinase kinase kinase; 8.71

- 417407; AA923278; Hs.290905; ESTs, Weakly similar to protease [H.sapiens]; ESTs, Weakly similar to protease [H.sapi]; 8.64
 407239; AA076350; Hs.57846; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4; leukocyte immunoglobulin-like receptor; ; 8.58
 436481; AA379597; Hs.5199; HSPC150 protein similar to ubiquitin-conjugating enzyme; HSPC150 protein similar to ubiquitin-con; 8.55
 412140; AA219691; Hs.73625; RAB6 interacting, kinesin-like (rabkinesin 6); RAB6 interacting, kinesin-like (rabkinesin); 8.52
 438091; AW373062; Hs.351546; nuclear receptor subfamily 1, group 1, member 3; nuclear receptor subfamily 1, group 1, m; 8.51
 424800; AL035588; Hs.153203; MyoD family inhibitor; MyoD family inhibitor; 8.45
 447198; H65423; Hs.17831; hypothetical protein DKFZp434E2135; hypothetical protein DKFZp434E2135; 8.45
 430056; X97548; Hs.228059; KRAB-associated protein 1; KRAB-associated protein 1; 8.42
 417389; BE260964; Hs.82045; midkine (neurite growth-promoting factor 2); midkine (neurite growth-promoting factor); 8.40
 430676; AF084866; Hs.72585; gb:Homo sapiens envelope protein RIC-3 (env) gene, complete cd; gb:Homo sapiens envelope protein RIC-3 (c); 8.38
 420759; T11832; Hs.127797; Homo sapiens cDNA FLJ11381 fs, clone HEMBA1000501; Homo sapiens cDNA FLJ11381 fs, clone HE; 8.38
 406621; X57809; Hs.181125; immunoglobulin lambda locus; immunoglobulin lambda locus; 8.37
 453914; NM_000507; Hs.574; fructose-1,6-bisphosphatase 1; fructose-1,6-bisphosphatase 1; 8.25
 423198; M81933; Hs.1634; cell division cycle 25A; cell division cycle 25A; 8.19
 418299; AA275300; Hs.835968; Integrin, beta 2 (antigen CD18 (p95), lymphocyte function-associated antigen 1; macrophage antigen 1 (mac-1) beta subunit); integrin, beta 2 (antigen CD18 (p95), ly; 8.17
 453968; AA847843; Hs.62711; High mobility group (nonhistone chromosomal) protein 4; High mobility group (nonhistone chromoso; 8.16
 453985; N44545; Hs.261865; ESTs; ESTs; 8.14
 451106; BE382701; Hs.25590; N-MYC oncogene; N-MYC oncogene; 8.10
 420347; AL033539; Hs.97124; Human DNA sequence from clone RP1-308H15 on chromosome 6p22.1-22.3 Contains a gene similar to HDGF (hepatoma-derived growth factor (high-mobility group protein 1-like)), ESTs, GSSs and a CpG Isl; Human DNA sequence from clone RP1-308H15; 8.03
 415857; AA866115; Hs.127797; Homo sapiens cDNA FLJ11381 fs, clone HEMBA1000501; Homo sapiens cDNA FLJ11381 fs, clone HE; 8.02
 425601; AW629485; Hs.140720; GSK-3 binding protein FRAT2; GSK-3 binding protein FRAT2; 7.90
 421016; AA504583; Hs.101047; transcription factor 3 (E2A immunoglobulin enhancer binding factors E12/E47); transcription factor 3 (E2A immunoglobul); 7.89
 432407; AA221036; ; gb:z03f12r1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 5' similar to SW:POL_BAEVM P10272 POL POLYPROTEIN 1; mRNA sequence; gb:z03f12r1 Stratagene NT2 neuronal pr; 7.83
 422846; BE513934; Hs.1583; neutrophil cytosolic factor 1 (47kD, chronic granulomatous disease, autosomal 1); neutrophil cytosolic factor 1 (47kD, chr; 7.80
 433228; F28212; Hs.14953; KIAA1491 protein; KIAA1491 protein; 7.73
 446528; AU076640; Hs.15243; nucleolar protein 1 (120kD); nucleolar protein 1 (120kD); 7.71
 447350; AJ375572; Hs.172634; v-erb-a avian erythroblastic leukemia viral oncogene homolog-like 4 (HERA); v-erb-a avian erythroblastic leukemia vi; 7.71
 448775; AB025237; Hs.388; nudix (nucleoside diphosphate linked moiety X)-type motif 1; nudix (nucleoside diphosphate linked mol; 7.71
 430253; AK001514; Hs.236844; hypothetical protein FLJ10652; hypothetical protein FLJ10652; 7.70
 444784; D12485; Hs.11851; ectonucleotide pyrophosphatase/phosphodiesterase 1 {Plasma-cell membrane glycoprotein PC-1}; ectonucleotide pyrophosphatase/phosphodi; 7.62
 443537; D13305; Hs.203; cholecystokinin B receptor; cholecystokinin B receptor; 7.57
 446291; BE397753; Hs.14623; interferon, gamma-inducible protein 30; interferon, gamma-inducible protein 30; 7.55
 410006; AW732308; Hs.57783; eukaryotic translation initiation factor 3, subunit 9 (ets, 116kD); eukaryotic translation initiation factor; 7.53
 430255; AK000703; Hs.323822; Homo sapiens mRNA for KIAA1551 protein, partial cds; Homo sapiens mRNA for KIAA1551 protein; ; 7.52
 411975; AB16058; Hs.144583; 3'UTR of: dead ringer (Drosophila)-like 1; 3'UTR of: dead ringer (Drosophila)-like ; 7.50
 439864; A1720078; Hs.291997; ESTs, Weakly similar to A47582 B-cell growth factor precursor [H.sapiens]; ESTs, Weakly similar to A47582 B-cell pr; 7.47
 440773; AA362702; Hs.37747; Homo sapiens, Similar to RIKEN cDNA 2700083B06 gene, clone MGC:4689, mRNA, complete cds; Homo sapiens, Similar to RIKEN cDNA 2700; 7.47
 417705; AW134952; Hs.175220; hypothetical protein FLJ14541; hypothetical protein FLJ14541; 7.47
 425367; BE271188; Hs.155975; protein tyrosine phosphatase, receptor type, C-associated protein; protein tyrosine phosphatase, receptor t; 7.47
 407710; AW022277; Hs.23616; ESTs; ESTs; 7.45
 445093; AJ207197; Hs.374149; ESTs; ESTs; 7.41
 418113; AJ272141; Hs.83484; SRY (sex determining region Y)-box 4; SRY (sex determining region Y)-box 4; 7.39
 417900; BE260127; Hs.82906; CDC20 (cell division cycle 20, S. cerevisiae, homolog); CDC20 (cell division cycle 20, S. cerevi; 7.37
 429469; M64590; Hs.111801; glycine dehydrogenase (decarboxylating); glycine decarboxylase, glycine cleavage system protein P; glycine dehydrogenase (decarboxylating; ; 7.33
 422726; U11680; Hs.1572; facioscapular dysplasia (Aarskog-Scott syndrome); facioscapular dysplasia (Aarskog-Scott sy; 7.33
 430504; H52761; Hs.44095; Homo sapiens, clone MGC:12617, mRNA, complete cds; Homo sapiens, clone MGC:12617, mRNA, com; 7.32
 448981; AJ968719; Hs.195387; ESTs; ESTs; 7.28
 413762; AW411479; Hs.848; FK506-binding protein 4 (59kD); FK506-binding protein 4 (59kD); 7.26
 435092; AL137310; Hs.4749; Homo sapiens mRNA; cDNA DKFZp761E13121 (from clone DKFZp761E13121); partial cds; Homo sapiens mRNA; cDNA DKFZp761E13121 (c; 7.25
 434414; AJ798376; ; gb:tr34607.x1 NCI_CGAP_Ov23 Homo sapiens cDNA clone 3 similar to TRC015475 O15475 UNNAMED HERV-H PROTEIN 1; mRNA sequence; gb:tr34607.x1 NCI_CGAP_Ov23 Homo sapiens; 7.24
 428977; AK001404; Hs.194698; cyclin B2; cyclin B2; 7.19
 434274; AA628538; Hs.57783; ESTs, Moderately similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Moderately similar to ALU1_HUMAN A; 7.19
 446700; AW206257; Hs.156328; Human DNA sequence from clone RP11-145L22 on chromosome 6p21.32-22.2. Contains the gene for myelin/oligodendrocyte glycoprotein MOG, (part of) the gene for a novel KRAB box containing C2H2 type zinc f; Human DNA sequence from clone RP11-145L2; 7.18
 420524; AB010575; Hs.98547; aniloride-sensitive cation channel 3, testis; aniloride-sensitive cation channel 3, te; 7.15
 439053; BE244588; Hs.6456; chaperonin containing TCP1, subunit 2 (beta); chaperonin containing TCP1, subunit 2 (b; 7.14
 445076; AJ206888; Hs.154131; ESTs; ESTs; 7.14
 448583; AJ970278; Hs.156905; KIAA1676; KIAA1676; 7.13
 429486; AF155827; Hs.203936; hypothetical protein FLJ10339; hypothetical protein FLJ10339; 7.10
 441362; BE614410; Hs.23044; RAD51 (S. cerevisiae) homolog (E. coli RecA homolog); RAD51 (S. cerevisiae) homolog (E. coli Re; 7.04
 433914; AF108138; Hs.112160; Homo sapiens DNA helicase homolog (PIF1) mRNA, partial cds; Homo sapiens DNA helicase homolog (PIF1); 7.02
 413278; BE563085; Hs.833; interferon-stimulated protein, 15 kDa; interferon-stimulated protein, 15 kDa; 7.02
 423765; R23858; Hs.143375; Homo sapiens, clone IMAGE:3840937, mRNA, partial cds; Homo sapiens, clone IMAGE:3840937, mRNA; 6.96
 418658; U03272; Hs.79432; fibrillin 2 (congenital contractual arachnodactyly); fibrillin 2 (congenital contractual ara; 6.92
 438450; AJ050865; Hs.65853; nodal, mouse, homolog; nodal, mouse, homolog; 6.90
 415323; BE269352; Hs.949; neutrophil cytosolic factor 2 (65kD, chronic granulomatous disease, autosomal 2); neutrophil cytosolic factor 2 (65kD, chr; 6.90
 444381; BE387335; Hs.283713; hypothetical protein BC014245; hypothetical protein BC014245; 6.89
 447582; BE293520; Hs.18910; prostate cancer overexpressed gene 1; prostate cancer overexpressed gene 1; 6.89
 424779; AL046851; Hs.153063; CD37 antigen; CD37 antigen; 6.89
 443907; AU076494; Hs.9963; TYRO protein tyrosine kinase binding protein; TYRO protein tyrosine kinase binding pro; 6.84
 427298; AA400495; ; ESTs; ESTs; 6.82
 414732; AW410978; Hs.77152; minichromosome maintenance deficient (S. cerevisiae) 7; minichromosome maintenance deficient (S; 6.81
 424959; NM_005781; Hs.153937; activated p21cdc42Hs kinase; activated p21cdc42Hs kinase; 6.81
 428866; U02330; Hs.172816; neuregulin 1; neuregulin 1; 6.80
 418203; X54942; Hs.83758; CDC28 protein kinase 2; CDC28 protein kinase 2; 6.80
 427521; AW973352; ; ESTs; ESTs; 6.75
 430397; AJ924533; Hs.105607; bicarbonate transporter related protein 1; bicarbonate transporter related protein ; 6.75
 427719; AJ393122; Hs.134726; ESTs; ESTs; 6.74

- 439453; BE264974; Hs.6566; thyroid hormone receptor interactor 13; thyroid hormone receptor interactor 13; 6.72
 453348; BE272318; Hs.8595; hypothetical protein FLJ12438; hypothetical protein FLJ12438; 6.71
 446113; AW967553; Hs.323518; Homo sapiens mRNA for FLJ00083 protein, partial cds; Homo sapiens mRNA for FLJ00083 protein; 6.70
 445363; NM_005993; Hs.12570; tubulin-specific chaperone d; tubulin-specific chaperone d; 6.70
 433701; AW445023; Hs.15155; ESTs; ESTs; 6.69
 418054; NM_002318; Hs.83354; lysyl oxidase-like 2; lysyl oxidase-like 2; 6.63
 441031; AJ110684; Hs.7645; fibrinogen, B beta polypeptide; fibrinogen, B beta polypeptide; 6.62
 439237; AW408158; Hs.318893; ESTs, Weakly similar to A47582 B-cell growth factor precursor [H.sapiens]; ESTs, Weakly similar to A47582 B-cell gr; 6.59
 424381; AA285249; Hs.146329; protein kinase Chk2 (CHEK2); protein kinase Chk2 (CHEK2); 6.58
 414821; M63835; Hs.77424; Fc fragment of IgG, high affinity Ia, receptor for (CD64); Fc fragment of IgG, high affinity Ia, re; 6.58
 418883; BE387036; Hs.1211; acid phosphatase 5, tartrate resistant; acid phosphatase 5, tartrate resistant; 6.57
 414161; AA136106; Hs.184852; KIAA1553 protein; KIAA1553 protein; 6.57
 437437; AA226869; Hs.351623; hypothetical protein DKFZp762L0311; hypothetical protein DKFZp762L0311; 6.55
 425769; U72513; Hs.159486; Human RPL13-2 pseudogene mRNA, complete cds; Human RPL13-2 pseudogene mRNA, complete; 6.55
 452363; AI582743; Hs.94953; Homo sapiens, Similar to complement component 1, q subcomponent, c polypeptide, clone MGC:77279, mRNA, complete cds; Homo sapiens, Similar to complement comp; 6.55
 422765; AW409701; Hs.1578; baculoviral IAP repeat-containing 5 (survivin); baculoviral IAP repeat-containing 5 (sur; 6.51
 409693; AW247090; Hs.57101; minichromosome maintenance deficient (S. cerevisiae) 2 (mifolin); minichromosome maintenance deficient (S.; 6.50
 418918; X07871; Hs.89476; CD2 antigen (p50), sheep red blood cell receptor; CD2 antigen (p50), sheep red blood cell; 6.49
 417911; AA333387; Hs.82916; chaperonin containing TCP1, subunit 6A (zeta 1); chaperonin containing TCP1, subunit 6A; 6.44
 427747; AW411426; Hs.180655; serine/threonine kinase 12; serine/threonine kinase 12; 6.43
 408142; AW952792; Hs.334612; SMC4 (structural maintenance of chromosomes 4, yeast)-like 1; SMC4 (structural maintenance of chromoso; 6.42
 430280; AA381258; Hs.237868; Interleukin 7 receptor; interleukin 7 receptor; 6.42
 432839; T27013; Hs.3132; steroidogenic acute regulatory protein; steroidogenic acute regulatory protein; 6.42
 422809; AK001379; Hs.421026; hypothetical protein FLJ10549; hypothetical protein FLJ10549; 6.40
 427578; AI591305; Hs.169084; ESTs, Highly similar to TUL3_HUMAN TUBBY RELATED PROTEIN 3 [H.sapiens]; ESTs, Highly similar to TUL3_HUMAN TUBBY; 6.40
 417115; AW952792; Hs.334612; small nuclear ribonucleoprotein polypeptide E; small nuclear ribonucleoprotein polypept; 6.39
 428227; AA321649; Hs.2248; small inducible cytokine subfamily B (Cys-X-Cys), member 10; small inducible cytokine subfamily B (C); 6.39
 441384; AA447849; Hs.288660; retinoic acid induced 3; retinoic acid induced 3; 6.38
 438915; AA280174; Hs.285681; Williams-Beuren syndrome chromosome region 14; Williams-Beuren syndrome chromosome regi; 6.34
 416773; AK000340; Hs.79828; hypothetical protein FLJ20333; hypothetical protein FLJ20333; 6.34
 451999; AW176401; Hs.27424; DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (S.cerevisiae CHL1-like helicase); DEAD/H (Asp-Glu-Ala-Asp/His) box polypep; 6.31
 444159; AF116846; Hs.10431; dead ringer (Drosophila)-like 2 (bright and dead ringer); dead ringer (Drosophila)-like 2 (bright); 6.31
 425274; BE281191; Hs.155462; minichromosome maintenance deficient (mif5, S. pombe) 6; minichromosome maintenance deficient (mif; 6.31
 436449; AA738254; Hs.165390; ESTs, Highly similar to A40350 transcription repressor protein YY1 [H.sapiens]; ESTs, Highly similar to A40350 transcrip; 6.30
 420507; AF093408; Hs.98397; A kinase (PRKA) anchor protein 3; A kinase (PRKA) anchor protein 3; 6.30
 415829; AW450188; Hs.163742; ESTs; ESTs; 6.28
 410342; R31350; Hs.743; Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide; Fc fragment of IgE, high affinity I, rec; 6.26
 446539; BE091828; Hs.16244; mitotic spindle coiled-coil related protein; mitotic spindle coiled-coil related prot; 6.25
 457465; AW301344; Hs.122908; DNA replication factor; DNA replication factor; 6.25
 428918; AL036957; Hs.2324; protamine 2; protamine 2; 6.24
 443523; AK001575; Hs.9536; hypothetical protein FLJ10713; hypothetical protein FLJ10713; 6.19
 424415; NM_001975; Hs.146580; enolase 2, (gamma, neuronal); enolase 2, (gamma, neuronal); 6.19
 407246; X90568; Hs.372004; titin; titin; 6.18
 458627; AW088642; Hs.97984; SRY (sex determining region Y)-box 17 (SOX17); SRY (sex determining region Y)-box 17 (S; 6.18
 421379; Y16221; Hs.103982; small inducible cytokine subfamily B (Cys-X-Cys), member 11; small inducible cytokine subfamily B (C); 6.16
 435099; AC004770; Hs.4756; flap structure-specific endonuclease 1; flap structure-specific endonuclease 1; 6.13
 424308; AW975531; Hs.154443; minichromosome maintenance deficient (S. cerevisiae) 4; minichromosome maintenance deficient (S.; 6.12
 430521; NM_016383; Hs.242183; HOM-TES-85 tumor antigen; HOM-TES-85 tumor antigen; 6.10
 444823; BE262989; Hs.12045; putative protein; putative protein; 6.10
 428484; AF104032; Hs.184601; solute carrier family 7 (cationic amino acid transporter, y system), member 5; solute carrier family 7 (cationic amino; 6.09
 402260; ; NM_001436; Homo sapiens fibrillarin (FBL), mRNA, transcript (F8A), mRNA; NM_001436; Homo sapiens fibrillarin (FBL); 6.09
 441321; H17182; Hs.7771; B-cell associated protein; B-cell associated protein; 6.05
 422283; AW411307; Hs.114311; CDC45 (cell division cycle 45, S.cerevisiae, homolog)-like; CDC45 (cell division cycle 45, S.cerevis; 6.04
 431629; AU077025; Hs.265827; interferon, alpha-inducible protein (clone IFI-6-16); Interferon, alpha-inducible protein (c; 6.04
 402678; ; Target Exon; Target Exon; 6.03
 453884; AA355925; Hs.36232; KIAA0186 gene product; KIAA0186 gene product; 6.01
 439753; BE262233; Hs.7423; hypothetical protein from EUROIMAGE 2168212; hypothetical protein from EUROIMAGE 2168; 6.01
 420596; NM_002692; Hs.99185; polymerase (DNA directed), epsilon 2; polymerase (DNA directed), epsilon 2; 6.01
 420676; AI434780; Hs.4248; vav 2 oncogene; vav 2 oncogene; 6.00
 418756; AA252254; Hs.226949; ESTs; ESTs; 5.99
 454438; AA224053; Hs.172405; cell division cycle 27; cell division cycle 27; 5.98
 407818; AL021938; Hs.40154; jumonji (mouse) homolog; jumonji (mouse) homolog; 5.98
 413313; NM_002047; Hs.293885; glycyl-tRNA synthetase; glycyl-tRNA synthetase; 5.96
 424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lysozyme (renal amyloidosis); 5.95
 417777; AJ823763; Hs.7055; ESTs, Weakly similar to I78685 serine/threonine-specific protein kinase [H.sapiens]; ESTs, Weakly similar to I78685 serine/th; 5.94
 449569; AI656634; Hs.195389; ESTs; ESTs; 5.92
 436576; AI458213; Hs.77542; ESTs; ESTs; 5.90
 438746; AI886815; Hs.184727; Human melanoma-associated antigen p97 (melanotransferrin) mRNA, 3' flank; Human melanoma-associated antigen p97 (m; 5.89
 420009; AW271108; Hs.133294; ESTs; ESTs; 5.89
 417208; S67773; Hs.81665; v-kit Hardy-Zuckerman 4 feline sarcoma viral oncogene homolog; v-kit Hardy-Zuckerman 4 feline sarcoma v; 5.88
 403171; ; C2001472:gi5809678[gb|AA841848.2] (U64675) sperm membrane protein BS-63 [Homo sapiens]; C2001472:gi5809678[gb|AA841848.2] (U64; 5.87
 448730; AB032983; Hs.21894; KIAA1157 protein; KIAA1157 protein; 5.87
 406137; ; NM_000179; Homo sapiens mutS (E. coli) homolog 6 (MSH6), mRNA, VERSION NM_000178.1 GI; NM_000179; Homo sapiens mutS (E. coli) h; 5.85
 423787; AJ295745; Hs.238204; nuclear pore complex protein; nuclear pore complex protein; 5.85
 425126; N32759; Hs.172944; chorionic gonadotropin, beta polypeptide; chorionic gonadotropin, beta polypeptide; 5.84
 452796; AB011100; Hs.30655; KIAA0528 gene product; KIAA0528 gene product; 5.84
 416322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK2-associated dual specificity phosphatase); cyclin-dependent kinase inhibitor 3 (CDK; 5.80
 447369; NM_012093; Hs.18268; adenylylase kinase 5; adenylylase kinase 5; 5.79
 420344; BE463721; Hs.97101; putative G protein-coupled receptor; putative G protein-coupled receptor; 5.78
 420297; AI628272; Hs.128757; ESTs, Weakly similar to ALU1_HUMAN ALU SUBFAMILY J SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Weakly similar to ALU1_HUMAN ALU S; 5.75
 414761; AU077228; Hs.77256; enhancer of zeste (Drosophila) homolog 2; enhancer of zeste (Drosophila) homolog 2; 5.75

- 430287; AW182459; Hs.125759; ESTs, Weakly similar to LEU5_HUMAN LEUKEMIA ASSOCIATED PROTEIN 5 [H.sapiens]; ESTs, Weakly similar to LEU5_HUMAN LEUK5; 5.74
436251; BE515055; Hs.295585; nucleolar protein (KKE/D repeat); nucleolar protein (KKE/D repeat); 5.73
421535; AB002359; Hs.105478; phosphoribosylformylglycinamide synthase (FGAR amidotransferase); phosphoribosylformylglycinamide synthase; 5.71
414883; AA926960; Hs.348669; CDC28 protein kinase 1; CDC28 protein kinase 1; 5.69
425159; NM_004341; Hs.154868; carbamoyl-phosphate synthetase 2, aspartate transcarbamylase, and dihydroorotase; carbamoyl-phosphate synthetase 2, aspartate; 5.69
401704; ; NM_021195; Homo sapiens claudin 6 (CLDN6), mRNA. VERSION NM_020982.1 GI; NM_021195; Homo sapiens claudin 6 (CLDN6); 5.66
425358; AL079558; Hs.338207; FK506 binding protein 12-rapamycin associated protein 1; FK506 binding protein 12-rapamycin associated protein 1; 5.65
402677; ; NM_000478; Homo sapiens alkaline phosphatase, liver/bone/kidney (ALPL), mRNA. alpha-hydroxylase, polypeptide 1 (CYP7B1), mRNA; NM_000478; Homo sapiens alkaline phosphatase; 5.64
409264; NM_014937; Hs.52463; KIAA0966 protein; KIAA0966 protein; 5.63
432185; AA221032; Hs.272838; hypothetical protein FLJ10494; hypothetical protein FLJ10494; 5.63
409012; AL117435; Hs.49725; DKFZP434I216 protein; DKFZP434I216 protein; 5.63
430252; AL638774; Hs.105328; testes development-related NYD-SP20; testes development-related NYD-SP20; 5.61
419359; AL043202; Hs.30073; chromosome segregation 1 (yeast homolog)-like; chromosome segregation 1 (yeast homolog); 5.61
452816; AA131789; Hs.61509; ESTs; ESTs; 5.60
402679; ; NM_000478; Homo sapiens alkaline phosphatase, liver/bone/kidney (ALPL), mRNA. alpha-hydroxylase, polypeptide 1 (CYP7B1), mRNA; NM_000478; Homo sapiens alkaline phosphatase; 5.69
414291; AJ288619; Hs.13040; G protein-coupled receptor 85; G protein-coupled receptor 85; 5.58
453028; AB006532; Hs.31442; RacQ protein-like 4; RacQ protein-like 4; 5.58
453905; NM_002314; Hs.36566; LIM domain kinase 1; LIM domain kinase 1; 5.56
411263; BE297802; Hs.69360; kinesin-like 6 (mitotic centromere-associated kinesin); kinesin-like 6 (mitotic centromere-associated); 5.55
419660; BE280337; Hs.194693; solute carrier family 7 (cationic amino acid transporter, y system), member 7; solute carrier family 7 (cationic amino acid transporter, y system), member 7; 5.55
446979; AL654443; Hs.197683; ESTs; ESTs; 5.54
424321; W74048; Hs.1765; lymphocyte-specific protein tyrosine kinase; lymphocyte-specific protein tyrosine kinase; 5.53
418962; AA714835; Hs.271863; ESTs; ESTs; 5.53
447388; AW630534; Hs.76277; Homo sapiens, clone MGC-9381, mRNA, complete cds; Homo sapiens, clone MGC-9381, mRNA, complete cds; 5.52
427247; AW504221; Hs.174103; integrin, alpha L (antigen CD11A (p180), lymphocyte function-associated antigen 1; alpha polypeptide); integrin, alpha L (antigen CD11A (p180)); 5.52
449322; AL638616; Hs.198586; ESTs; ESTs; 5.51
428450; NM_014791; Hs.184339; KIAA0175 gene product; KIAA0175 gene product; 5.51
415141; AA189099; Hs.268171; ESTs, Weakly similar to ALU7_HUMAN ALU SUBFAMILY SQ SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Weakly similar to ALU7_HUMAN ALU S; 5.48
454048; H05626; Hs.6921; ESTs; ESTs; 5.46
417079; U65590; Hs.81134; Interleukin 1 receptor antagonist; Interleukin 1 receptor antagonist; 5.45
434699; AA643687; Hs.149425; Homo sapiens cDNA FLJ11880 f1s, clone HEMBB1001304; Homo sapiens cDNA FLJ11880 f1s, clone HE; 5.44
414334; AA824298; Hs.21331; hypothetical protein FLJ10036; hypothetical protein FLJ10036; 5.44
452291; AF015592; Hs.28853; CDC7 (cell division cycle 7, S. cerevisiae, homolog)-like 1; CDC7 (cell division cycle 7, S. cerevisiae); 5.44
438564; AA381553; Hs.198253; major histocompatibility complex, class II, DQ alpha 1; major histocompatibility complex, class II, DQ alpha 1; 5.44
427668; AA288760; Hs.180191; hypothetical protein FLJ14904; hypothetical protein FLJ14904; 5.43
449437; AL702038; Hs.100057; Homo sapiens cDNA: FLJ22902 f1s, clone KAT05581; Homo sapiens cDNA: FLJ22902 f1s, clone K; 5.41
453653; AA357001; Hs.34045; hypothetical protein FLJ20764; hypothetical protein FLJ20764; 5.40
450746; D82873; Hs.278599; general transcription factor II, I; general transcription factor II, I; 5.40
425966; NM_001781; Hs.1973; cyclin F; cyclin F; 5.39
418134; AA397769; Hs.86617; ESTs; ESTs; 5.38
432141; BE410964; Hs.272736; nuclear receptor binding protein; nuclear receptor binding protein; 5.37
417141; U22662; Hs.347353; nuclear receptor subfamily 1, group H, member 3; nuclear receptor subfamily 1, group H, member 3; 5.36
428329; AA426091; Hs.98453; ESTs, Moderately similar to R27328 2 [H.sapiens]; ESTs, Moderately similar to R27328 2 [H.]; 5.35
406811; U82979; Hs.67848; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4; leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 4; 5.34
415818; AL077330; Hs.360791; transcription elongation factor A (SII), 1; transcription elongation factor A (SII), 1; 5.33
448133; AA723157; Hs.73769; folate receptor 1 (adulf); folate receptor 1 (adulf); 5.33
424762; AL119442; Hs.183884; eukaryotic translation initiation factor 4 gamma, 2; eukaryotic translation initiation factor; 5.32
421958; AW751497; Hs.98370; cytochrome P450, subfamily IIS, polypeptide 1; cytochrome P450, subfamily IIS, polypeptide; 5.32
429271; AF039950; Hs.198515; dead ringer (Drosophila)-like 1; dead ringer (Drosophila)-like 1; 5.32
456373; BE247706; Hs.86693; membrane-spanning 4-domains, subfamily A, member 2 (CD20 antigen); membrane-spanning 4-domains, subfamily A; 5.30
414807; X90725; Hs.77597; polo (Drosophila)-like kinase; polo (Drosophila)-like kinase; 5.30
422997; BE018212; Hs.122908; DNA replication factor; DNA replication factor; 5.29
440014; AW960782; Hs.6856; ash2 (absent, small, or homeotic, Drosophila, homolog)-like; ash2 (absent, small, or homeotic, Drosop); 5.28
418399; AF131781; Hs.84753; hypothetical protein FLJ12442; hypothetical protein FLJ12442; 5.26
416176; AL808627; Hs.192822; serologically defined breast cancer antigen NY-BR-81; serologically defined breast cancer antigen; 5.21
450377; AB030309; Hs.355925; KIAA1265 protein; KIAA1265 protein; 5.20
409670; AL368109; Hs.375604; KIAA1856 protein; KIAA1856 protein; 5.20
429063; Y09397; Hs.227817; BCL2-related protein A1; BCL2-related protein A1; 5.20
449523; NM_000579; Hs.54443; chemokine (C-C motif) receptor 5; chemokine (C-C motif) receptor 5; 5.20
408908; BE296227; Hs.250822; serine/threonine kinase 15; serine/threonine kinase 15; 5.19
429732; U20158; Hs.2488; lymphocyte cytosolic protein 2 (SH2 domain-containing leukocyte protein of 75kD); lymphocyte cytosolic protein 2 (SH2 domain-containing leukocyte protein of 75kD); 5.19
436088; W05391; Hs.351546; nuclear receptor subfamily 1, group I, member 3; nuclear receptor subfamily 1, group I, member 3; 5.18
437623; D63880; Hs.5719; chromosome condensation-related SMC-associated protein 1; chromosome condensation-related SMC-associated protein 1; 5.15
448181; AF272833; Hs.279763; hypothetical protein FLJ10504; hypothetical protein FLJ10504; 5.15
436540; BE397032; Hs.14468; hypothetical protein MGC14226; hypothetical protein MGC14226; 5.14
422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor type, C; protein tyrosine phosphatase, receptor type, C; 5.14
426752; X69490; Hs.172004; ttn; ttn; 5.13
415007; BE244332; Hs.77770; adaptor-related protein complex 3, mu 2 subunit; adaptor-related protein complex 3, mu 2 subunit; 5.13
400263; ; Hs.75309; Eos Control; Eos Control; 5.13
437099; N77793; Hs.48669; ESTs, Highly similar to S14458 laminin alpha-1 chain precursor [H.sapiens]; ESTs, Highly similar to S14458 laminin alpha-1 chain precursor [H.sapiens]; 5.12
427209; H05509; Hs.92423; KIAA1566 protein; KIAA1566 protein; 5.10
407347; AA829847; ; gbcd40d07.s1 NCL_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:1370413 3' similar to contains Alu repetitive element, mRNA sequence.; gbcd40d07.s1 NCL_CGAP_GCB1 Homo sapiens; 5.10
458933; AL638429; Hs.24763; RAN binding protein 1; RAN binding protein 1; 5.10
450431; AW136797; Hs.268041; ESTs; ESTs; 5.09
434608; AA805443; Hs.179909; hypothetical protein FLJ22995; hypothetical protein FLJ22995; 5.08
410423; AW402432; Hs.63489; protein tyrosine phosphatase, non-receptor type 6; protein tyrosine phosphatase, non-receptor type 6; 5.08
417929; R27219; Hs.74647; Human T-cell receptor active alpha-chain mRNA from JM cell line, complete cds; Human T-cell receptor active alpha-chain; 5.05
412723; AA648459; Hs.335851; hypothetical protein AF301222; hypothetical protein AF301222; 5.05

- 447321; AW271217; Hs.281434; Homo sapiens cDNA FLJ14028 fis, clone HEMBA1003838; Homo sapiens cDNA FLJ14028 fis, clone HE; 5.03
 417866; AW067903; Hs.82772; collagen, type XI, alpha 1; collagen, type XI, alpha 1; 5.03
 410082; AA081594; Hs.158311; Musashi (Drosophila) homolog 1; Musashi (Drosophila) homolog 1; 5.02
 433592; NM_004642; Hs.3436; deleted in oral cancer (mouse, homolog) 1; deleted in oral cancer (mouse, homolog); 5.02
 425811; AL039104; Hs.159557; karyopherin alpha 2 (RAG cohort 1, Importin alpha 1); karyopherin alpha 2 (RAG cohort 1, impor; 5.00
 425237; U07695; Hs.155227; EphB4; EphB4; 5.00
 414809; AI434699; Hs.77356; transferrin receptor (p90, CD71); transferrin receptor (p90, CD71); 4.99
 402145; ; Target Exon; Target Exon; 4.99
 432126; AA865239; Hs.37196; ESTs; ESTs; 4.99
 408279; AF216955; Hs.44095; Homo sapiens, clone MGC:12617, mRNA, complete cds; Homo sapiens, clone MGC:12617, mRNA, com; 4.98
 419525; T79257; Hs.1269; asialoglycoprotein receptor 2; asialoglycoprotein receptor 2; 4.97
 424439; AA578635; Hs.1770; ligase I, DNA, ATP-dependent; ligase I, DNA, ATP-dependent; 4.97
 427667; AK001279; Hs.180171; Homo sapiens cDNA FLJ10417 fis, clone NT2RP1000112; Homo sapiens cDNA FLJ10417 fis, clone NT; 4.96
 457313; AF047002; Hs.241520; transcriptional coactivator; transcriptional coactivator; 4.96
 448589; BE382657; Hs.21496; signal transducer and activator of transcription 1, 91kD; signal transducer and activator of trans; 4.94
 426427; M66699; Hs.169840; TTK protein kinase; TTK protein kinase; 4.91
 440129; AA865818; Hs.368523; ESTs, Weakly similar to S71886 Ste20-like protein kinase [H.sapiens]; ESTs, Weakly similar to S71886 Ste20-like; 4.91
 453922; AF053306; Hs.36708; budding uninhibited by benzimidazoles 1 (yeast homolog), beta; budding uninhibited by benzimidazoles 1; 4.90
 435602; AF217515; Hs.283532; uncharacterized bone marrow protein BM039; uncharacterized bone marrow protein BM03; 4.89
 452598; NM_001295; Hs.301921; chemokine (C-C motif) receptor 1; chemokine (C-C motif) receptor 1; 4.88
 445333; BE537641; Hs.44278; hypothetical protein FLJ12538 similar to ras-related protein RAB17; hypothetical protein FLJ12538 similar to; 4.88
 437102; AW005605; Hs.5464; thyroid hormone receptor coactivating protein; thyroid hormone receptor coactivating pr; 4.87
 441600; AA939347; Hs.127223; Homo sapiens cysteine knot protein (ZSIC61) mRNA, complete cds; Homo sapiens cysteine knot protein (ZSIC; 4.87
 421350; AW301608; Hs.278188; ESTs, Moderately similar to IS4374 gene NF2 protein [H.sapiens]; ESTs, Moderately similar to IS4374 gene; 4.87
 409093; BE248634; Hs.50441; CGI-04 protein; CGI-04 protein; 4.86
 424304; NM_001395; Hs.144879; dual specificity phosphatase 9; dual specificity phosphatase 9; 4.86
 437696; Z83844; Hs.5790; hypothetical protein DJ37E16.5; hypothetical protein DJ37E16.5; 4.86
 417381; AF164142; Hs.82042; solute carrier family 23 (nucleoside transporters), member 1; solute carrier family 23 (nucleoside tra; 4.84
 416445; AL043004; Hs.79337; KIAA0135 protein; KIAA0135 protein; 4.83
 448939; BE267799; Hs.22595; hypothetical protein FLJ10637; hypothetical protein FLJ10637; 4.82
 413566; AW604451; Hs.285814; sprouty (Drosophila) homolog 4; sprouty (Drosophila) homolog 4; 4.82
 424081; NM_006413; Hs.139120; ribonuclease P (30kD); ribonuclease P (30kD); 4.81
 425474; Z48054; Hs.158084; peroxisome receptor 1; peroxisome receptor 1; 4.81
 412278; BE262621; Hs.73793; macrophage migration inhibitory factor (glycosylation-inhibiting factor); macrophage migration inhibitory factor (i; 4.81
 422689; AW856665; Hs.299797; gb:RC3-CT0297-290100-013-d03 CT0297 Homo sapiens cDNA, mRNA sequence; gb:RC3-CT0297-290100-013-d03 CT0297 Homo; 4.80
 409101; NM_004297; Hs.50612; guanine nucleotide binding protein (G protein), alpha 14; guanine nucleotide binding protein (G pr; 4.79
 412760; AW379030; Hs.41324; ESTs; ESTs; 4.79
 447250; AJ878909; Hs.17883; protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform; protein phosphatase 1G (formerly 2C), ma; 4.79
 429345; R11141; Hs.199695; hypothetical protein; hypothetical protein; 4.78
 448950; AF286687; Hs.8275; CGI-152 protein; CGI-152 protein; 4.78
 412926; AJ879076; Hs.75061; macrophage myristoylated alanine-rich C kinase substrate; macrophage myristoylated alanine-rich C; 4.78
 412641; M16660; Hs.74335; heat shock 90kD protein 1, beta; heat shock 90kD protein 1, beta; 4.76
 420261; AW206093; Hs.748; fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome); fibroblast growth factor receptor 1 (fms; 4.76
 421905; AI650247; Hs.32689; ESTs, Weakly similar to LIV-1 protein [H.sapiens]; ESTs, Weakly similar to LIV-1 protein [H.s]; 4.75
 413880; AJ660842; Hs.110915; interleukin 22 receptor; interleukin 22 receptor; 4.75
 424805; NM_002497; Hs.153704; NIMA (never in mitosis gene a)-related kinase 2 (NEK2); NIMA (never in mitosis gene a)-related k; 4.74
 418356; L42563; Hs.1165; ATPase, H⁺ transporting, nongastric, alpha polypeptide; ATPase, H⁺ transporting, nongastric, alp; 4.74
 435905; AW997484; Hs.5003; KIAA0456 protein; KIAA0456 protein; 4.74
 428024; Z29067; Hs.2236; NIMA (never in mitosis gene a)-related kinase 3; NIMA (never in mitosis gene a)-related k; 4.74
 421846; AA017707; Hs.1432; protein kinase C substrate 80K-H; protein kinase C substrate 80K-H; 4.72
 419138; U48508; Hs.89631; ryanodine receptor 1 (skeletal); ryanodine receptor 1 (skeletal); 4.72
 437296; AA350994; Hs.20281; KIAA1700; KIAA1700; 4.70
 450142; AW207469; Hs.24485; chondroitin sulfate proteoglycan 6 (bemar); chondroitin sulfate proteoglycan 6 (bemar; 4.70
 421733; AL119671; Hs.1420; fibroblast growth factor receptor 3 (achondroplasia, thanatophoric dwarfism); fibroblast growth factor receptor 3 (ach; 4.69
 449475; AJ348027; Hs.129828; hypothetical protein PP1057; hypothetical protein PP1057; 4.69
 420082; AW411096; Hs.94785; TGF(beta)-induced transcription factor 2; TGF(beta)-induced transcription factor 2; 4.69
 429335; AB005038; Hs.199270; cytochrome P450, subfamily XXVIIIB (25-hydroxyvitamin D-1-alpha-hydroxylase), polypeptide 1; cytochrome P450, subfamily XXVIIIB (25-hy; 4.69
 436858; AJ469355; Hs.127310; ESTs; ESTs; 4.68
 406937; U14622; ; gb:Human transketolase-like protein gene, partial cds.; gb:Human transketolase-like protein gene; 4.67
 411296; BE207307; Hs.10114; growth suppressor 1; growth suppressor 1; 4.67
 426726; AA488915; Hs.171955; trophoblast associated protein (tastin); trophoblast associated protein (tastin); 4.67
 409132; AJ224538; Hs.50732; protein kinase, AMP-activated, beta 2 non-catalytic subunit; protein kinase, AMP-activated, beta 2 no; 4.67
 449230; BE613348; Hs.356392; melanoma cell adhesion molecule; melanoma cell adhesion molecule; 4.66
 431681; AK000378; Hs.287568; hypothetical protein FLJ20371; hypothetical protein FLJ20371; 4.66
 443623; AA345519; Hs.9641; complement component 1, q subcomponent, alpha polypeptide; complement component 1, q subcomponent, ; 4.65
 441595; AW206035; Hs.356457; ESTs; ESTs; 4.64
 423419; R55336; Hs.23539; ESTs; ESTs; 4.64
 415724; NM_003580; Hs.78687; neutral sphingomyelinase (N-SMase) activation associated factor; neutral sphingomyelinase (N-SMase) activ; 4.63
 435045; BE297155; Hs.143698; ESTs; ESTs; 4.62
 424441; X14850; Hs.147097; H2A histone family, member X; H2A histone family, member X; 4.62
 414972; BE263782; Hs.77895; KIAA0008 gene product; KIAA0008 gene product; 4.62
 436885; W28681; Hs.5288; Homo sapiens mRNA; cDNA DKFZp434M245 (from clone DKFZp434M245); Homo sapiens mRNA; cDNA DKFZp434M245 (fr; 4.62
 449515; AI653378; Hs.302012; ESTs; ESTs; 4.61
 425998; AF076629; Hs.165950; fibroblast growth factor receptor 4; fibroblast growth factor receptor 4; 4.61
 420027; AU009746; Hs.94395; ATP-binding cassette, sub-family D (ALD), member 4; ATP-binding cassette, sub-family D (ALD); 4.61
 438469; AK001455; Hs.5198; Down syndrome critical region gene 2; Down syndrome critical region gene 2; 4.61
 413441; AI929374; Hs.75367; Src-like-adaptor; Src-like-adaptor; 4.60
 456847; AJ360456; Hs.86088; ESTs; ESTs; 4.58
 421505; BE302798; Hs.105097; thymidine kinase 1, soluble; thymidine kinase 1, soluble; 4.57
 426935; NM_000088; Hs.172928; collagen, type I, alpha 1; collagen, type I, alpha 1; 4.57
 428782; X12830; Hs.193400; interleukin 6 receptor; interleukin 6 receptor; 4.56
 409430; R21945; Hs.346735; splicing factor, arginine/serine-rich 5; splicing factor, arginine/serine-rich 5; 4.56
 412773; H15785; Hs.74573; similar to vaccinia virus HindIII K4L ORF; similar to vaccinia virus HindIII K4L OR; 4.55

- 443066; AI188710; Hs.374480; ESTs; ESTs; 4.55
 441607; NM_005010; Hs.7912; neuronal cell adhesion molecule; neuronal cell adhesion molecule; 4.54
 453227; AW135852; Hs.243991; ESTs; ESTs; 4.52
 438459; T49300; Hs.35304; Homo sapiens cDNA FLJ13655 fis, clone PLACE1011503; Homo sapiens cDNA FLJ13655 fis, clone PL; 4.51
 422585; BE258035; Hs.118400; slinged (Drosophila)-like (sea urchin fascin homolog like); slinged (Drosophila)-like (sea urchin fas); 4.51
 463613; F06838; Hs.374476; ESTs; ESTs; 4.50
 413900; AW409747; Hs.75612; stress-induced-phosphoprotein 1 (Hsp70/Hsp90-organizing protein); stress-induced-phosphoprotein 1 (Hsp70/H); 4.50
 412507; L36545; Hs.73964; EphA4; EphA4; 4.50
 419034; NM_002110; Hs.89555; hemopoietic cell kinase; hemopoietic cell kinase; 4.49
 413431; AW246428; Hs.75355; ubiquitin-conjugating enzyme E2N (homologous to yeast UBC13); ubiquitin-conjugating enzyme E2N (homolo); 4.49
 406547; ; Target Exon; Target Exon; 4.49
 443216; WB0487; Hs.324521; hypothetical protein DC50; hypothetical protein DC50; 4.48
 417497; AW402482; Hs.82212; CD53 antigen; CD53 antigen; 4.47
 448695; AB014544; Hs.21572; KIAA0644 gene product; KIAA0644 gene product; 4.47
 445350; AF052112; Hs.12540; lysophospholipase I; lysophospholipase I; 4.46
 446238; NM_006293; Hs.301; TYRO3 protein tyrosine kinase; TYRO3 protein tyrosine kinase; 4.46
 429150; AF120103; Hs.197366; smoothened (Drosophila) homolog; smoothened (Drosophila) homolog; 4.46
 420340; NM_000734; Hs.37087; CD32 antigen, zeta polypeptide (TIT3 complex); CD32 antigen, zeta polypeptide (TIT3 com); 4.46
 413428; U88837; Hs.75354; GCN1 (general control of amino-acid synthesis 1, yeast)-like 1; GCN1 (general control of amino-acid synt); 4.44
 421819; NM_013403; Hs.108665; zinedin; zinedin; 4.44
 409512; AW979167; Hs.293591; melanoma differentiation associated protein-5; melanoma differentiation associated prot; 4.44
 428995; AW004975; Hs.194716; MAD (mothers against decapentaplegic, Drosophila) homolog interacting protein, receptor activation anchor; MAD (mothers against decapentaplegic, D); 4.43
 434551; BE397162; Hs.280858; ESTs, Highly similar to A35661 DNA excision repair cross-complementing protein ERCC3 (H.sapiens); ESTs, Highly similar to A35661 DNA excis; 4.43
 418295; AW970043; Hs.238039; hypothetical protein FLJ11090; hypothetical protein FLJ11090; 4.42
 409243; AB037761; Hs.51743; KIAA1340 protein; KIAA1340 protein; 4.42
 437103; AW139408; Hs.152940; ESTs; ESTs; 4.42
 413166; AJ077141; Hs.374548; solute carrier family 16 (monocarboxylic acid transporters), member 1; solute carrier family 16 (monocarboxylic); 4.42
 456362; AW973003; Hs.179909; hypothetical protein FLJ22995; hypothetical protein FLJ22995; 4.40
 424078; AB006626; Hs.139033; paternally expressed 3; paternally expressed 3; 4.39
 448153; Y10805; Hs.20521; HMT1 (hnRNP methyltransferase, S. cerevisiae)-like 2; HMT1 (hnRNP methyltransferase, S. cerevi; 4.37
 410134; U68140; Hs.58927; nuclear VCP-like; nuclear VCP-like; 4.36
 435523; T62849; Hs.11090; membrane-spanning 4-domains, subfamily A, member 7; membrane-spanning 4-domains, subfamily A; 4.35
 400440; X83957; Hs.83870; nabulin; nabulin; 4.35
 437218; AL117497; Hs.68185; ESTs, Weakly similar to T42727 proliferation potential-related protein - mouse [M.musculus]; ESTs, Weakly similar to T42727 prolifer; 4.34
 430473; NM_014349; Hs.241535; apolipoprotein L, 3; apolipoprotein L, 3; 4.34
 432744; AA988835; Hs.38664; ESTs; ESTs; 4.33
 423173; AA442655; Hs.124942; protein phosphatase 2A 48 kDa regulatory subunit; protein phosphatase 2A 48 kDa regulatory; 4.33
 415995; NM_004573; Hs.355888; phospholipase C, beta 2; phospholipase C, beta 2; 4.33
 408728; AL137379; Hs.47125; hypothetical protein FLJ13912; hypothetical protein FLJ13912; 4.30
 431222; X56777; Hs.273790; zona pellucida glycoprotein 3A (sperm receptor); zona pellucida glycoprotein 3A (sperm re; 4.30
 427792; M63928; Hs.180841; tumor necrosis factor receptor superfamily, member 7; tumor necrosis factor receptor superfam; 4.29
 426227; U67058; Hs.154299; Human proteinase activated receptor-2 mRNA, 3'UTR; Human proteinase activated receptor-2 mR; 4.29
 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIB, receptor for (CD16); Fc fragment of IgG, low affinity IIB, r; 4.29
 434826; AF155661; Hs.22265; pyruvate dehydrogenase phosphatase; pyruvate dehydrogenase phosphatase; 4.29
 412314; AA825247; Hs.358084; downstream of: G protein-coupled receptor 27 (GPR27) (SREB1); downstream of: G protein-coupled receptor; 4.28
 447827; U37272; Hs.19718; protein tyrosine phosphatase, receptor type, U; protein tyrosine phosphatase, receptor t; 4.28
 426108; AA622037; Hs.166468; programmed cell death 5; programmed cell death 5; 4.28
 428820; AA436187; Hs.172631; integrin, alpha M (complement component receptor 3, alpha; also known as CD11b (p170), macrophage antigen alpha polypeptide); integrin, alpha M (complement component; 4.27
 437908; AJ082424; Hs.351043; ESTs; ESTs; 4.27
 444664; N26362; Hs.11616; map kinase phosphatase-like protein MK-STYX; map kinase phosphatase-like protein MK-S; 4.27
 429002; AW248439; Hs.2340; junction plakoglobin; junction plakoglobin; 4.26
 439334; AJ148976; Hs.112062; ESTs; ESTs; 4.26
 425308; M97639; Hs.155585; receptor tyrosine kinase-like orphan receptor 2; receptor tyrosine kinase-like orphan rec; 4.25
 413809; NM_000878; Hs.75588; Interleukin 2 receptor, beta; Interleukin 2 receptor, beta; 4.25
 453648; W21493; Hs.380100; hypothetical protein FLJ14005; hypothetical protein FLJ14005; 4.24
 447200; BE543148; Hs.281434; Homo sapiens cDNA FLJ14028 fis, clone HEMBA1003538; Homo sapiens cDNA FLJ14028 fis, clone HE; 4.24
 447528; AJ612027; Hs.76277; Homo sapiens, clone MGC:9381, mRNA, complete cds; Homo sapiens, clone MGC:9381, mRNA, comp; 4.23
 452721; AJ269529; Hs.301871; solute carrier family 37 (glycerol-3-phosphate transporter), member 1; solute carrier family 37 (glycerol-3-pho; 4.22
 445810; AB008681; Hs.23994; activin A receptor, type IIB; activin A receptor, type IIB; 4.22
 447198; D61523; Hs.283435; ESTs; ESTs; 4.22
 416714; AF283770; Hs.79530; CD79A antigen (immunoglobulin-associated alpha); CD79A antigen (immunoglobulin-associated; 4.22
 425358; BE244879; Hs.155939; inositol polyphosphate-5-phosphatase, 145kD; inositol polyphosphate-5-phosphatase, 14; 4.22
 422605; H16646; Hs.118666; hypothetical protein PP591; hypothetical protein PP591; 4.21
 444535; AF011456; Hs.122575; EDG-4 (endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 4); EDG-4(endothelial differentiation, lys; 4.21
 417088; M54915; Hs.61170; pim-1 oncogene; pim-1 oncogene; 4.20
 421707; NM_014921; Hs.107054; leclomedin-2; leclomedin-2; 4.20
 408717; AF045458; Hs.47061; unc-51 (C. elegans)-like kinase 1; unc-51 (C. elegans)-like kinase 1; 4.20
 438485; W57578; Hs.378718; RAB7, member RAS oncogene family; RAB7, member RAS oncogene family; 4.19
 419452; U33835; Hs.90572; PTK7 protein tyrosine kinase 7; PTK7 protein tyrosine kinase 7; 4.18
 418755; Y14443; Hs.88218; zinc finger protein 200; zinc finger protein 200; 4.18
 417212; AW952823; Hs.351547; NS1-binding protein; NS1-binding protein; 4.17
 413686; AI469213; Hs.71404; ESTs; ESTs; 4.17
 419344; U94905; Hs.277445; diacylglycerol kinase, zeta (104kD); diacylglycerol kinase, zeta (104kD); 4.16
 418870; AF147204; Hs.89414; chemokine (C-X-C motif), receptor 4 (fus); chemokine (C-X-C motif), receptor 4 (fus; 4.16
 408482; NM_000676; Hs.45743; adenosine A2b receptor; adenosine A2b receptor; 4.16
 422391; D63479; Hs.115907; diacylglycerol kinase, delta (130kD); diacylglycerol kinase, delta (130kD); 4.15
 409421; AA189883; Hs.67624; ESTs; ESTs; 4.15
 415938; BE383507; Hs.78921; A kinase (PRKA) anchor protein 1; A kinase (PRKA) anchor protein 1; 4.14
 415198; AW009480; Hs.943; natural killer cell transcript 4; natural killer cell transcript 4; 4.14
 424685; W21223; Hs.151734; nuclear transport factor 2 (placental protein 15); nuclear transport factor 2 (placental pr; 4.13

- 428479; Y00272; Hs.334562; cell division cycle 2, G1 to S and G2 to M; cell division cycle 2, G1 to S and G2 to M; 4.13
- 423728; AW891294; Hs.132136; solute carrier family 4, sodium bicarbonate cotransporter, member 8; solute carrier family 4, sodium bicarbonate; 4.13
- 433436; BE545277; Hs.340959; Ts translation elongation factor, mitochondrial; Ts translation elongation factor, mitochondrial; 4.13
- 420253; A1656055; Hs.95200; neighbor of A-kinase anchoring protein 95; neighbor of A-kinase anchoring protein 95; 4.12
- 5 412584; X54870; Hs.74085; DNA segment on chromosome 12 (unique) 2489 expressed sequence; DNA segment on chromosome 12 (unique) 24; 4.12
- 400205; Hs.81848; NM_006265; Homo sapiens RAD21 (S. pombe) homolog (RAD21), mRNA. (APO-1/CD95 (Fas)-associated phosphatase) (PTPN13), mRNA; NM_006265; Homo sapiens RAD21 (S. pombe); 4.12
- 425322; U63630; Hs.155637; protein kinase, DNA-activated, catalytic polypeptide; protein kinase, DNA-activated, catalytic; 4.11
- 10 419607; RS2557; Hs.91578; Homo sapiens clone 23783 mRNA sequence; Homo sapiens clone 23783 mRNA sequence; 4.10
- 459035; AW291109; Hs.332563; ESTs, Weakly similar to T31611 hypothetical protein Y50E8A.g - *Caenorhabditis elegans* [C.elegans]; ESTs, Weakly similar to T31611 hypothetical; 4.10
- 432512; NM_003284; Hs.3017; transition protein 1 (during histone to protamine replacement); transition protein 1 (during histone to ; 4.10
- 452875; BE275760; Hs.30928; DNA segment on chromosome 19 (unique) 1177 expressed sequence; DNA segment on chromosome 19 (unique) 11; 4.09
- 423804; AW403448; Hs.1706; interferon-stimulated transcription factor 3, gamma (48kD); Interferon-stimulated transcription factor 3, gamma; 4.09
- 15 413745; AW247252; Hs.75514; nucleoside phosphorylase; nucleoside phosphorylase; 4.09
- 442081; AW770493; Hs.182674; guanine nucleotide binding protein (G protein) alpha 12; guanine nucleotide binding protein (G protein) alpha 12; 4.09
- 425003; AF119046; Hs.154149; apurinic/apyrimidinic endonuclease(APEX nuclease)-like 2 protein; apurinic/apyrimidinic endonuclease(APEX); 4.08
- 421859; AA356620; Hs.106947; KIAA0050 gene product; KIAA0050 gene product; 4.08
- 432841; M93425; Hs.62; protein tyrosine phosphatase, non-receptor type 12; protein tyrosine phosphatase, non-receptor type 12; 4.08
- 20 452058; AB028949; Hs.183994; KIAA1026 protein; KIAA1026 protein; 4.08
- 425059; AA687465; Hs.298184; potassium voltage-gated channel, shaker-related subfamily, beta member 2; potassium voltage-gated channel, shaker-related; 4.07
- 418526; BE019020; Hs.85838; solute carrier family 16 (monocarboxylic acid transporters), member 3; solute carrier family 16 (monocarboxylic acid transporters), member 3; 4.07
- 424517; A1539443; Hs.137447; Homo sapiens cDNA FLJ12168 fis, clone MAMMA1000643; Homo sapiens cDNA FLJ12168 fis, clone MA; 4.07
- 434224; AA380731; Hs.84; interleukin 2 receptor, gamma (severe combined immunodeficiency); interleukin 2 receptor, gamma (severe combined immunodeficiency); 4.06
- 25 446791; A1632276; Hs.195922; ESTs; ESTs; 4.06
- 432055; AA401039; Hs.2903; protein phosphatase 4 (formerly X), catalytic subunit; protein phosphatase 4 (formerly X), catalytic; 4.06
- 431194; D43704; Hs.250712; calcium channel, voltage-dependent, beta 3 subunit; calcium channel, voltage-dependent, beta 3; 4.06
- 418751; BE389014; Hs.372548; phosphoinositide-3-kinase, regulatory subunit, polypeptide 3 (p55, gamma); phosphoinositide-3-kinase, regulatory subunit, polypeptide 3 (p55, gamma); 4.06
- 425923; NM_005026; Hs.162808; phosphoinositide-3-kinase, catalytic, delta polypeptide; phosphoinositide-3-kinase, catalytic, delta; 4.05
- 30 408892; AL040127; Hs.34074; dipeptidylpeptidase VI; dipeptidylpeptidase VI; 4.04
- 448272; BE266912; Hs.14601; hematopoietic cell-specific Lyn substrate 1; hematopoietic cell-specific Lyn substrate 1; 4.04
- 439176; A1446444; Hs.190394; ESTs, Weakly similar to B28096 line-1 protein ORF2 [H.sapiens]; ESTs, Weakly similar to B28096 line-1 protein ORF2 [H.sapiens]; 4.04
- 417890; BE241595; Hs.82848; selectin L (lymphocyte adhesion molecule 1); selectin L (lymphocyte adhesion molecule 1); 4.04
- 35 410068; A1633888; Hs.58435; FYN-binding protein (FYN-120/130); FYN-binding protein (FYN-120/130); 4.03
- 410539; BE269047; Hs.65234; hypothetical protein FLJ20595; hypothetical protein FLJ20595; 4.03
- 427716; L38951; Hs.180448; karyopherin (importin) beta 1; karyopherin (importin) beta 1; 4.03
- 451050; AW937420; Hs.351868; ESTs; ESTs; 4.02
- 449687; AB023227; Hs.23860; KIAA1010 protein; KIAA1010 protein; 4.02
- 448499; BE613280; Hs.77550; p53-regulated DDA3; p53-regulated DDA3; 4.01
- 40 437527; A1241019; Hs.145644; ESTs; ESTs; 4.01
- 425118; AU076611; Hs.154872; methylene tetrahydrofolate dehydrogenase (NAD dependent), methylenetetrahydrofolate cyclohydrolase; methylene tetrahydrofolate dehydrogenase (NAD dependent), methylenetetrahydrofolate cyclohydrolase; 4.00
- 451931; AK000208; Hs.27267; Homo sapiens cDNA FLJ20201 fis, clone COLF12410; Homo sapiens cDNA FLJ20201 fis, clone CO; 4.00
- 412939; AW411491; Hs.75089; eukaryotic translation elongation factor 1 gamma; eukaryotic translation elongation factor 1 gamma; 4.00
- 408581; U66243; Hs.55039; mitogen-activated protein kinase 12; mitogen-activated protein kinase 12; 3.99
- 433577; AW007080; Hs.284102; ESTs; ESTs; 3.99
- 439963; AW247529; Hs.6793; platelet-activating factor acetylhydrolase, isoform 1b, gamma subunit (29kD); platelet-activating factor acetylhydrolase, isoform 1b, gamma subunit (29kD); 3.99
- 418528; BE247550; Hs.86859; growth factor receptor-bound protein 7; growth factor receptor-bound protein 7; 3.99
- 448533; AA311426; Hs.21636; tubulin, gamma 1; tubulin, gamma 1; 3.98
- 50 420298; ; C19000263.g[3108023]gb|AAC15755.1| (AC004659) BC62940_2 [Homo sapiens]||56335; C19000263.g[3108023]gb|AAC15755.1| (AC004659) BC62940_2 [Homo sapiens]||56335; 3.97
- 408414; A114888; Hs.193400; ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]; ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]; 3.97
- 415012; NM_004383; Hs.77793; c-src tyrosine kinase; c-src tyrosine kinase; 3.97
- 416084; L16591; Hs.79006; deoxythymidylate kinase (thymidylate kinase); deoxythymidylate kinase (thymidylate kinase); 3.95
- 422051; AW327546; Hs.111024; solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1; solute carrier family 25 (mitochondrial carrier, citrate transporter), member 1; 3.95
- 55 447887; AA114050; Hs.211610; caspase 8, apoptosis-related cysteine protease; caspase 8, apoptosis-related cysteine protease; 3.95
- 430770; AA765894; Hs.123296; ESTs; ESTs; 3.94
- 442894; A1026718; Hs.18954; ESTs; ESTs; 3.94
- 420333; AJ001383; Hs.97064; lymphocyte antigen 94 (mouse) homolog (activating NK-receptor; NK-p46); lymphocyte antigen 94 (mouse) homolog (activating NK-receptor; NK-p46); 3.94
- 438458; AA913381; Hs.279763; ESTs; ESTs; 3.94
- 60 422598; BE387202; Hs.118638; non-metastatic cells 1, protein (NM23A) expressed in; non-metastatic cells 1, protein (NM23A) expressed in; 3.93
- 420162; BE378432; Hs.95577; cyclin-dependent kinase 4; cyclin-dependent kinase 4; 3.93
- 424829; NM_002507; Hs.1827; nerve growth factor receptor (TNFR superfamily, member 16); nerve growth factor receptor (TNFR superfamily, member 16); 3.93
- 447574; AF162666; Hs.18895; tousel-like kinase 1; tousel-like kinase 1; 3.93
- 425797; AF002386; Hs.159545; platelet activating receptor homolog; platelet activating receptor homolog; 3.93
- 65 421910; NM_014586; Hs.109437; hormonally upregulated neu tumor-associated kinase; hormonally upregulated neu tumor-associated kinase; 3.92
- 413781; J05272; Hs.850; IMP (inosine monophosphate) dehydrogenase 1; IMP (inosine monophosphate) dehydrogenase 1; 3.92
- 434334; AA912476; Hs.116750; Homo sapiens cDNA FLJ13221 fis, clone NT2RP4002075; Homo sapiens cDNA FLJ13221 fis, clone NT; 3.92
- 400262; Hs.75309; Eos Control; Eos Control; 3.90
- 424877; AA349289; Hs.100057; Homo sapiens cDNA: FLJ22902 fis, clone KAT05581; Homo sapiens cDNA: FLJ22902 fis, clone K; 3.90
- 409799; D11928; Hs.76845; phosphoserine phosphatase-like; phosphoserine phosphatase-like; 3.90
- 435206; A1432364; Hs.160594; ESTs; ESTs; 3.90
- 438853; BE547830; Hs.375208; paired immunoglobulin-like receptor beta; paired immunoglobulin-like receptor beta; 3.90
- 413627; BE182082; Hs.246973; intron of Bicaudal D homolog 1; intron of Bicaudal D homolog 1; 3.90
- 75 426265; AA421069; Hs.97896; ESTs; ESTs; 3.89
- 451063; AW163702; Hs.25911; HLA-B associated transcript-2; HLA-B associated transcript-2; 3.89
- 407013; U35637; Hs.83870; gb|Human nebulin mRNA, partial cds; gb|Human nebulin mRNA, partial cds; 3.89
- 437239; AW503395; Hs.5541; ATPase, Ca transporting, ubiquitous; ATPase, Ca transporting, ubiquitous; 3.88
- 400261; Hs.1802; Eos Control; Eos Control; 3.88
- 404047; AF212223; Hs.25010; hypothetical protein P15-2; hypothetical protein P15-2; 3.88
- 80 422293; X94453; Hs.114366; pyrroline-5-carboxylate synthetase (glutamate gamma-semialdehyde synthetase); pyrroline-5-carboxylate synthetase (glutamate gamma-semialdehyde synthetase); 3.87
- 414251; AL042306; Hs.97689; VASA protein; VASA protein; 3.87
- 417767; BE242241; Hs.82542; acylxyacyl hydrolase (neutrophil); acylxyacyl hydrolase (neutrophil); 3.87
- 414443; AU077268; Hs.76144; platelet-derived growth factor receptor, beta polypeptide; platelet-derived growth factor receptor, beta polypeptide; 3.87

- 444099; D87432; Hs.10315; solute carrier family 7 (cationic amino acid transporter, y system), member 6; solute carrier family 7 (cationic amino ; 3.86
 419593; BE379320; Hs.91448; MKP-1 like protein tyrosine phosphatase; MKP-1 like protein tyrosine phosphatase; 3.86
 427022; AW245839; Hs.173255; small nuclear ribonucleoprotein polypeptide A; small nuclear ribonucleoprotein polypept; 3.86
 443661; AA336609; Hs.10862; Homo sapiens cDNA: FLJ23313 fis, clone HEP11919; Homo sapiens cDNA: FLJ23313 fis, clone H; 3.86
 408056; AA312329; Hs.42331; ephrin-A4; ephrin-A4; 3.86
 410552; X66945; Hs.748; fibroblast growth factor receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome); fibroblast growth factor receptor 1 (fms; 3.85
 450778; U81375; Hs.25450; solute carrier family 29 (nucleoside transporters), member 1; solute carrier family 29 (nucleoside tra; 3.85
 418978; T85295; Hs.268606; ESTs; ESTs; 3.84
 429903; AL134197; Hs.93597; cyclin-dependent kinase 5, regulatory subunit 1 (p35); cyclin-dependent kinase 5, regulatory su; 3.84
 442980; AA857025; Hs.8878; kinesin-like 1; kinesin-like 1; 3.84
 447232; AW499834; Hs.327; Interleukin 10 receptor, alpha; Interleukin 10 receptor, alpha; 3.84
 434688; AF154115; Hs.4076; CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1; CTD (carboxy-terminal domain, RNA polyme; 3.83
 432539; AL138168; Hs.278378; karyopherin beta 2b, transportin; karyopherin beta 2b, transportin; 3.83
 415684; D59356; Hs.374480; sorbitol dehydrogenase; sorbitol dehydrogenase; 3.83
 451598; N29102; Hs.79658; ESTs; ESTs; 3.82
 449433; A167208; Hs.9012; ESTs, Weakly similar to S26650 DNA-binding protein 5 [H.sapiens]; ESTs, Weakly similar to S26650 DNA-bind; 3.82
 426359; AA376409; Hs.10862; Homo sapiens cDNA: FLJ23313 fis, clone HEP11919; Homo sapiens cDNA: FLJ23313 fis, clone H; 3.81
 435160; AB002374; Hs.4791; KIAA0376 protein; KIAA0376 protein; 3.80
 443402; U77848; Hs.9295; elastin (supravalvular aortic stenosis, Williams-Beuren syndrome); elastin (supravalvular aortic stenosis, ; 3.80
 422753; A1928999; Hs.1575; small nuclear ribonucleoprotein D3 polypeptide (18kD); small nuclear ribonucleoprotein D3 polyp; 3.79
 421508; NM_004833; Hs.105115; absent in melanoma 2; absent in melanoma 2; 3.79
 414806; D14694; Hs.77329; phosphatidylserine synthase 1; phosphatidylserine synthase 1; 3.79
 428023; AL038843; Hs.374530; Homo sapiens cDNA: FLJ23602 fis, clone LNG15735; Homo sapiens cDNA: FLJ23602 fis, clone L; 3.79
 421654; AW163267; Hs.106469; suppressor of var1 (Scerelvisae) 3-like 1; suppressor of var1 (Scerelvisae) 3-like; 3.79
 439668; A1091277; Hs.302634; frizzled (Drosophila) homolog 8; frizzled (Drosophila) homolog 8; 3.78
 411126; AA151647; Hs.68677; cytochrome b-245, alpha polypeptide; cytochrome b-245, alpha polypeptide; 3.78
 429170; NM_001394; Hs.2359; dual specificity phosphatase 4; dual specificity phosphatase 4; 3.78
 425354; U62027; Hs.155935; complement component 3a receptor 1; complement component 3a receptor 1; 3.78
 423909; AL223183; Hs.135194; immunoglobulin superfamily, member 6; immunoglobulin superfamily, member 6; 3.78
 429667; A1675749; Hs.211608; nucleoporin 153kD; nucleoporin 153kD; 3.77
 414177; A1351359; Hs.356303; uncharacterized hypothalamus protein HARP11; uncharacterized hypothalamus protein HAR; 3.77
 414135; NM_004419; Hs.2128; dual specificity phosphatase 5; dual specificity phosphatase 5; 3.77
 445817; NM_003642; Hs.13340; histone acetyltransferase 1; histone acetyltransferase 1; 3.77
 410422; AL042014; Hs.63348; Homo sapiens, clone MGC:15203, mRNA, complete cds; Homo sapiens, clone MGC:15203, mRNA, com; 3.76
 412146; M92444; Hs.73722; APEX nuclease (multifunctional DNA repair enzyme); APEX nuclease (multifunctional DNA repair; 3.76
 413011; AW068115; Hs.821; biglycan; biglycan; 3.76
 428157; A1738718; Hs.198427; hexokinase 2; hexokinase 2; 3.76
 400288; X08258; Hs.149609; Integrin, alpha 5 (fibronectin receptor, alpha polypeptide); integrin, alpha 5 (fibronectin receptor, ; 3.75
 427378; BE515037; Hs.177556; melanoma antigen, family D, 1; melanoma antigen, family D, 1; 3.75
 405484; ; C3002124*gi12737280[refXP_006682.2] keratin 18 [Homo sapiens]||6533; C3002124*gi12737280[refXP_006682.2] k; 3.75
 450998; BE387614; Hs.25797; splicing factor 3b, subunit 4, 49kD; splicing factor 3b, subunit 4, 49kD; 3.75
 432460; H12812; Hs.274691; adenylate kinase 3; adenylate kinase 3; 3.75
 428816; AA004986; Hs.193852; ATP-binding cassette, sub-family C (CFTR/MRP), member 2; ATP-binding cassette, sub-family C (CFTR; 3.74
 431884; AA521246; Hs.210792; ESTs, Weakly similar to ALU8_HUMAN ALU SUBFAMILY SX SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Weakly similar
 to ALU8_HUMAN ALU S; 3.74
 453329; T97205; Hs.193400; ESTs, Weakly similar to 2109260A B cell growth factor [H.sapiens]; ESTs, Weakly similar to 2109260A B cell; 3.74
 426440; BE382756; Hs.168902; solute carrier family 2 (facilitated glucose transporter), member 1; solute carrier family 2 (facilitated glu; 3.74
 438330; AW450572; Hs.257316; ESTs; ESTs; 3.74
 419911; L15301; Hs.1276; BN51 (BHK21) temperature sensitivity complementing; BN51 (BHK21) temperature sensitivity com; 3.74
 452695; AW780199; Hs.30327; mitogen-activated protein kinase-activated protein kinase 5; mitogen-activated protein kinase-activat; 3.73
 442233; AW867149; Hs.28439; ESTs, Weakly similar to I38022 hypothetical protein [H.sapiens]; ESTs, Weakly similar to I38022 hypothet; 3.73
 451295; A1557212; Hs.17132; ESTs, Moderately similar to I54374 gene NF2 protein [H.sapiens]; ESTs, Moderately similar to I54374 gene ; 3.73
 410772; BE275297; Hs.194685; Homo sapiens clone 24875 mRNA sequence; Homo sapiens clone 24875 mRNA sequence; 3.73
 426251; A424283; Hs.168383; intercellular adhesion molecule 1 (CD54), human rhinovirus receptor; intercellular adhesion molecule 1 (CD54); 3.72
 449843; R85337; Hs.24030; solute carrier family 31 (copper transporters), member 2; solute carrier family 31 (copper transpor; 3.71
 423523; AW293828; Hs.193580; ESTs; ESTs; 3.71
 413407; A1956293; Hs.75339; inositol polyphosphate phosphatase-like 1; inositol polyphosphate phosphatase-like; 3.71
 448336; R53848; Hs.44976; ESTs; ESTs; 3.70
 422083; NM_001141; Hs.111256; arachidonate 15-lipoxygenase, second type; arachidonate 15-lipoxygenase, second typ; 3.70
 416087; AF046184; Hs.79008; SKI-INTERACTING PROTEIN; SKI-INTERACTING PROTEIN; 3.70
 442200; AW590572; Hs.235768; ESTs; ESTs; 3.70
 414280; BE410769; Hs.75873; zyxlin; zyxlin; 3.69
 409354; N68188; Hs.159472; Homo sapiens cDNA: FLJ22224 fis, clone HRC01703; Homo sapiens cDNA: FLJ22224 fis, clone H; 3.69
 415276; U88666; Hs.78353; SFRS protein kinase 2; SFRS protein kinase 2; 3.69
 439659; AW970780; Hs.58483; leucine-rich repeat-containing G protein-coupled receptor 6 (LGR6) mRNA; leucine-rich repeat-containing G protein; 3.69
 446522; NM_003876; Hs.15196; putative receptor protein; putative receptor protein; 3.68
 422785; A1824114; Hs.289088; heat shock 90kD protein 1, alpha; heat shock 90kD protein 1, alpha; 3.68
 401083; ; NM_016582; Homo sapiens peptide transporter 3 (LOC51295), mRNA, VERSION NM_016579.1 GI; NM_016582; Homo sapiens peptide transpor; 3.68
 413048; M93221; Hs.75182; mannose receptor, C type 1; mannose receptor, C type 1; 3.68
 452690; A1536070; Hs.16065; ESTs; ESTs; 3.68
 428981; BE313077; Hs.93135; ESTs, Weakly similar to ALU2_HUMAN ALU SUBFAMILY SB SEQUENCE CONTAMINATION WARNING ENTRY [H.sapiens]; ESTs, Weakly similar
 to ALU2_HUMAN ALU S; 3.68
 415010; NM_004203; Hs.77783; membrane-associated tyrosine- and threonine-specific cdc2-inhibitory kinase; membrane-associated tyrosine- and threon; 3.68
 428578; NM_005756; Hs.184942; G protein-coupled receptor 64; G protein-coupled receptor 64; 3.68
 446430; AA346837; Hs.15075; hypothetical protein DKFZp434E2216; hypothetical protein DKFZp434E2216; 3.68
 442013; AA506478; Hs.375009; Human DNA sequence from clone RP11-353C18 on chromosome 20 Contains ESTs, STSs, GSSs and CpG Islands. Contains the NIFS gene for
 cysteine desulfurase, two genes for novel proteins and the gene for the; Human DNA sequence from clone RP11-353C1; 3.66
 416602; NM_006159; Hs.367895; Protein kinase C-binding protein NELL2; Protein kinase C-binding protein NELL2; 3.65
 441226; BE563042; Hs.118820; Homo sapiens, Similar to RIKEN cDNA 0510012G03 gene, clone MGC:14132, mRNA, complete cds; Homo sapiens, Similar to RIKEN cDNA 0610;
 3.65
 413076; U10584; Hs.75188; wee1 (S. pombe) homolog; wee1 (S. pombe) homolog; 3.65
 429303; AW137635; Hs.44238; ESTs, Weakly similar to G65657 alpha-1C-adrenergic receptor splice form 2 [H.sapiens]; ESTs, Weakly similar to G65657 alpha-1C; 3.65
 452060; W26980; Hs.349089; ATP-binding cassette, sub-family F (GQN2), member 2; ATP-binding cassette, sub-family F (GQN2; 3.65

- 451558; NM_001089; Hs.26630; ATP-binding cassette, sub-family A (ABC1), member 3; ATP-binding cassette, sub-family A (ABC1); 3.65
 414774; X02419; Hs.77274; plasminogen activator, urokinase; plasminogen activator, urokinase; 3.65
 417426; NM_002291; Hs.82124; laminin, beta 1; laminin, beta 1; 3.65
 450296; AL041949; Hs.24756; hepatocyte growth factor-regulated tyrosine kinase substrate; hepatocyte growth factor-regulated tyrosine kinase; 3.64
 437689; AI358105; Hs.123164; ESTs, Weakly similar to match to ESTs AA657999 [H.sapiens]; ESTs, Weakly similar to match to ESTs AA; 3.64
 414029; BE297731; Hs.75709; mannose-6-phosphate receptor (cation dependent); mannose-6-phosphate receptor (cation dep); 3.64
 444368; AB033058; Hs.11101; KIAA1232 protein; KIAA1232 protein; 3.64
 425910; AA830797; Hs.184760; CCAAT-box-binding transcription factor; CCAAT-box-binding transcription factor; 3.63
 451484; AV648896; Hs.283771; hypothetical protein; hypothetical protein; 3.63
 444613; H29627; Hs.79092; hypothetical protein FLJ14427; hypothetical protein FLJ14427; 3.63
 447495; AW401884; Hs.18720; programmed cell death 8 (apoptosis-inducing factor); programmed cell death 8 (apoptosis-induc); 3.62
 408101; AW968504; Hs.278346; CDC2-related protein kinase 7; CDC2-related protein kinase 7; 3.62
 424732; D80001; Hs.152629; KIAA0179 protein; KIAA0179 protein; 3.62
 411168; NM_000169; Hs.69089; galactosidase, alpha; galactosidase, alpha; 3.62
 422112; BE540240; Hs.111783; Lsm1 protein; Lsm1 protein; 3.62
 453020; AL162038; Hs.31422; Homo sapiens mRNA; cDNA DKFZp434M229 (from clone DKFZp434M229); Homo sapiens mRNA; cDNA DKFZp434M229 (fr; 3.61
 438798; AA825792; Hs.377119; gb:od84b11.s1 NCL CGAP_Ov2 Homo sapiens cDNA clone, mRNA sequence; gb:od84b11.s1 NCL CGAP_Ov2 Homo sapiens; 3.61
 445515; BE388865; Hs.179999; Homo sapiens, clone IMAGE:3457003, mRNA; Homo sapiens, clone IMAGE:3457003, mRNA; 3.61
 407797; AK000524; Hs.39850; hypothetical protein FLJ20517; hypothetical protein FLJ20517; 3.60
 423217; NM_000094; Hs.1840; collagen, type VII, alpha 1 (epidermolysis bullosa, dystrophic, dominant and recessive); collagen, type VII, alpha 1 (epidermolys; 3.60
 444885; AJ677737; Hs.380100; hypothetical protein FLJ14005; hypothetical protein FLJ14005; 3.60
 433764; AW753676; Hs.39982; zinc finger protein RINZF (NM_023929); zinc finger protein RINZF (NM_023929); 3.59
 427857; AL133017; Hs.288679; hypothetical protein FLJ22865; hypothetical protein FLJ22865; 3.59
 415020; BE249315; Human DNA sequence from clone RP11-127L20 on chromosome 10. Contains ESTs, STGs, GSSs and CpG Islands. Contains the gene for a novel
 glutathione S-transferase and five novel genes; Human DNA sequence from clone RP11-127L2; 3.59
 415149; X12451; Hs.78056; cathepsin L; cathepsin L; 3.57
 458715; AK000973; Hs.1706; hypothetical protein FLJ10111; hypothetical protein FLJ10111; 3.57
 423576; NM_000383; Hs.129829; autoimmune regulator (autoimmune polyendocrinopathy candidiasis ectodermal dystrophy); autoimmune regulator (autoimmune polyen; 3.57
 404070; NM_015988; Hs.7120; cytokine receptor-like molecule 9; cytokine receptor-like molecule 9; 3.57
 434883; AW381538; Hs.19807; hypothetical protein MGC12959; hypothetical protein MGC12959; 3.57
 404976; ; NM_014323; Homo sapiens zinc finger protein 278 (ZNF278), transcript variant 1, mRNA; NM_014323; Homo sapiens zinc finger prot; 3.57
 449656; AA020008; Hs.188633; ESTs; ESTs; 3.56
 413796; AL040178; Hs.142003; ESTs; ESTs; 3.56
 408859; AI581134; Hs.181357; laminin receptor 1 (87kD, ribosomal protein SA); laminin receptor 1 (87kD, ribosomal prot; 3.56
 411030; BE387193; Hs.67896; 7-60 protein; 7-60 protein; 3.56
 447079; AA280057; Hs.105280; ESTs, Weakly similar to dJ963K23.2 [H.sapiens]; ESTs, Weakly similar to dJ963K23.2 [H.s]; 3.56
 424263; M77640; Hs.1767; L1 cell adhesion molecule (hydrocephalus, stenosis of aqueduct of Sylvius 1, MASA (mental retardation, aphasia, shuffling gait and adducted thumbs)
 syndrome, spastic paraplegia 1); L1 cell adhesion molecule (hydrocephalus; 3.55
 413472; BE242870; Hs.75379; solute carrier family 1 (glial high affinity glutamate transporter), member 3; solute carrier family 1 (glial high aff; 3.55
 443466; BE243123; Hs.321045; IKK-related kinase epsilon; inducible IkappaB kinase; IKK-related kinase epsilon; Inducible Ik; 3.55
 426746; J03626; Hs.2057; uridine monophosphate synthetase (orotate phosphoribosyl transferase and orotidine-5'-decarboxylase); uridine monophosphate synthetase (orotat; 3.55
 450931; N25158; Hs.25648; tumor necrosis factor receptor superfamily, member 5; tumor necrosis factor receptor superfam; 3.55
 425836; AW956696; Hs.90960; ESTs; ESTs; 3.54
 441054; AA913591; Hs.126480; ESTs; ESTs; 3.54
 440692; AL137268; Hs.7285; KIAA0759 protein; KIAA0759 protein; 3.54
 458946; AA009716; Hs.42311; ESTs; ESTs; 3.53
 449027; AJ271216; Hs.22880; dipeptidylpeptidase III; dipeptidylpeptidase III; 3.53
 421852; NM_014141; Hs.106552; cell recognition molecule Caspr2; cell recognition molecule Caspr2; 3.53
 422732; AA577455; Hs.24937; transformer-2 alpha (hra-2 alpha); transformer-2 alpha (hra-2 alpha); 3.53
 424870; T16545; Hs.244624; ESTs; ESTs; 3.52
 442794; AJ744130; Hs.356753; hypothetical protein MGC2975; hypothetical protein MGC2975; 3.52
 417840; D30857; Hs.82353; protein C receptor, endothelial (EPCR); protein C receptor, endothelial (EPCR); 3.51
 419971; AA400027; Hs.296234; ESTs, Weakly similar to T31613 hypothetical protein Y50E8A.1 - Caenorhabditis elegans [C.elegans]; ESTs, Weakly similar to T31613 hypotheti; 3.51
 410257; BE244044; Hs.61469; hypothetical protein; hypothetical protein; 3.51
 424837; BE276113; Hs.333034; N-acetyltransferase, homolog of S. cerevisiae ARD1; N-acetyltransferase, homolog of S. cerev; 3.51
 421921; H83363; Hs.355893; translocase of inner mitochondrial membrane 10 (yeast) homolog; translocase of inner mitochondrial membr; 3.50
 454128; AL031259; Hs.367900; programmed cell death 2; programmed cell death 2; 3.50
 434049; AA501430; Hs.5771; amyotrophic lateral sclerosis 2 (juvenile) chromosome region, candidate 2; amyotrophic lateral sclerosis 2 (juvenil; 3.50
 453641; AA444140; Hs.90960; ESTs; ESTs; 3.50
 429592; AB028041; Hs.209646; KIAA1118 protein; KIAA1118 protein; 3.49
 430847; AC003682; Hs.127988; ESTs, Weakly similar to Z211_HUMAN ZINC FINGER PROTEIN 211 [H.sapiens]; ESTs, Weakly similar to Z211_HUMAN ZINC; 3.47
 410855; X97795; Hs.66718; RAD54 (S.cerevisiae)-like; RAD54 (S.cerevisiae)-like; 3.44
 413372; H55532; Hs.349695; tubulin, alpha 2; tubulin, alpha 2; 3.07
 437224; AL117628; Hs.97808; ESTs; ESTs; 2.77
 430439; AL133661; ; DKFZP434B061 protein; DKFZP434B061 protein; 2.76
 435897; AF268223; Hs.128322; t-complex 11 (a murine top homolog); t-complex 11 (a murine top homolog); 2.53
 417592; AA204664; Hs.182437; ESTs, Weakly similar to 154383 chromosome segregation protein smc1 [H.sapiens]; ESTs, Weakly similar to 154383 chromosome; 2.46
 412026; AA383618; Hs.73073; testis-specific ankyrin motif containing protein; testis-specific ankyrin motif containing; 2.35
 422789; AK001113; Hs.120842; hypothetical protein FLJ10251; hypothetical protein FLJ10251; 2.33
 425627; AF012369; Hs.185885; ESTs; ESTs; 2.12
 438983; AF085884; Hs.20025; proscosin binding protein sp32 precursor; proscosin binding protein sp32 precursor; 2.07
 426709; AA383076; Hs.159274; outer dense fibre of sperm tails 1; outer dense fibre of sperm tails 1; 1.99
 433724; AI827749; Hs.144924; serine/threonine protein kinase SSTK; serine/threonine protein kinase SSTK; 1.68
 420710; NM_007009; Hs.99875; zona pellucida binding protein; zona pellucida binding protein; 1.54

TABLE 57B

Pkey:	Unique Eos probeset identifier number	
CAT number:	Gene cluster number	
Accession:	Genbank accession numbers	
Pkey	CAT Number	Accession

417886	1031334_1	AA210987 D57294 AA214564 AA207006 D56572
432407	MH1429_12	BG036675 BF772005 BF771866 BG960386 BG960381 NM_005712 AF110315 BE074534 BE182776 BE158000 BE157999 BE714315 AW818104
5		AW847519 AA099426 AW817981 AW856396 BG961122 AA224498 AA308542 AW821833 BF902155 AI732411 BG778834 BG283641 BE748279
		BE748870 BG319640 BE748864 BF739224 BG988155 AK057283 BI861466 AA663341 AA457591 BG949294 AW392886 AA071122 AA227849
		AA584918 BG969570 BF773486 AL041698 BF959013 R87170 C16859 BF770411 BF771298 AK075321 L13623 AA216700 BF771864 AW861859
		BE537068 C18935 AA155719 BF771172 BF769107 BF804964 AW818172 AW818143 AW392930 AW817057 AW858044 BF746211 AA179928
		AW861687 AW821826 BI055726 BF242643 AA207189 BF770412 BF771157 BG430030 AA065592
10	434414 35978_1	AF134164 BF809407 AA218557 BF842863 AI267168 BF876178 BG999253 AW861851 AW858362 AI817548 BF771300 AA113928 AA223422
		AA055556 BF773400 BF998869 BE081333 BE073424 BE142245 H59571 H59570 BF871558 BF871064 BE001132 BF826831 AW754298
		AA223267 BG997695 BG997697 AW991957 AA534354 BG319501 BF736309 AI694265 AA045564 BG950256 AI829309 BG987850 BE093175
		BF854337
	427298 115241_1	AA933717 BF081897 AW628327 AA641788 AA400495
	427521 513212_1	AW973352 BF222929 AW016853 BF059130 AI651829 BE551767 AA558414 AI339359 BF059601 AI961162 AI341422 AI206248 AI206165
15	407347 810943_1	AA548735 AA768578 AI539081 AW025967 AA736837 N79575 AW594357 AA480892
	430439 6760_2	T23514 AI655785
		AL133561 AL117481 AL122069 AW436292 AI968826 AL041090

TABLE 57C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham L. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham L. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
402199	8576116	Minus	84187-84744
402680	8113438	Plus	137634-137768,139702-139893,140475-14050
402260	3399665	Minus	113765-113910,115663-115765,116808-11694
402678	8113438	Plus	37395-37514,37866-37981
403171	9838164	Minus	74502-74703
406137	9166422	Minus	30487-31058
401704	3087841	Plus	24712-25374
402677	8113438	Plus	22135-22309,23063-23238
402679	8113438	Plus	132079-132216
402145	8018280	Plus	113086-114800
406547	7711513	Minus	172780-174358
402398	4082817	Minus	24019-24973
405484	5922025	Plus	199214-199579,199672-199920,200262-20049
401083	3242744	Plus	33192-33360
404976	3419864	Minus	139625-140632

TABLE 58A: 434 genes upregulated in bladder cancer relative to normal body tissues

Table 58A lists about 434 genes upregulated in bladder cancer relative to normal body tissues that are likely to encode proteins amenable to modulation by small molecules, peptides, or antibodies. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression. The protein products of these genes often contain one or more domains indicative of have oncogenic function or of transducing intracellular signals, or of being modulatable by small molecules, peptides, or antibodies (e.g. pkinase, death-domain, 7tm, phosphatase, or ion transporter). Certain predicted protein domains are noted.

Pkey: Unique Eos probeset identifier number
ExAccn: Exemplar accession number, GenBank accession number
UniGeneID: UniGene number
Pred.Prod.Domains: Certain predicted protein domains. Abbreviations used: TM, transmembrane domain; SS, signal sequence; =Y, very likely to contain; =M, likely to contain; other protein domain abbreviations are from PFAM (Nucleic Acids Research, 2002, 30:276-280).
UniGene Title: UniGene gene title
R1 90th percentile of bladder tumor AIs divided by the 50th percentile of normal tissue AIs

Pkey; ExAccn; UniGeneID; UniGene Title; Pred.Prod.Domains; R1

430630; AW269920; Hs.2621; cystatin A (stefin A); cystatin;TM=M; 35.25
 422282; AF019225; Hs.114309; apolipoprotein L; MotA_ExtB;TM=Y;SS=M; 33.25
 414655; N98568; Hs.76422; phospholipase A2, group IIA (platelets, ; phoslip;TM=M;SS=Y; 31.68
 415182; D17793; Hs.78183; aldo-keto reductase family 1, member C3; aldo_ket_red;TM=M; 31.04
 417771; AA804698; Hs.82547; retinoic acid receptor responder (tazarot; none;none; 28.50
 439180; AI393742; Hs.199087; v-erb-b2 avian erythroblastic leukemia v; Furin-like,pkinase,Recep_L_domain,Peptidase_M24; 27.43
 417079; U65590; Hs.81134; interleukin 1 receptor antagonist; IL1;SS=M; 25.98
 413859; AW992356; Hs.8364; Homo sapiens pyruvate dehydrogenase kinase; SAM_PNT;none; 25.38
 418818; AA228899; Hs.101307; Homo sapiens HUT11 protein mRNA, partial; UT;none; 25.28
 425397; J04088; Hs.156346; topoisomerase (DNA) II alpha (170kD); DNA_gyrase3,DNA_topoisolv,HATPase_c;SS=M; 23.58
 421733; AL119671; Hs.1420; fibroblast growth factor receptor 3 (act; lg.pkinase;TM=Y;SS=M; 21.24
 424008; R02740; Hs.137555; putative chemokine receptor; GTP-binding; 7tm_1;TM=Y;SS=M; 20.45
 447343; AA256841; Hs.23684; ESTs, Highly similar to S02392 alpha-2-m; none;none; 19.78
 408243; Y00787; Hs.624; interleukin 8; HLH,PAS,IL8;TM=M; 18.90
 427490; Z95152; Hs.178695; mitogen-activated protein kinase 13; pkinase;TM=M; 18.75
 410687; U24389; Hs.65436; lysyl oxidase-like 1; Lysyl_oxidase;SS=M; 18.63
 444381; BE387335; Hs.283713; ESTs, Weakly similar to 864054 hypohep; Collagen;TM=M;SS=M; 18.60
 452747; BE153855; Hs.61460; Ig superfamily receptor LNIR; Ig,Rhbd_glycop;TM=Y;SS=M; 18.55
 415444; BE247295; Hs.78452; solute carrier family 20 (phosphate tran; PHO4,LIM;TM=M; 18.25

- 413132; NM_006823; Hs.75209; protein kinase (cAMP-dependant, catalytic); PKD;SS=M; 17.73
 427337; Z46223; Hs.176663; Fc fragment of IgG, low affinity IIb, γ_2 ; Ig;TM=Y;SS=M; 17.68
 450746; D82673; Hs.278589; general transcription factor II, γ ; none;SH3,PK; 17.12
 418945; BE246762; Hs.89499; arachidonate 5-lipoxygenase; lipoxygenase,PLAT;TM=M; 16.88
 420981; L40904; Hs.100724; peroxisome proliferative activated recep; hormone_rec,zf-C4;TM=M; 16.78
 439941; AI392640; Hs.18272; amino acid transporter system A1; Aa_trans;TM=Y; 16.75
 431846; BE019924; Hs.271580; uroplakin 1B; transmembrane4;TM=Y;SS=M; 16.56
 424247; X14008; Hs.234734; lysozyme (renal amyloidosis); lys,lg,FAD_Synth,kdh,kdh_C,pkinase;SS=M; 16.43
 414883; AA926960; CDC28 protein kinase 1; CKS; 16.20
 438091; AW373062; nuclear receptor subfamily 1, group 1, m; hormone_rec,zf-C4;none; 15.80
 439963; AW247529; Hs.6793; platelet-activating factor acetylhydrolase PAF-AH1b, lipase_GDSL;TM=M; 15.70
 428450; NM_014791; Hs.184339; KIAA0175 gene product; KA1,pkinase;TM=M; 15.63
 422278; AF072873; Hs.114216; frizzled (Drosophila) homolog 6; Fz,Frizzled,7tm_2;TM=Y;SS=M; 15.45
 434293; NM_004445; Hs.3798; EphB6; EPH1bd,fn3,pkinase,SAM;TM=Y;SS=M; 15.43
 417880; BE241595; Hs.82848; selectin L (lymphocyte adhesion molecule); EGF,lectin_c,sushi;TM=M;SS=M; 15.28
 443991; NM_002250; Hs.10082; potassium intermediate/small conductance; CaMBD,SK_channel,ion_trans;TM=Y;SS=M; 15.10
 416305; AU076628; Hs.78187; coxsackie virus and adenovirus receptor; Ig;TM=Y;SS=M; 14.90
 432306; Y18207; Hs.303090; protein phosphatase 1, regulatory (inhib; CBM_21;TM=M; 14.80
 413076; U10554; Hs.75188; wee1 (S. pombe) homolog; pkinase;TM=M; 14.73
 429345; R11141; Hs.199695; hypothetical protein; K,letra,SAM; 14.58
 449230; BE613348; Hs.211679; melanoma cell adhesion molecule; ig,isochr,Ribosomal_L6,F-box;TM=Y;SS=M; 14.55
 421508; NM_004533; Hs.105115; absent in melanoma 2; PAAD_DAPIN,HIN;TM=M; 14.53
 446008; NM_004403; Hs.13530; deafness, autosomal dominant 5; none;TM=M;SS=M; 14.35
 429555; AW139399; Hs.98988; ESTs; none;TM=M; 14.18
 416224; NM_002902; Hs.79088; reticulocalbin 2, EF-hand calcium bindin; ehand;SS=M; 14.13
 429573; AA884407; Hs.211695; protein tyrosine phosphatase, non-recept; Y_phosphatase,Band_41,PDZ;SS=M; 13.90
 426657; NM_015865; Hs.171713; solute carrier family 14 (urea transport; UT;TM=Y; 13.83
 428157; AJ738719; Hs.198427; hexokinase 2; hexokinase,hexokinase2,none; 13.80
 400843; ; NM_003105*Homo sapiens sortilin-related; EGF,fn3,ldl_recept_g,ldl_recept_b,granulin,BNR;TM=Y;SS=M; 13.78
 439453; BE264974; Hs.6566; thyroid hormone receptor interactor 13; AAA,ABC_tran,Cose;TM=M; 13.38
 432314; AA533447; Hs.312989; ESTs; Xlrk,none; 13.25
 413109; AW389845; Hs.110865; ESTs; PHO4,none; 13.15
 424490; AJ278016; Hs.55555; ankyrin repeat domain 3; ank,pkinase;TM=M; 13.13
 426490; NM_001621; Hs.170087; aryl hydrocarbon receptor; PAC,PAS;TM=M; 12.93
 426155; NM_001982; Hs.199067; v-erb-b2 avian erythroblastic leukemia v; Furin-like,pkinase,Recep_L_domain,Furin-like,pkinase,Recep_L_domain,Peptidase_M24; 12.43
 440249; AI245580; Hs.249175; ESTs; TaD_DNase,pkinase,death,none; 12.38
 425177; AF127577; Hs.155017; nuclear receptor interacting protein 1; none;SS=M; 12.38
 404942; U03825; ; splicing factor, arginine/serine-rich 9; CD38;TM=Y;SS=M; 12.03
 439569; AW602166; Hs.222399; CEGP1 protein; EGF,TNFR_p6,granulin,CUB,Keratin_B2,TIL;TM=M;SS=M; 11.93
 443195; BE148235; Hs.193063; Homo sapiens cDNA FLJ14201 fis, clone NT; Aa_trans,none; 11.88
 408000; L11690; Hs.198689; bulbus pemphigoid antigen 1 (230240kD); ehand,spectrin,GAS2,SH3,Plectin,RA,Xylose_isom,FLID,bZIP,Tropomyosin,Myc-LZ,M,ldh_C,CH,ALP3;TM=M; 11.88
 412182; AA205588; Hs.155180; Splicing factor, arginine/serine-rich, 4; rrm,hormone_rec,zf-C4,sugar_tr; 11.85
 433470; AF990584; ; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 11.80
 425118; AU076611; Hs.154672; methylene tetrahydrofolate dehydrogenase; myb_DNA-binding,THF_DHG_C,THF_DHG_C,THF_DHG_C,CAP_GLY,AAA,LON,Peptidase_C9,bZIP,Mxan_ur permease,HCO3_cotransp;TM=M; 11.69
 418870; AF147204; Hs.89414; chemokine (C-X-C motif), receptor 4 (fus; 7tm_1,7tm_2;TM=Y;SS=M; 11.50
 426761; AJ015709; Hs.172089; Homo sapiens mRNA; cDNA DKFZp586I2022 (f; none;TM=Y;SS=M; 11.48
 439760; AL359053; Hs.57664; Homo sapiens mRNA full length insert cDNA; IMPDH_C,IMPDH_N,CBS,Integrin_B,Ricln_B,lectin; 11.38
 446742; AA232119; Hs.16085; putative G-protein coupled receptor; none;TM=Y;SS=M; 11.23
 436729; BE21807; ; transmembrane 4 superfamily member 1; none;TM=Y;SS=M; 11.18
 409960; BE261944; Hs.339673; hexokinase 1; none,none; 11.02
 426539; AB011155; Hs.170290; discs, large (Drosophila) homolog 5; SH3,PDZ,Guanylate_kin;TM=M; 10.78
 417821; BE245149; Hs.82643; protea tyrosine kinase 9; cofilin_ADF;SS=M; 10.63
 427654; AA410183; Hs.137475; ESTs; lon_trans,vwc,IGFBP,isp_1; 10.58
 418004; U37519; Hs.87539; aldehyde dehydrogenase 3 family, member; aldedh;TM=M;SS=M; 10.53
 447365; BE383676; Hs.334; Rho guanine nucleotide exchange factor 1; SH3,PH,RhoGEF;TM=M; 10.53
 449437; AJ702038; Hs.100057; Homo sapiens cDNA; FLJ22902 fis, clone K; none,none; 10.52
 436856; AI469355; Hs.127310; ESTs; pkinase,rrm;TM=M; 10.48
 451035; AU076785; Hs.430; plasmin 1 (1 isoform); ehand,CH,Adaptin_N;SS=M; 10.38
 418299; AA278530; Hs.83988; integrin, beta 2 (antigen CD18 (p95), β_2 ; Integrin_B,EGF,PS;TM=Y;SS=M; 10.35
 431890; X17033; Hs.271986; integrin, alpha 2 (CD49B, alpha 2 subunit; vwa,Integrin_A,FG-GAP;TM=Y;SS=M; 10.34
 440006; AK000517; Hs.6844; hypothetical protein FLJ20510; AAA,NB-ARC,PAAD_DAPIN,NA;NA; 10.25
 420344; BE463721; Hs.97101; putative G protein-coupled receptor; Methyltransf_5;TM=Y;SS=M; 10.18
 437852; BE001836; Hs.256897; ESTs, Weakly similar to dJ365O12.1 (Hsa; GPS,7tm_2;TM=Y; 10.13
 400752; ; NM_003105*Homo sapiens sortilin-related; EGF,fn3,ldl_recept_a,ldl_recept_b,granulin,BNR;TM=Y;SS=M; 10.08
 427700; AA282294; Hs.180383; dual specificity phosphatase 6; Rhodanese,DSPC;TM=M; 10.05
 426728; NM_007118; Hs.171957; triple functional domain (PTPRF interact; SH3,lg,pkinase,PH,spectrin,RhoGEF;TM=M; 10.05
 400496; ; ENSP00003224716*GTP-binding protein SAR; none;TM=Y; 10.01
 413899; AF083692; Hs.75608; tight junction protein 2 (zone occludens; SH3,PDZ,Guanylate_kin;TM=M; 10.00
 404568; ; NM_022071*Homo sapiens hypothetical pro; SH2;TM=M; 10.00
 444823; BE262989; Hs.12045; putative protein; Mra1,MBOAT;TM=M;SS=Y; 9.93
 421425; AK001564; Hs.104222; hypothetical protein FLJ10702; ehand,kazal,arf,ras,7tm_1;TM=M; 9.90
 413441; AI929374; Hs.75367; Src-like-adaptor; SH2,SH3;TM=M; 9.90
 424954; NM_000546; Hs.1846; tumor protein p53 (Li-Fraumeni syndrome); P53,WD40,JRK;TM=M; 9.88
 452289; BE568205; Hs.28827; mitogen-activated protein kinase kinase ; pkinase;TM=M; 9.85
 439223; AW238299; Hs.250618; UL16 binding protein 2; ldl_recept_a,PKD,MHC_J;TM=M;SS=Y; 9.83
 429238; NM_002849; Hs.198288; protein tyrosine phosphatase, receptor t; Y_phosphatase;TM=Y;SS=M; 9.80
 414135; NM_004419; Hs.2126; dual specificity phosphatase 5; Rhodanese,DSPC,Y_phosphatase;TM=M; 9.73
 452239; AW379378; Hs.170121; protein tyrosine phosphatase, receptor t; none,none; 9.73
 418322; AA284166; Hs.84113; cyclin-dependent kinase inhibitor 3 (CDK; Y_phosphatase,DSPC;TM=M; 9.72
 403912; ; CS000394*gi12737280refXP_006682.2) k; none;TM=M; 9.70
 427315; AA179949; Hs.175563; Homo sapiens mRNA; cDNA DKFZp564N0763 (f; none,spectrin,SH3,PH,CH; 9.70

- 428428; AL037544; Hs.184290; cyclin-dependent kinase 7 (homolog of Xc; pkinase; TM=M; 9.68
 422241; Y00062; Hs.170121; protein tyrosine phosphatase, receptor t; kinesin, fn3, Y_phosphatase; TM=M; 9.63
 429083; Y09397; Hs.227817; BCL2-related protein A1; Bcl-2; TM=M; 9.63
 425322; U63630; Hs.155837; protein kinase, DNA-activated, catalytic; PI3_P14_kinase, FAT, FATC; TM=M; 9.55
 430259; BE5650182; Hs.127826; RafGEF-like protein 3, mouse homolog; fn3, RA, RasGEF; TM=M; SS=M; 9.50
 428520; AA331961; Hs.184736; hypothetical protein FLJ10097; none; TM=M; 9.50
 418969; W33191; Hs.28907; hypothetical protein FLJ20258; SH3; TM=M; 9.50
 448913; AA194422; Hs.22564; myosin VI; mm, zf-RanBP, pkinase, GST_C, Ets, SAM_PNT, ABC2_membrane, myosin_head, IQ, Myosin_N, bZIP, zf-C2H2, PHD, BTB, TFIIS, AT_hock, SAM; TM=M; 9.50
 414911; NM_000107; Hs.77602; damage-specific DNA binding protein 2 (4; WD40, homeobox, LIM; TM=M; 9.48
 451295; AI557212; Hs.17132; ESTs, Moderately similar to 154374 gene; pkinase, DAG_PE-bind, pkinase_C, OPR; none; 9.45
 402328; ; Target Exon; pkinase; TM=M; 9.44
 443710; AI928136; Hs.9691; Homo sapiens cDNA: FLJ23249 fls, clone C; G-alpha; none; 9.42
 414987; AA524394; Hs.294022; hypothetical protein FLJ14950; SH2; TM=M; 9.42
 434375; BE277910; Hs.3833; 3'-phosphoadenosine 5'-phosphosulfate sy; APS_kinase, ATP-sulfurylase, PRK, Thymidylate_kin; SS=M; 9.40
 418827; BE327311; Hs.47166; HT021; none; TM=M; 9.40
 440578; AW005054; Hs.47883; ESTs, Weakly similar to KCC1_HUMAN CALCI; pkinase; none; 9.35
 433376; AI249361; Hs.74122; caspase 4, apoptosis-related cysteine pr; CARD, ICE_p10, ICE_p20; SS=M; 9.28
 410668; BE379794; Hs.65403; hypothetical protein; death, TNFR_c6; TM=Y; SS=M; 9.25
 430024; AJ808780; Hs.227730; integrin, alpha 6; integrin_A, FG-GAP; TM=Y; SS=M; 9.23
 452696; AJ826645; Hs.211534; ESTs; ArfGap, PH, ank, Guanylate_kin, PDZ, SH3; 9.13
 434263; N34895; Hs.44648; ESTs; ig; none; 9.13
 407949; W21874; Hs.247057; ESTs, Weakly similar to 2109260A B cell; Ribosomal_S14, ank, pkinase, death; none; 9.10
 429332; AF030403; Hs.189263; Sla-20 related kinase; pkinase, metalthio; TM=M; SS=M; 9.03
 417426; NM_002291; Hs.82124; laminin, beta 1; laminin_EGF, laminin_Nterm, integrin_B; SS=M; 9.08
 443951; F13272; Hs.111334; fibrin, light polypeptide; PMP22_Claudin; none; 9.07
 414368; W70171; Hs.75939; uridine monophosphate kinase; PRK_CoA; 8.98
 451292; AB037716; Hs.26204; KIAA1295 protein; SH3; TM=M; 8.93
 438000; AI825880; Hs.5985; non-kinase Cdc42 effector protein SPEC2; none; TM=M; 8.90
 446520; AA128808; Hs.179802; transporter-like protein; none; TM=Y; SS=M; 8.90
 436075; BE090176; Hs.179902; transporter-like protein; none; TM=Y; SS=M; 8.88
 437056; AI147061; ; gbok33a11.1; Soares_NSF_F8_9W_OT_PA_P_S; none, spectrin, SH3, PH, C4; 8.78
 445496; AB007880; Hs.12802; development and differentiation enhancer; SH3, ank, PH, ArfGap; TM=M; 8.78
 418203; XS4942; Hs.83758; CDC28 protein kinase 2; CKS; 8.75
 434608; AA805443; Hs.179809; hypothetical protein FLJ22995; none; TM=M; 8.70
 445033; AV652402; Hs.72901; mucin 13, epithelial transmembrane; ank; 8.68
 417640; D30857; Hs.82353; protein C receptor, endothelial (EPCR); none; TM=M; SS=M; 8.65
 432841; M93425; Hs.62; protein tyrosine phosphatase, non-recept Y_phosphatase; SS=M; 8.65
 430397; AI924533; Hs.105607; bicarbonate transporter related protein; HCO3_cotransp; TM=Y; 8.64
 448658; AW196563; Hs.200242; caspase recruitment domain protein 6; CARD; TM=M; 8.60
 442994; AI026718; Hs.16954; ESTs; ank, pkinase, death, Ribosomal_S14; 8.60
 429109; AL006637; Hs.196352; neutrophil cytosolic factor 4 (40kD); SH3, OPR, PX; TM=M; 8.60
 455439; AW945484; Hs.184252; ESTs, Weakly similar to ALU8_HUMAN ALU S; none, 7m_1; 8.55
 437763; AA489369; Hs.5831; tissue inhibitor of metalloproteinase 1; TIMP, pkinase, DAG_PE-bind, RBD; 8.43
 417035; AA192455; Hs.22968; Homo sapiens clone IMAGE451939, mRNA seq; none, none; 8.40
 418478; U38945; Hs.1174; cyclin-dependent kinase inhibitor 2A (me; ank; 8.39
 448209; AW160488; Hs.20709; tetraspan 5; transmembrane4; TM=Y; SS=M; 8.33
 450139; AK001838; Hs.296323; serum/glucocorticoid regulated kinase; none, none; 8.33
 446350; AF052112; Hs.12540; lysophospholipase I; atylhydrolase_2; TM=M; 8.31
 427509; M62505; Hs.2161; complement component 5 receptor 1 (C5a I; 7m_1; TM=Y; SS=M; 8.30
 445633; AI45386; Hs.17287; ESTs, Weakly similar to S26689 hypothetical; IRK; none; 8.28
 446719; W33900; Hs.301872; hypothetical protein MGC4840; AAA, SKI; TM=M; 8.23
 424762; AL119442; Hs.183684; eukaryotic translation initiation factor; none, none; 8.20
 427274; NM_005211; Hs.174142; colony stimulating factor 1 receptor, for; ig, pkinase; TM=Y; SS=M; 8.18
 416094; AW995512; Hs.225977; nuclear receptor coactivator 3; none, none; 8.15
 419262; AA834664; Hs.29131; nuclear receptor coactivator 2; PAS, zf-C2H2, SET; 8.15
 417386; AL037228; Hs.82043; D123 gene product; NUDIX, secY, E1_dehydrog, transket_pyr; TM=Y; SS=M; 8.13
 431238; AV656840; Hs.285116; interleukin 13 receptor, alpha 1; fn3; TM=Y; SS=M; 8.10
 439658; AA332057; Hs.6639; hypothetical protein MGC15440; none; TM=M; SS=M; 8.09
 425424; NM_004954; Hs.157199; ELKL motif kinase; pkinase, UBA, KA1; TM=M; 8.08
 422573; AW297986; Hs.295726; integrin, alpha V (vitronectin receptor; FG-GAP, integrin_A; none; 8.05
 408912; AB011084; Hs.48924; KIAA0512 gene product; ALEX2; Armadillo_seg; TM=M; SS=M; 8.03
 447674; BE270640; Hs.19192; cyclin-dependent kinase 2; pkinase; SS=M; 8.03
 404891; ; Target Exon; none, none; 7.95
 414278; AA330116; Hs.77273; Human glucose transporter pseudogene; none, none; 7.93
 452888; AW955464; Hs.30942; ephrin-B2; Ephrin, fn2; TM=Y; SS=M; 7.93
 433211; H11850; Hs.12808; MARK; pkinase, UBA, KA1; SS=M; 7.91
 436486; W57578; Hs.237955; RAB7, member RAS oncogene family; pkinase, ABC1; none; 7.90
 413219; AA678200; Hs.118727; Homo sapiens cDNA FLJ13692 fls, clone PL; HLH, death, TNFR_c6, Acyl-CoA_hydro; 7.90
 417381; AF164142; Hs.82042; solute carrier family 23 (nucleobase tra; xan_ur_permease, RA; 7.88
 427122; AW057736; Hs.323910; HER2 receptor tyrosine kinase (c-erb-b2; Furin-like, pkinase, Recept_L_domain, YLP; TM=Y; SS=M; 7.86
 405036; ; NM_021628; Homo sapiens arachidonate lip; lipoxigenase, complex1_49kd, PLAT; TM=M; 7.83
 418529; AW005595; Hs.250897; TRK-fused gene; Band_41, ERM, pkinase, LRR, LRRCT, MAM, Nucleoplasm, Tropomyosin, OPR, filament, bZIP, G-gamma_M, DUF164; TM=M; 7.83
 431912; AI660552; Hs.76549; ESTs, Weakly similar to A56154 Abi subst; none, Acyl-CoA_ch, Acyl-CoA_ch_M, Acyl-CoA_ch_N; 7.80
 432981; NM_002733; Hs.3136; protein kinase, AMP-activated, gamma 1 n; CBS, Aa_trans; TM=M; 7.78
 422940; BE077458; ; gbRC1-BT0605-090500-015-b04 BT0606 Homo; Sec7, PH, ANF_receptor, ig_chan, WD40, IRK; 7.78
 446636; AC002563; Hs.15767; citron (rho-interacting, cerine/threonin; CNH, DAG_PE-bind, PH, Involucrin, M; TM=M; 7.78
 431183; NM_008855; Hs.250696; KDEL (Lys-Asp-Glu-Leu) endoplasmic retic; ER_lumen_recept; TM=M; SS=M; 7.78
 400845; ; NM_003105; Homo sapiens sortilin-related; EGF, fn3, kL_recept, ald_recept, bgranulin, BNR; TM=Y; SS=M; 7.73
 409142; AL136877; Hs.50758; SMC4 (structural maintenance of chromosom; ABC_tran, M, SMC_N, SMC_C, DUF164; none; 7.73
 437192; AW975786; Hs.75355; ubiquitin-conjugating enzyme E2N (homolo; UQ_con, Y_phosphatase, SH2; 7.70
 403212; ; NM_018695; Homo sapiens Intersectin 2 (IT; SH3, effhand, C2, PH, RhoGEF; TM=M; 7.70
 441190; H09073; Hs.25046; ESTs; E1-E2_ATPase, Cation_ATPase_C, Cation_ATPase_N, Hydrolase; none; 7.68

- 408745; AA077391; ; gb:7B14E12 Chromosome 7 Fetal Brain cDNA; 7m_1,zf-C3HC4,m3,SPRY,KRAB,zf-C2H2,rve,zf-B_box;TM=Y;SS=M; 7.68
- 428840; M15990; Hs.194148; v-yes-1 Yamaguchi sarcoma viral oncogene; SH2,SH3,pkinase;SS=M; 7.65
- 447898; AW969638; Hs.112318; 6.2 kd protein; none;none; 7.65
- 425289; AW139342; Hs.155530; interferon, gamma-inducible protein 16; PAAD_DAPIN,HIN;SS=M; 7.63
- 401927; ; C17000914*gi18394367ref|NP_058549.1|s; none; 7.60
- 407347; AA829847; ; gb:cd040d07.s1 NCI_CGAP_GCB1 Homo sapiens; RhoGAP,SH2,pkinase,POLO_box;none; 7.58
- 449924; W30681; Hs.146233; Homo sapiens cDNA: FLJ22130 fls, clone H; SH3;none; 7.57
- 429952; AF080158; Hs.226673; inhibitor of kappa light polypeptide gen; pkinase,ubiquitin,Enterotoxin_A,PHO4,pkinase,ubiquitin; 7.55
- 445800; AA126419; Hs.32944; inositol polyphosphate-4-phosphatase; ty; none;none; 7.55
- 421489; AF922821; Hs.32433; ESTs; none,PI-PLC-X,PI-PLC-Y,C2; 7.53
- 430486; BE062109; Hs.241551; chloride channel, calcium activated, fam; none;TM=Y;SS=M; 7.53
- 431605; AW972407; Hs.124370; gb:EST384498 MAGE resequences, MAGL Homo; adenylylkinase,SRP54;TM=M; 7.50
- 430670; A1417881; Hs.292464; ESTs; 7m_2,Fz,Frizzled;none; 7.50
- 431441; U81961; Hs.2794; sodium channel, nonvoltage-gated 1 alpha; ASC;TM=Y; 7.48
- 420676; A1434780; Hs.4248; vav 2 oncogene; RhoGEF,PH,CH,SH2,SH3,DAG_PE-bind;none; 7.48
- 444252; R21135; Hs.54985; ESTs; none;none; 7.47
- 414914; U49844; Hs.77613; ataxia telangiectasia and Rad3 related; FAT,FATC,PI3_P14_kinase;TM=M; 7.47
- 443428; AF098158; Hs.9329; chromosome 20 open reading frame 1; none;TM=M; 7.45
- 418546; AA224827; ; gb:nc32g04.s1 NCI_CGAP_Py2 Homo sapiens; vwa,Integrin_A,FG-GAP;none; 7.45
- 437860; AA333063; Hs.279898; Homo sapiens cDNA: FLJ23165 fls, clone L; none;NA;NA; 7.43
- 452007; AA428234; Hs.34908; ESTs, Weakly similar to T17210 hypothet; none,pkinase; 7.40
- 432407; AA221036; ; gb:z03f12.1 Stratagene NT2 neuronal pr; DEAD,helicase_C,rmr,Ndr,Cys_knot,TIL,vwa,vwc,vwd,QJ,RIIa,abhydrolase,TGF-beta,DUF139,TPR,DSPC,isp_1,Ribosomal_S21,rvp;TM=M; 7.40
- 424943; AJ077260; Hs.153924; death-associated protein kinase 1; ank,pkinase,death,SPRY,SAP,Ribosomal_L24e,SRP54,dDENN,DENN,uDENN;TM=M; 7.40
- 421429; NM_014922; Hs.104305; death effector filament-forming Ced-4-l; LRR,PAAD_DAPIN,AAA,CARD,NB-ARC;NA;NA; 7.38
- 417141; U22682; Hs.347353; nuclear receptor subfamily 1, group H, m; hormone_rec,zf-C4;SS=M; 7.38
- 430016; NM_004736; Hs.227656; xenotropic and polytropic retrovirus rec; SPX,EXS;TM=Y; 7.38
- 422813; AV656574; Hs.121068; transmembrane 4 superfamily member 6; transmembrane4;TM=Y;SS=M; 7.32
- 433390; AA586950; Hs.260180; Homo sapiens mRNA; cDNA DKFZp781G18121 (; none,spectrin,SH3,PH,CH; 7.26
- 409213; U81412; Hs.51133; PTK6 protein tyrosine kinase 6; SH2,SH3,pkinase;TM=M; 7.24
- 444745; AF117754; Hs.11861; thyroid hormone receptor-associated prot; none;TM=M; 7.23
- 452817; AA322859; Hs.284275; Homo sapiens PAK2 mRNA, complete cds; pkinase,PBD;TM=M; 7.19
- 407591; NM_000910; Hs.37125; neuropeptide Y receptor Y2; 7m_1;TM=Y; 7.18
- 427231; AW851989; Hs.285814; sprouty (Drosophila) homolog 4; SH2,SH3;TM=M;SS=M; 7.18
- 450285; AW383258; Hs.24752; spectrin SH3 domain binding protein 1; SH3;TM=M; 7.18
- 403344; ; NM_000341; Homo sapiens solute carrier fa; alpha-amylase;TM=Y; 7.15
- 427268; X78520; Hs.174139; chloride channel 3; CBS,voltage_CLC;TM=Y; 7.14
- 442213; N36110; Hs.305971; solute carrier family 2 (facilitated glu; sugar_tr;TM=Y;SS=M; 7.14
- 404876; ; NM_022819; Homo sapiens phospholipase A2; phospho;SS=M; 7.11
- 433618; AA802539; Hs.345494; ESTs; G-alpha_A_deaminase; 7.10
- 417165; R80137; Hs.302738; Homo sapiens cDNA: FLJ21425 fls, clone C; Sulfate_transp,STAS,HMG_box; 7.08
- 413073; AL038165; Hs.75187; translocase of outer mitochondrial membr; MAS20,zf-A20,VPS9;TM=M;SS=M; 7.05
- 426655; AL049589; Hs.171723; neuronal cell death-related protein; TFIID-31;TM=M; 7.05
- 423387; AJ012074; ; vasocutic intestinal peptide receptor 1; 7m_2,HRM,CSD;TM=Y;SS=M; 7.03
- 400211; ; NM_003898; Homo sapiens PAK-Interacting ; SH3,PH,RhoGEF,Terpena_synth;TM=M; 7.03
- 438150; AA037634; Hs.342874; transforming growth factor, beta recepto; zona_pellucida;none; 6.93
- 431341; AA307211; Hs.251531; proteasome (prosome, macropain) subunit; proteasome;TM=M; 6.93
- 405275; AB028989; ; mitogen-activated protein kinase 8 inter; Cys_knot,TGF-beta,vwa,vwc,vwd,TIL,DUF139;SS=M; 6.93
- 415392; Z44057; Hs.10957; ESTs; PIP5K;none; 6.89
- 429355; AW973253; Hs.292689; ESTs; pkinase,bZIP,Armadillo_seg;none; 6.88
- 426683; M88874; Hs.211587; phospholipase A2, group IVA (cytosolic; C2,PLA2_B;TM=M; 6.85
- 427832; AF035362; Hs.180930; TBP-associated factor 172; SNF2_N,helicase_C,Armadillo_seg,HEAT;TM=M; 6.83
- 447887; AA114050; Hs.18949; caspase 8, apoptosis-related cysteine pr; ICE_p10,ICE_p20,DED;TM=M; 6.80
- 400158; ; ENSP0000024302; cDNA FLJ11591 fls, clone Sm;SS=M; 6.78
- 401917; AL050149; ; RAN binding protein 3; Orexin,SH2,STAT,STAT_bind,STAT_prot,lon_trans,PAC,PAS;none; 6.78
- 400844; ; NM_003105; Homo sapiens sortilin-related; EGF,m3,lid_recept_a,lid_recept_b,granulin,BNR;TM=Y;SS=M; 6.73
- 457239; U07358; Hs.211601; mitogen-activated protein kinase kinase ; pkinase; 6.73
- 404440; ; NM_021048; Homo sapiens melanoma antigen; MAGE;TM=M; 6.73
- 424241; AW995948; Hs.182339; Homo sapiens pyruvate dehydrogenase kina; Ets,SAM_PNT;TM=M; 6.70
- 426746; J03626; Hs.2057; uridine monophosphate synthetase (orlat; Pribosyltran,OMPdecase;TM=M; 6.70
- 429429; AA829725; Hs.334437; hypothetical protein MGC4248; none,transmembrane4; 6.65
- 450825; AC005954; Hs.25527; tight junction protein 3 (zona occludens; PDZ,Guanylate_kin;SS=M; 6.64
- 408639; AW451353; Hs.173328; ESTs; B55;none; 6.63
- 408058; AA312328; Hs.42331; ephrin-A4; Ephrin;TM=M;SS=M; 6.61
- 401057; BE563196; ; eukaryotic translation elongation factor; lon_trans,IQ;TM=Y; 6.60
- 446528; H89616; Hs.296290; Homo sapiens cDNA FLJ13357 fls, clone PL; none;none; 6.60
- 400528; ; NM_020975; Homo sapiens rel proto-oncoge; cadherin,pkinase;TM=Y;SS=M; 6.58
- 418562; R60869; Hs.124831; CGI-67 protein; none,Skp1,AAA; 6.57
- 453826; AL138129; ; gb:DKFZp547F152_r1 547 (synonym: htrb1) ; PK,PK_C;none; 6.55
- 437412; BE069288; Hs.34744; Homo sapiens mRNA; cDNA DKFZp547C136 (fr; ABC_tran,ABC_membrana;none; 6.54
- 415086; AJ077288; Hs.296323; serum/glucocorticoid regulated kinase; none;none; 6.50
- 453489; AA300067; Hs.33032; hypothetical protein DKFZp434N185; F5_F8_type_C,pkinase,Ets,F5_F8_type_C,pkinase,Ets; 6.47
- 439866; AA280717; Hs.6727; Ras-GTPase activating protein SH3 domain; rmr,NTF2;TM=M; 6.46
- 456376; AA663904; Hs.89652; TNFRSF1A-associated via death domain; death;TM=M; 6.45
- 441712; AW391927; Hs.7946; KIAA1288 protein; ALP3;TM=M; 6.44
- 414557; AA340111; Hs.100009; acyl-Coenzyme A oxidase 1, palmitoyl; pkinase,7m_1; 6.43
- 432211; BE274530; Hs.273333; hypothetical protein FLJ10986; FGGY_C;TM=M; 6.43
- 432945; AL043683; Hs.8173; hypothetical protein FLJ10803; none;TM=M;SS=M; 6.40
- 438941; AF075947; Hs.31864; ESTs; Ca_channel_B,SH3,art;none; 6.40
- 441466; AW673081; Hs.54828; ESTs; pkinase,zf-C2H2,KRAB;none; 6.33
- 438698; AW297855; Hs.125815; ESTs, Weakly similar to I38022 hypothet; lipoxygenase,PLAT;none; 6.33
- 433255; AL274270; Hs.96840; KIAA1527 protein; MHCK_EF2_kinase;TM=M;SS=M; 6.33
- 427801; AW979155; Hs.298275; amino acid transporter 2; Aa_trans;TM=M;SS=M; 6.32

- 407970; AW403814; Hs.41714; BCL2-associated athanogene; ubikulin, BAG, Tropomyosin; 6.30
 439464; AA669735; Hs.324743; protein phosphatase 4 regulatory subunit; none; none; 6.30
 453977; AA865006; Hs.250427; ESTs; pklnase, P2X_receptor, E1-E2_ATPase, Hydrolase; 6.30
 412491; W31589; Hs.73957; RAB5A, member RAS oncogene family; ras, arf, P2C; TM=M; 6.30
 413235; BE243445; Hs.75248; topoisomerase (DNA) II beta (180kD); DNA_gyraseB, DNA_topoisolV, HATPase_c, DNA_gyraseB, DNA_topoisolV, HATPase_c; 6.29
 404342; ; C7002192; g|7299207|gb|AAAF54404.1| (AEQ); none; TM=M; 6.27
 409274; NM_003930; Hs.52644; SKAP55 homologue; SH3, PH, SS=M; 6.25
 419593; AA133749; Hs.301350; FYD domain-containing ion transport reg; ATP1G1_PLM_MAT8; TM=Y; SS=M; 6.23
 405429; ; Target Exon; Y_phosphatase; none; 6.23
 404975; AL042278; ; uncharacterized hypothalamus protein HT0; kringler; TM=Y; SS=M; 6.20
 452929; AW954938; Hs.172816; neuregulin 1; Neuregulin, EGF, ig, Neuregulin, EGF, ig; 6.18
 446883; AW452756; Hs.16364; hypothetical protein FLJ10955; DEAD, helicase_C, nm, Ndr, Cys_knot, TIL, vwa, vwc, vwd, IQ, RIIa, abhydrolase, TGF-beta, DUF139, TPR, DSPc, tss_1, Ribosomal_S21, rvp; TM=M; 6.18
 433233; AB040927; Hs.301804; KIAA1494 protein; SH3, zf-C3HC4; TM=M; 6.15
 458791; BE615453; Hs.346509; dedicator of cyto-kinesis 1; none; TM=Y; 6.15
 421836; AF109219; Hs.108787; phosphatidylinositol glycan, class N; none; none; 6.14
 447727; AI421079; ; tumor necrosis factor receptor superfamily; none; synaptobrevin; 6.13
 401536; ; NM_002530; Homo sapiens neurotrophic tyrosine kinase, type 3, receptor-like; LRR, LRRNT, LRRCT; TM=M; SS=M; 6.11
 444317; AI140568; Hs.143436; ESTs, Weakly similar to PLHU plasmin [H; PAN, kringler, trypsin, PI-PLC-X, C2, SH2, PH, SH3, PI-PLC-Y, PAN; 6.10
 427557; NM_002659; Hs.179557; plasminogen activator, urokinase receptor; UPAR_LY6, ET, PLA2_inh; SS=M; 6.08
 450447; AF212223; Hs.25010; hypothetical protein P15-2; NTF2; TM=M; 6.08
 450107; AI873287; Hs.257812; ESTs; ICE_p20, DED; TM=M; 6.05
 418175; AW967054; Hs.206312; ESTs, Weakly similar to I38022 hypothetical; zf-C2H2, BTB, K_tetra, Synlaxin; none; 6.05
 408963; NM_000492; Hs.663; cystic fibrosis transmembrane conductance; ABC_tran, ABC_membrane, PRK, Bac_export_3; TM=Y; 6.05
 439738; BE246502; Hs.9598; sema domain, immunoglobulin domain (Ig); Sema, PSI, integrin_B; TM=Y; 6.03
 427625; AF008216; Hs.285013; putative human HLA class II associated protein; none; none; 6.03
 409430; R21945; Hs.346735; splicing factor, arginine/serine-rich 5; DSPc, Rhodanese; none; 6.03
 440650; AB016825; Hs.15813; solute carrier family 22 (organic cation, sugar_tr); TM=Y; SS=M; 6.03
 405102; ; C15001220; g|4469558|gb|AAD21311.1| (AF); DAG, PE-binding, PH, RhoGEF, DC1; SS=M; 6.03
 400121; ; Eos Control; SH3, PH, RhoGEF, Terpene_synth; TM=M; 6.03
 415327; H27489; ; gb|ym54c02.r1 Soares infant brain 1N1B H; SH3, PDZ, Guanylate_kin; SS=M; 6.03
 404148; ; NM_002944; Homo sapiens v-ros avian UR2; fn3, pklnase, DUF139; TM=Y; SS=M; 6.03
 405531; ; Target Exon; PDZ, CARD, Guanylate_kin; TM=M; 6.00
 433363; AA584829; Hs.275163; non-metastatic cells 2, protein (NM23B); NDK; none; 6.00
 427270; H47921; Hs.174139; chloride channel 3; voltage_CLC, CBS; none; 5.99
 423774; L33054; Hs.1702; interleukin 9 receptor; none; TM=M; SS=M; 5.98
 424124; AA335609; Hs.7589; ESTs, Weakly similar to A46010 X-linked; pklnase, TBC; 5.98
 411040; AF007393; Hs.177674; protein-kinase, interferon-inducible dou; HLH; TM=M; 5.95
 423422; AC005175; Hs.128425; NY-REN-24 antigen; Sulfotransfer, 7tm_1; none; 5.88
 453902; BE502341; Hs.3402; ESTs; none; none; 5.88
 409636; AA305729; Hs.18272; amino acid transporter system A1; Aa_trans; TM=Y; 5.86
 436154; AA764950; Hs.119898; ESTs; ethanol_DAG_PE-binding, DAGKa, PHD, DAGKc, PSL; none; 5.85
 455358; AW902641; ; gb|CV3-NN1024-100500-181-d08 NN1024 Homo; Sulfatase, Somatomedin_B, Phosphodiesterase; none; 5.83
 414108; AI287592; Hs.75761; SFRS protein kinase 1; ank, PH, Cholesterol_BP, pklnase; TM=M; 5.82
 452547; AA335295; Hs.74120; adipose specific 2; LEA; TM=M; 5.82
 415204; T27434; ; gb|hbc2294 Human pancreatic islet Homo s; Na_Ca_Ex, Calx-beta; none; 5.80
 435563; NM_0210317; Hs.95497; solute carrier family 2 (facilitated glr; sugar_tr; TM=Y; 5.78
 456097; C15702; Hs.288028; ESTs, Moderately similar to I54374 gene; dsrm, FKBP; 5.78
 422445; M23114; Hs.1626; ATPase, Ca transporting, cardiac muscle; E1-E2_ATPase, Cation_ATPase_C, Cation_ATPase_N, Hydrolase; TM=Y; 5.77
 436246; AW403953; Hs.119991; ESTs; none, DNA_gyraseB, DNA_topoisolV, HATPase_c; 5.75
 422953; AA488860; Hs.245043; hypothetical protein FLJ14297; ABC_tran, PRK; TM=Y; SS=M; 5.75
 425854; AA749190; ; ESTs; RhoGAP, SH2, pklnase, POLO_box; none; 5.74
 424160; T74062; ; gb|yc81f01.r1 Soares infant brain 1N1B H; ROK; none; 5.70
 417389; BE260964; Hs.82046; midkine (neurotrophic growth-promoting factor); PTN_MK; TM=M; SS=Y; 5.69
 437613; R19892; Hs.10267; MLL1 protein; none; none; 5.68
 410820; BE391493; Hs.16476; Human DNA sequence from clone RP5-852M4; TBC; SS=M; 5.68
 423393; R37772; Hs.21420; p21-activated protein kinase 6; pklnase, PBD; TM=M; 5.66
 426500; NM_014638; Hs.170156; KIAA0450 gene product; C2, PI-PLC-Y; TM=M; 5.63
 406930; U04891; ; gb|Human olfactory receptor (OR17-219) g; none; TM=Y; SS=M; 5.60
 401044; ; Target Exon; none, ICE_p20, ICE_p10, CARD, Peptidase_M1; 5.56
 428479; Y00272; Hs.234582; cell division cycle 2, G1 to S and G2 to M; pklnase, ICE_p10, ICE_p20; TM=M; SS=M; 5.55
 421970; AF227156; Hs.110103; RNA polymerase I transcription factor RR; none, permesases, pyridoxal_deC, bromodomain, PHD, MBD, AF_huok, DDT, PI3_P14_klnase, FAT, FATC, BoIA, RUN; TM=M; 5.53
 426248; T18988; Hs.293668; ESTs; pklnase; none; 5.50
 418426; NM_003804; Hs.296327; receptor (TNFRSF)-interacting serine-thr; pklnase, death; TM=M; 5.43
 417086; AA194446; ; ESTs, Weakly similar to S55024 nebulin; ank, death, ZU5, EGF, kringler, trypsin, Nebulin, LIM; SS=M; 5.43
 447437; U07225; Hs.339; purinergic receptor P2Y, G-protein coupled; 7tm_1, SH2; TM=Y; SS=M; 5.40
 412247; AF022375; Hs.73793; vascular endothelial growth factor; PDGF; SS=M; 5.40
 434938; AW500718; Hs.8115; Homo sapiens, clone MGC16169, mRNA, cont; pklnase, TBC, Rhodanese; TM=M; 5.38
 418355; AA428520; Hs.90061; progesterone binding protein; heme_1; TM=Y; SS=M; 5.35
 411188; BE161168; ; gb|PMO-HT0425-170100-002-at0 HT0425 Homo; adenylate kinase; none; 5.35
 422461; NM_003417; Hs.117077; zinc finger protein 284; zf-C2H2, KRAB, TFIIS; TM=M; 5.28
 426348; BE46586; Hs.17433; hypothetical protein FLJ20967; none; none; 5.25
 429170; NM_001039; Hs.2359; dual specificity phosphatase 4; Rhodanese, DSPc, Y_phosphatase, Ribosomal_S3_N; TM=M; 5.23
 429592; AB029041; Hs.209646; KIAA1118 protein; Tropomyosin, Exo_endo_phos, IQ; TM=M; 5.22
 434821; AA159111; Hs.284281; Human putative ribosomal protein S1 mRNA; ER_lumen_recept, Ribosomal_L11, Ribosomal_L11_N; TM=Y; SS=M; 5.21
 434368; AW518020; Hs.73893; dopamine receptor D2; pklnase, SH3; none; 5.15
 405586; ; NM_000299; Homo sapiens plakophilin 1 (ec; Armadillo_seg; TM=M; 5.13
 408176; AK001553; Hs.43436; adenylate kinase 3 alpha like; adenylate kinase; none; 5.12
 407443; AF227138; ; gb|Homo sapiens candidate taste receptor; none; TM=Y; SS=M; 5.11
 415817; AA398045; Hs.104679; ESTs; Furin-like, pklnase, Recept_L_domain, fn3; none; 5.10
 401886; ; NM_021783; Homo sapiens XEDAR (XEDAR), mR; TNFR_c6; TM=M; SS=M; 5.08
 410314; AW680708; Hs.18851; hypothetical protein FLJ10875; myb_DNA-binding, PAR, BAH, bromodomain, PHD, SET; TM=M; 5.08

- 401579; AL031447; : Homo sapiens, clone IMAGE:4053044, mRNA; Neur_chan_LBD, Neur_chan_memb, none; 5.05
 445873; AA250970; Hs.251946; poly(A)-binding protein, cytoplasmic 1-; PABP, rrm, pkinase, 14-3-3; 5.05
 417528; AA203634; : gb:zx58b09.r1 Soares_fetal_liver_spleen.; pkinase, UBA, KA1, none; 5.03
 417527; AA203524; : gb:zx58e10.r1 Soares_fetal_liver_spleen.; SH3; SS=M; 4.98
 407722; BE252241; Hs.38041; pyridoxal (pyridoxine, vitamin B6) kinase; pK8; TM=M; 4.95
 431321; AW136372; Hs.1852; acid phosphatase, prostate; acid_phosphat, none; 4.93
 404298; : : C6001238*gl|121715|sp|P26697|GTA3_CHICK; none, GST_C, GST_N, pkinase; 4.85
 407603; AW955705; Hs.62604; Homo sapiens, clone IMAGE:4299322, mRNA; none; TM=M; 4.82
 424099; AF071202; Hs.139336; ATP-binding cassette, sub-family C (CFTR; ABC_tran, ABC_membrane; TM=Y; 4.73
 422366; T83882; Hs.97927; ESTs; pkinase, none; 4.64
 424905; NM_002497; Hs.153704; NIMA (never in mitosis gene a)-related k; pkinase; TM=M; 4.48
 426925; NM_001196; Hs.315689; Homo sapiens cDNA: FLJ22373 fls, clone H; Esterase, enolase, Peptidase_S9; TM=M; 4.45
 439606; W79123; Hs.58561; G protein-coupled receptor 87; 7tm_1; TM=Y; SS=M; 4.40
 400749; : : NM_003105* Homo sapiens sortilin-related; EGF, fn3, ldl_recept_a, ldl_recept_b, granulin, BNR; TM=Y; SS=M; 4.38
 425721; AC002115; Hs.159309; uroplakin 1A; transmembrane4; TM=Y; SS=M; 4.33
 444008; BE395085; Hs.10086; type I transmembrane protein Fnt4; kld_recept_a, PKD, MHC.; TM=M; SS=Y; 4.31
 400751; : : NM_003105* Homo sapiens sortilin-related; EGF, fn3, ldl_recept_a, ldl_recept_b, granulin, BNR; TM=Y; SS=M; 4.18
 408908; BE296227; Hs.250822; serine/threonine kinase 15; pkinase; SS=M; 3.90
 422152; AA909249; Hs.112282; solute carrier family 30 (zinc transport; none, none; 3.88
 458760; AI498631; Hs.111334; ferritin, light polypeptide; cystatin, ferritin, histone, HCO3_cotransp, SH3, RhoGAP, xan_vr_permease, FCH; SS=M; 3.85
 441218; BE327561; Hs.202345; ESTs; none, WD40, E1-E2_ATPase, Calton_ATPase_C, Calton_ATPase_N, Hydrolase; 3.78
 419073; AW372170; Hs.183918; Homo sapiens cDNA FLJ12797 fls, clone NT; death, ZU5; SS=M; 3.76
 451385; AA017656; : gb:ze33h01.r1 Soares retina N2b4HR Homo; Atrophin-1, enolase, Atrophin-1_Y, phosphatase, SH2, fibrinogen_C, TIM; 3.60
 412604; AW978324; Hs.1904; protein kinase C, iota; pkinase, DAG_PE_bind, pkinase_C, OPR; TM=M; 3.30
 409582; R27430; Hs.271565; ESTs; none, Neur_chan_LBD, Neur_chan_memb; 3.28
 441155; AW161008; Hs.7719; GABA(A) receptor-associated protein; MAP1_LC3; SS=M; 3.23
 436740; AW975133; : gb:EST387239 IMAGE resequences, MAGN Homo; none, EPH_1, fn3, pkinase, SAM; 3.20
 418319; AW611703; Hs.190173; ESTs, Weakly similar to A46010 X-linked; none, IRK; 3.20
 409744; AW675258; Hs.56265; Homo sapiens mRNA; cDNA DKFZp586P2321 (f; none; NA; NA; 3.13
 418764; NK0531; Hs.42215; protein phosphatase 1, regulatory subunit; none, none; 3.10
 400848; : : sortilin-related receptor, L(DLR class); EGF, fn3, ldl_recept_a, ldl_recept_b, granulin, BNR; TM=Y; SS=M; 3.09
 422005; BE266558; Hs.110702; Homo sapiens mRNA; cDNA DKFZp761E212 (fr; none, Na_H_Exchange; 3.03
 426440; BE382755; Hs.169902; solute carrier family 2 (facilitated glr; sugar_tr; TM=Y; SS=M; 3.02
 424187; AA336551; Hs.17287; ESTs, Weakly similar to S26689 hypothet; IRK, none; 2.98
 425852; AK001504; Hs.159651; death receptor 6, TNF superfamily member; death, TNFR_p5; TM=Y; SS=M; 2.93
 401279; : : C13000351*gl|2494033|sp|Q54398|KDGQ_MES; none, none; 2.88
 406671; AA129547; Hs.285754; met proto-oncogene (hepatocyte growth fa; Sema, pkinase, TIG, PSI, none; 2.83
 447081; Y13896; Hs.17287; potassium inwardly-rectifying channel, s; IRK; TM=Y; 2.80
 453619; H87648; Hs.33922; Homo sapiens, clone MGC:9084, mRNA, comp; pkinase; TM=M; 2.75
 441699; AW511128; Hs.127572; ESTs; none, Aa_trans; 2.73
 458781; AI444821; Hs.63085; ESTs, Weakly similar to MPP3_HUMAN MAGUK; SH3, PDZ, Guanylate_kin, L27; TM=M; 2.73
 446913; AA430650; Hs.16529; transmembrane 4 superfamily member (tet; transmembrane4; TM=Y; SS=M; 2.70
 453487; R31770; Hs.56562; ESTs; 7tm_1, none; 2.68
 421279; AW664878; Hs.106645; ESTs; pkinase, none; 2.68
 419720; AA249131; Hs.337778; hypothetical protein FLJ11068; none, none; 2.65
 452345; AA293279; Hs.29173; hypothetical protein FLJ20515; DSPc; TM=M; 2.63
 422247; U18244; Hs.113602; solute carrier family 1 (high affinity a; SDF; TM=Y; 2.62
 425212; AW962253; Hs.171618; ESTs; pkinase, none; 2.60
 427344; NM_000869; Hs.2142; 5-hydroxytryptamine (serotonin) receptor; Neur_chan_LBD, Neur_chan_memb; TM=Y; SS=M; 2.58
 423629; AW021173; Hs.18812; Homo sapiens cDNA: FLJ21909 fls, clone H; voltage_CLC, CBS, none; 2.55
 458737; BE247203; Hs.124831; C61-67 protein; abhydrolase_2; TM=M; SS=M; 2.53
 421585; U95628; Hs.302043; chemokine (C-C motif) receptor-like 2; 7tm_1; TM=Y; SS=M; 2.53
 424028; AK005044; Hs.153692; Homo sapiens cDNA FLJ14354 fls, clone Y7; none, none; 2.50
 448324; AI571356; Hs.34174; ESTs, Moderately similar to ALU8_HUMAN A; ICE_p20, CARD, ICE_p10, none; 2.50
 402268; : : Target Exon; pkinase, UBA, none; 2.43
 452258; AK000933; Hs.28661; Homo sapiens cDNA FLJ10071 fls, clone HE; GDI, 7tm_1, none; 2.40
 419168; AW851980; Hs.262346; ESTs, Weakly similar to S72482 hypothet; none, spectrin, SH3, PH, CH; 2.40
 420634; S42457; Hs.1323; cyclic nucleotide gated channel alpha 1; cNMP_binding, lon_trans; TM=Y; 2.35
 419630; W57756; : gb:zd20g10.r1 Soares_fetal_heart_NbHH19W; zf-C3HC4, none; 2.35
 426227; U87058; Hs.154295; Human proteinase activated receptor-2 mR; 7tm_1; TM=Y; SS=M; 2.35
 400704; : : Target Exon; lig_chan, SBP_bac_3, ANF_receptor; TM=Y; SS=M; 2.33
 400149; : : Eos Control; acid_phosphat; TM=Y; SS=M; 2.30
 459327; AW149706; Hs.7859; gb:xt41d02.x1 NC1_CGAP_Bm50 Homo sapiens; PHD, PWWP, SET, pkinase; lg; 2.30
 452220; BE158008; Hs.212296; ESTs; Integrin_A, FG-GAP, none; 2.25
 416690; H84078; Hs.108551; ESTs; pkinase, none; 2.23
 408354; AJ382803; Hs.159235; ESTs; none, none; 2.23
 452203; X57522; : transporter 1, ATP-binding cassette, sub; ABC_tran, ABC_membrane, SRP54, Thymidylate_kin; TM=Y; SS=M; 2.21
 405093; : : C12001101*gl|7522643|pi|T32733 AMPA g; none, none; 2.20
 412723; AA648458; Hs.335951; hypothetical protein AF301222; none; TM=M; 2.20
 418738; AW388633; Hs.6682; solute carrier family 7, (cationic amino; none, none; 2.18
 417185; NM_002484; Hs.81469; nucleotide binding protein 1 (E.coli Min; Parafer4_NIH, ArsA_ATPase; TM=M; 2.18
 433222; AW514472; Hs.238415; dickkopf (Xenopus laevis) homolog 4; none, PHO4; 2.18
 413627; BE182082; Hs.246973; ESTs; Armadillo_seg, IBB; TM=M; 2.18
 407415; AF073328; : gb:Homo sapiens tetracycline transporter.; none, none; 2.15
 450592; AI701555; Hs.202562; ESTs; pkinase, none; 2.15
 428767; AI421972; Hs.98802; ESTs, Moderately similar to T14342 NSD1; none, pkinase; lg; 2.15
 429012; AW829596; Hs.194726; BCL2-associated atlanogene 4; Sm, BAG; SS=M; 2.15
 419122; AI401380; Hs.44410; ESTs; ABC_tran, ABC_membrane, none; 2.10
 446420; AW015693; Hs.135614; ESTs; lon_trans, none; 2.05
 420076; AA827850; Hs.293717; ESTs; DUF59, pkinase; 2.05
 409416; AW388359; Hs.10667; ESTs; transmembrane4; TM=Y; SS=M; 2.03
 428766; AA477989; Hs.98800; ESTs; TPR, 7tm_1; 2.03
 427001; NM_005482; Hs.173135; dual-specificity tyrosine-(Y)-phosphoryl; pkinase; TM=M; 2.03

453709; AL119133; ; protein kinase C substrate 80K-H; none,histone; 2.03
 423341; AW242394; Hs.108660; ESTs; none,none; 2.00
 466772; AW604297; Hs.129711; hepatitis A virus cellular receptor 1; ig;TM=Y;SS=M; 1.88
 427786; BE407863; Hs.256871; ESTs; none,FG-GAP,7m,1; 1.65
 423508; AW604297; Hs.129711; hepatitis A virus cellular receptor 1; ig;TM=Y;SS=M; 1.00
 447993; AW139525; Hs.170362; ESTs; none,none; 1.00

TABLE 588

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
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438091	22448_1	A10054860 AV652198 AV652192 AV652138 AV652127 AV652194 BE935919 AV652017 AV651995 AV651548 AV646063 AV651985 AV646164 AV646179 AW860409 AA345002 BF155189 BE068931 X56197 AL603014 AW953629 BM263546 BE550772 AA701084 A1681352 AA356689 AW938841 BF438147 W05391 H75313 BF326185 AV646335 AV651589 AV646340 AV651992 AV646384 AV646384 AV667497 BF155183 AV646370 AW797876 A1906821 X58196 BE833835 AA626440 BE833808 BF224205 AA709126 BE673807 A1923886 AA947932 A1276125 A1185720 AW510698 AA987230 BE467708 AW896628 AW898644 A1146984 AW043642 A1286245 A1186932 A1635262 A1139455 A1298739 A1813854 A1024768 BE699445 BE699444 A1707807 D52654 A1214518 A1004723 A1698085 AW087420 A1565133 AA845571 AW888622 BF110144 AW513280 A1081128 BF362770 A1268839 A1435818 BF476318 A1024767 BE174213 AA757598 AA513019 AA902859 A1860794 A1334784 BF108411 BM310532 AW513771 A1951391 A1337671 BF095606 BF095601 BF095468 AW890091 BF095753 AW243400 AW898607 AW898616 BF362762 A1922204 AW898625 BE699445 BE174186 AW102923 D52715 BE699466 D52477 D56017 BF955933 BG623563 AV646254 AA463522 B1003244 A1299190 W40186 BE174210 BF939031 BF434180 AW579001 T55662 H01811 T52522 BF945037 BF955938 D54679 D53933 R67100 BG925552 BF999056 RB3430 Z28822 T85791 W03942 H63289 A1091537 BF096583 AA345570 H48870 H00720 T83523 B1039626 B1037700 R00353 BE155184 N98343 N79072 H01812 T55581 X76684 AL573167 A1445461 A153743 A198365 A156464 AA977180 A1694111 A1591358 AW071625 A1678712 A1720339 A1927769 BE439796 A1963432 AA292958 AW192593 A1865838 A1866905 A1424384 A1161312 A1911921 A1597801 B1494959 A1240988 A1492554 AW262737 BE044033 AW008570 AW629505 B1494958 AA088439 AA706057 BF222820 BF583608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA043217 BE219784 A1799814 AA129575 A1671727 A170033 BE646195 AW779725 AA903050 AA147228 AA04570 A1075878 W38161 A1972739 AW673152 AA723200 C06123 BF057147 AA627686 AA157944 A1990245 AA662517 T32487 A1800106 A1333170 A1859160 W45410 A1990827 AW275048 AA182640 AA478328 A1298935 AW085158 AW471421 AW103470 AW300456 AW191997 A1823466 AA962397 AA136658 A1251817 AW339104 AA724739 AA411100 AA191349 AA757735 AA037696 A1769516 AW772283 AA010631 A1692846 A1061065 H08983 R79933 A1950693 A1245632 A1349390 AA148284 A1798502 AA487893 A1621320 AW194272 C06365 AA953883 BE858936 A1918523 A1872628 A1927217 A1453453 A1189366 AW338678 A1261359 A1500576 BF477735 A1032569 A1972899 A1985583 Z28771 A1363829 A1693030 AA603586 BE773488 AW339301 BE773489 BE773462 BE773495 A1650338 BE773499 A1745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398 BE811388 BE811352 BE773501 BE773494 BE773486 BE773474 BE773473 BE773470 BE773461 BE811350 BE811337 BF593847 BG055071 AW675302 BF003068 AA719173 BE811348 A1582462 A1868240 BE773500 A1244845 A1565439 A1918453 A1472527 A1446740 AA035576 AA191414 AW674145 C05782 A1589284 D57558 A1468237 A1432033 AA989662 R21762 BF002457 AA988297 A1574095 AL576200 AL571074 AL574525 AL578810 BG498381 A1928364 BE797932 AA479834 AA479712 C17732 BM091258 BF843901 AW820230 C17476 BE327120 AA1129574 AA136645 BF843900 AW808193 AA502832 AA649494 A1568520 AL547960 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380 BE811399 BF997171 BF757734 BE926037 A1377596 C06111 AW088968 BE811404 BE811472 A1865912 A1925607 A1871950 A1093510 BE905927 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 B1044896 A1744233 AW984527 C17504 BF843883 A1248307 BE773483 A1567995 W60075 BF941183 A1738844 BE811458 BE773481 A1262930 AA948565 BE706942 BE156360 T65026 AW242958 AW197954 BE905184 AA722206 A1344943 A1348877 A1334860 BE811857 BE156280 AA454099 AA037722 BF843897 AW805183 AA043216 BG482886 AA182734 AA877242 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 B1755027 BG506731 BC008442 BC010166 AL550134 AL553096 AL548700 AL550751 AL547978 AL545286 AL540643 AU118627 AL601379 B1259821 BG741786 B1868522 AU135866 B1552770 B1259210 B1256520 B1255569 BG485098 B1258228 BG498501 BM044512 AU133984 AL566586 BE745111 B1222633 AU133917 BG288151 B1260715 B1550550 BG500773 B1551761 BG707601 B1818593 BF691383 BG721129 BG541578 BE906666 BG751098 B1224135 BG400746 BG478065 BE790436 AW080238 AU137549 BG429896 BE392486 AW961686 BG721056 BE908365 BE546656 BG541235 AW583735 BG528290 B1260895 AW651691 BM048974 BM043805 BG142185 AA315188 A1446615 C06300 BG497644 AA088544 A1815987 BG528631 BE819182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA376800 D68120 AA343532 AA308636 F00422 AA376086 AA316968 AA343799 B1870221 BE910282 BG538748 AW960564 AV732879 D18854 AA192519 BF922148 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE088964 AA921353 R21800 AA011222 T97525
436729	6524_1	X76684 AL573167 A1445461 A153743 A198385 A156464 AA977180 A1694111 A1591358 AW071625 A1678712 A1720339 A1927769 BE439796 A1963432 AA292958 AW192593 A1865838 A1866905 A1424384 A1161312 A1911921 A1597801 B1494959 A1240988 A1492554 AW262737 BE044033 AW008570 AW629505 B1494958 AA088439 AA706057 BF222820 BF583608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA043217 BE219784 A1799814 AA129575 A1671727 A170033 BE646195 AW779725 AA903050 AA147228 AA04570 A1075878 W38161 A1972739 AW673152 AA723200 C06123 BF057147 AA627686 AA157944 A1990245 AA662517 T32487 A1800106 A1333170 A1859160 W45410 A1990827 AW275048 AA182640 AA478328 A1298935 AW085158 AW471421 AW103470 AW300456 AW191997 A1823466 AA962397 AA136658 A1251817 AW339104 AA724739 AA411100 AA191349 AA757735 AA037696 A1769516 AW772283 AA010631 A1692846 A1061065 H08983 R79933 A1950693 A1245632 A1349390 AA148284 A1798502 AA487893 A1621320 AW194272 C06365 AA953883 BE858936 A1918523 A1872628 A1927217 A1453453 A1189366 AW338678 A1261359 A1500576 BF477735 A1032569 A1972899 A1985583 Z28771 A1363829 A1693030 AA603586 BE773488 AW339301 BE773489 BE773462 BE773495 A1650338 BE773499 A1745717 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398 BE811388 BE811352 BE773501 BE773494 BE773486 BE773474 BE773473 BE773470 BE773461 BE811350 BE811337 BF593847 BG055071 AW675302 BF003068 AA719173 BE811348 A1582462 A1868240 BE773500 A1244845 A1565439 A1918453 A1472527 A1446740 AA035576 AA191414 AW674145 C05782 A1589284 D57558 A1468237 A1432033 AA989662 R21762 BF002457 AA988297 A1574095 AL576200 AL571074 AL574525 AL578810 BG498381 A1928364 BE797932 AA479834 AA479712 C17732 BM091258 BF843901 AW820230 C17476 BE327120 AA1129574 AA136645 BF843900 AW808193 AA502832 AA649494 A1568520 AL547960 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380 BE811399 BF997171 BF757734 BE926037 A1377596 C06111 AW088968 BE811404 BE811472 A1865912 A1925607 A1871950 A1093510 BE905927 BE811435 AA191387 AW772000 BE811453 BE614379 BF844522 B1044896 A1744233 AW984527 C17504 BF843883 A1248307 BE773483 A1567995 W60075 BF941183 A1738844 BE811458 BE773481 A1262930 AA948565 BE706942 BE156360 T65026 AW242958 AW197954 BE905184 AA722206 A1344943 A1348877 A1334860 BE811857 BE156280 AA454099 AA037722 BF843897 AW805183 AA043216 BG482886 AA182734 AA877242 AW372926 H27252 R38114 BF851858 BE156214 AA190427 T91762 AA035067 AA837326 T10930 BF906587 B1755027 BG506731 BC008442 BC010166 AL550134 AL553096 AL548700 AL550751 AL547978 AL545286 AL540643 AU118627 AL601379 B1259821 BG741786 B1868522 AU135866 B1552770 B1259210 B1256520 B1255569 BG485098 B1258228 BG498501 BM044512 AU133984 AL566586 BE745111 B1222633 AU133917 BG288151 B1260715 B1550550 BG500773 B1551761 BG707601 B1818593 BF691383 BG721129 BG541578 BE906666 BG751098 B1224135 BG400746 BG478065 BE790436 AW080238 AU137549 BG429896 BE392486 AW961686 BG721056 BE908365 BE546656 BG541235 AW583735 BG528290 B1260895

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NM_003899 C63476 BM456434 AA778936 AA452871 AI052466 AW014138 AA448725 BE673088 AW02198 BI856378 BM150466 BM150674 BM148451 AW500880 AA180228 BE243507 BM144903 AA333656 AW503767 AA305470 AW504819 AA978184 AW500776 BE872488 AI032663 AA704686 AA652189 AA179463 AI535925 BE275744 BE277708 BE275715 AW504259 AA354483 BE244197 BE246232 D17055 AW013876 AW014877 T09464 T08407 AA830246 AW897881 BE501192 BE501195 AL044634 AA258853 BI037915 AA448037 BM461769 BI825965 BE763352 AW167531 Z45588 AV721881 AA527273 AI573219 AA457036 AW439651 AW264418 AA577618 AI802964 AA902292 AA468752 AI380374 AA722690 AI687708 AA916982 AI291576 AW190427 AI338089 AI653744 AI306665 AW513541 AW440077 AI370014 AA904269 AW188378 AI671644 AW193386 AI261832 AA775336 BF436811 AI582703 AI278635 BE440186 AA617898 AA648948 BI491837 BF590311 AA448633 F27048 F37022 AW770819 AA258808 AI369564 AW503675 AA777194 BE501048 BF222087 AA042973 AI868087 AA911460 Z41274 AI919082 T16746 AA447634 AI282427 F22455 T15901 AA825298 AW007436 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65	456358 415204 425854	1160035_1 1865508_1 2838_3	
70	424160 417088	5320_3 1154_2	
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453709 59915_1

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BG272488 A1628769 A1628764 A1189390 W84635 AA399496 AA761672 AA699520 A1200406 N68093 A143913 AA593133 AA613306 A1050971
AA651905 AA722687 A1749977 AA829345 BG057324 BF001339 AA910169 AA765133 A1360722 A1701849 A1365083 H95974 A1830377 A1312866
A1370491 BE858907 N62185 AA705746 BE379632 W93803 A1440333 AW367670 AW367640 N77131 BF993216 A1858263 W52329 N68106 R83113
R85153 BE380058 AA082537 AA729731 W23495 W31190 BF995236 BF968827 BF355168 N24508 AA215711 BF170735 AA280395 BE738851
AW367707 AA630879 AA428420 R76236 BG567847 N25931 AA173568 A1073687 AA004957 A1539585 N95093 H98798 H95072 H56853 AA251712
AA034214 R85096 H82051 H80794 R44954 AA278972 H68352 H68346 R94750 R89010 R67951 H65817 N24891 AA173731 A1693577 BE181027
AA709461 BE181002 W60239 BF987598 BF995279 H17483 R76237 AL119133 BF964815 AW663315 H65903 H17591 R20167 AA310039 R56734
R58508

TABLE 58C

Pkey: Unique number corresponding to an Eos probeset
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400843	9188605	Plus	5863-5970,7653-7784,8892-9023,9573-9807
404942	7382153	Plus	92095-92252
400752	7331445	Minus	36215-36481
400496	9743564	Plus	41515-41695
404568	9966995	Minus	92893-93116
403912	7710730	Minus	72000-72290,72431-72700,72929-73199
402328	4464283	Minus	13758-13922,14558-14752
404891	7329392	Plus	84874-85125
405036	7543748	Minus	121857-122129
400845	9188605	Plus	34428-34612
403212	7630897	Minus	156037-156210
401927	3873185	Minus	112000-112137

Table 59A lists about 1170 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03
GeneChip array such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 5.2. The "average" prostate cancer level was set to the
75th percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 50th percentile amongst non-malignant tissues. In order to remove gene-specific
background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the
ratio was evaluated.

TABLE 59A: ABOUT 1170 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

Pkey:	Unique Eos probeset identifier number			
ExAcct:	Exemplar Accession number, Genbank accession number			
UnigeneID:	Unigene number			
Unigene Title:	Unigene gene title			
R1:	Ratio of prostate tumor to normal adult body tissue			
Pkey	ExAcct	Unigene ID	Unigene Title	R1
428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	108.1
426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	102.5
420823	AF097021	Hs.273321	differentially expressed in hematopoietic	90.5
416854	H40164	Hs.80295	Purkinje cell protein 4	79.8
425075	AA506324	Hs.1852	acid phosphatase, prostate	71.6
431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	70.6
434666	AF151103	Hs.112259	T cell receptor gamma locus	69.1
419551	AW582256	Hs.91011	anterior gradient 2 (Xenopus laevis) hom	66.4
413859	AW992356	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	66.4
420154	A1093155	Hs.95420	JM27 protein	63.9
428336	AA503115	Hs.183752	microsomal protein, beta-	61.4
400287	S39329	Hs.181350	kallikrein 2, prostatic	59.7
416602	NM_006159	Hs.79389	nal (chicken)-like 2	54.6
428398	A1249368	Hs.98558	ESTs	54.6
432441	AW292425	Hs.163484	ESTs	54.6
414569	AF109298	Hs.118258	prostate cancer associated protein 1	54.2
417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	54.2
448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	53.7

5	437145	AF007216	Hs.5482	solute carrier family 4, sodium bicarbon	49.6
	446057	AJ420227	Hs.149358	ESTs, Weakly similar to A46010 X-linked	48.0
	431579	AW971082	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	46.8
	400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	45.0
	427674	NM_003528	Hs.2178	H2B histone family, member Q	44.9
	432374	V68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	44.5
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	44.5
	416314	N88802	Hs.5422	glycoprotein M6B	43.2
10	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	41.9
	409262	AK000531	Hs.52256	hypothetical protein FLJ20624	41.1
	423582	BE000831	Hs.23837	Homo sapiens cDNA FLJ11812 fis, clone HE	40.5
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	39.5
	439176	AJ464444	Hs.190394	ESTs, Weakly similar to B28096 line-1 pr	39.3
15	416585	X54162	Hs.79385	kelomodulin 1 (smooth muscle)	39.0
	447725	AL137638	Hs.19368	matrilin 2	38.6
	426174	AA547959	Hs.115838	ESTs	38.1
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	38.0
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	37.6
20	414217	AJ309298	Hs.279898	Homo sapiens cDNA: FLJ23165 fis, clone L	37.0
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	36.5
	400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb	36.1
	453096	AW294631	Hs.11325	ESTs	35.1
	419239	AA468183	Hs.184588	Homo sapiens cDNA: FLJ23241 fis, clone C	34.9
25	427665	AF134803	Hs.180141	cofilin 2 (muscle)	34.9
	415639	AJ733881	Hs.72472	BMP-R18	34.9
	428411	AW291464	Hs.10338	ESTs	34.6
	428819	AL135623	Hs.193914	KIAA0575 gene product	34.3
	401424			NM_001172:Homo sapiens arginase, type II	34.0
30	452114	N22687	Hs.8236	ESTs	34.0
	420990	AL044315	Hs.173694	Homo sapiens mRNA for KIAA1750 protein,	33.8
	448045	AJ297436	Hs.20166	prostate stem cell antigen	33.1
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	32.9
	432101	AJ918950	Hs.123642	EphA3	32.7
35	427398	AW390020	Hs.20415	chromosome 21 open reading frame 11	32.4
	426716	NM_006379	Hs.171921	sarna domain, immunoglobulin domain (Ig),	32.4
	434025	AF114264	Hs.216381	Homo sapiens clone HH409 unknown mRNA	32.4
	414591	AJ888490	Hs.55802	ESTs, Weakly similar to ALU8_HUMAN ALU S	32.3
	453355	AW295374	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	31.9
40	406380	AF123050	Hs.44532	diubiquitin	31.6
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytostatin)	31.4
	453370	AI70523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	31.3
	408369	R38438	Hs.182575	solute carrier family 15 (H???) transport	31.2
	408901	AA046458	Hs.95296	ESTs	30.8
45	440274	R24595	Hs.7122	scrapie responsive protein 1	30.7
	417332	AW972717	Hs.288462	hypothetical protein FLJ21511	30.3
	442983	BE018662	Hs.186195	ATPase, Class I, type 8B, member 1	30.2
	433404	T32982	Hs.102720	ESTs	29.6
	459247	N48243	Hs.110373	ESTs, Highly similar to T42626 secreted	29.6
50	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	29.3
	459290	NM_001546	Hs.34853	Inhibitor of DNA binding 4, dominant neg	29.2
	418827	BE327311	Hs.47166	HTO21	29.0
	410330	AW023630	Hs.45786	ESTs	28.6
	450377	AB033091	Hs.74313	KIAA1265 protein	28.6
55	424012	AW358377	Hs.137569	tumor protein 83 kDa with strong homology	28.5
	441633	AW958544	Hs.112242	normal mucosa of esophagus specific 1	28.2
	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	27.7
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	27.7
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	27.6
60	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	27.4
	446100	AW967109	Hs.13804	hypothetical protein dJ462023.2	27.4
	407202	N58172	Hs.109370	ESTs	27.4
	434078	AW880709	Hs.283683	chromosome 8 open reading frame 4	27.4
	442870	N45018	Hs.8769	hypothetical protein DKFZp761J17121	27.3
65	403047			NM_005656*:Homo sapiens transmembrane pr	27.2
	407709	AA456135	Hs.23023	ESTs	27.0
	433444	AW975324	Hs.129816	ESTs	26.8
	415889	AJ267700	Hs.317584	ESTs	26.8
	430539	AK001489	Hs.242894	ADP-ribosylation factor-like 1	26.5
70	408221	AA912183	Hs.47447	ESTs	26.5
	448519	AW175665	Hs.278695	Homo sapiens protein mRNA, complete cds	26.4
	437179	AA393508	Hs.300642	serologically defined colon cancer anti	26.4
	426457	AW894667	Hs.159955	chimerin (chimaerin) 1	26.2
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	26.2
75	400292	AA250737	Hs.72472	BMP-R18	26.0
	433647	AA603367	Hs.222294	ESTs	26.0
	429220	AW207206	Hs.136319	ESTs	25.8
	427871	AW992405	Hs.58622	Homo sapiens, clone IMAGE:3507281, mRNA,	25.6
	448105	AJ800470	Hs.171941	ESTs	25.5
80	415992	C05837	Hs.145807	hypothetical protein FLJ13593	25.5
	452792	AB037765	Hs.30652	KIAA1344 protein	25.3
	407910	AA650274	Hs.41296	fibronectin laucine rich transmembrane p	25.2
	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	24.9
	416951	AW957646	Hs.23023	ESTs	24.8

	451027	AW519204	Hs.40808	ESTs	24.5
	413517	N76712	Hs.44829	ESTs, Weakly similar to I3B022 hypothe	24.5
	409731	AA125985	Hs.55145	thymosin, beta, identified in neuroblast	24.4
5	418396	A1765805	Hs.26691	ESTs	24.1
	412088	A1689496	Hs.108932	ESTs	24.1
	429673	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	24.0
	411644	H92064	Hs.278626	Arg/Abi-interacting protein ArgBP2	24.0
	409619	AK001015	Hs.55220	BCL2-associated athanogene 2	23.9
10	433466	AA508353	Hs.105314	relaxin 1 (H1)	23.7
	431667	AI345227	Hs.105448	ESTs, Weakly similar to B34087 hypothe	23.6
	440995	T57773	Hs.10263	ESTs	23.5
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	23.2
	428695	AI355647	Hs.189999	purinergic receptor (family A group 5)	23.1
15	424720	M89907	Hs.152292	SW/SNF related, matrix associated, acti	22.9
	440260	AI972857	Hs.7130	copline IV	22.5
	443622	AI911527	Hs.11805	ESTs	22.2
	426418	M90464	Hs.169825	collagen, type IV, alpha 5 (Alport syndr	22.0
	425383	D63407	Hs.156007	Down syndrome critical region gene 1-lik	21.9
20	450642	R39773	Hs.7130	copline IV	21.9
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	21.8
	435981	H74319	Hs.188620	ESTs	21.8
	450693	AW450461	Hs.203965	ESTs	21.7
	444784	D12485	Hs.11951	ectonucleotide pyrophosphatase/phosphodi	21.7
25	423242	AL039402	Hs.125783	DEME-6 protein	21.7
	408621	AI970672	Hs.46538	chromosome 11 open reading frame 8	21.6
	408000	L11890	Hs.620	bullous pemphigoid antigen 1 (230/240kD)	21.5
	404210			NM_005936:Homo sapiens myeloid/lymphoid	21.5
	417622	AW298163	Hs.82318	WAS protein family, member 3	21.5
30	419526	AI821895	Hs.193481	ESTs	21.5
	442799	AI564739	Hs.68505	ESTs	21.4
	424846	AU077324	Hs.1832	neuropeptide Y	21.3
	420195	N44348	Hs.26243	Homo sapiens cDNA FLJ111177 fis, clone PL	21.3
	429922	Z97630	Hs.226117	H1 histone family, member 0	21.3
35	422511	AU076442	Hs.117938	collagen, type XVII, alpha 1	21.3
	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	21.2
	431474	AL133990	Hs.190642	ESTs	21.2
	430887	N66801	Hs.260287	KIAA1841 protein	21.1
40	416655	AW868613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	21.1
	408912	AB011084	Hs.48924	KIAA0512 gene product; ALEX2	21.1
	445133	AW157648	Hs.153505	ESTs	21.0
	421513	X00949	Hs.105314	relaxin 1 (H1)	21.0
	413745	AA133243	Hs.171553	ESTs, Moderately similar to CLC3_HUMAN C	20.8
	446795	AI797713	Hs.156471	ESTs	20.7
45	440774	AI420611	Hs.127832	ESTs	20.7
	407168	R45175	Hs.117183	ESTs	20.6
	417511	AL049175	Hs.82223	chordin-like	20.6
	431130	NM_006103	Hs.2719	epididymis-specific, whey-acidic protein	20.6
50	451277	AK001123	Hs.26176	hypothetical protein FLJ10261	20.6
	411800	N39342	Hs.103042	microtubule-associated protein 1B	20.5
	446469	BE094848	Hs.15113	homogentisate 1,2-dioxygenase (homogeni	20.5
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	20.5
	409758	AW474960	Hs.182258	ESTs, Weakly similar to I78895 serine/th	20.5
	424897	D53216	Hs.153684	fizzled-related protein	20.5
55	430280	AA361258	Hs.237868	interleukin 7 receptor	20.4
	401197			ENSP00000229263:HSPC213.	20.3
	452814	AI092790	Hs.334703	hypothetical protein FLJ14629	20.3
	429918	AW873986	Hs.118363	ESTs	20.2
	423073	BE252922	Hs.123118	MAD (mothers against decapentaplegic, Dr	20.2
60	453469	AB014533	Hs.33010	KIAA0633 protein	20.2
	444822	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	20.0
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	20.0
	419440	AB020689	Hs.90419	KIAA0882 protein	20.0
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	19.9
65	441890	R81733	Hs.33106	ESTs	19.9
	423690	AA329648	Hs.23804	ESTs, Weakly similar to PNO099 son3 prot	19.8
	423044	AA320829	Hs.97266	protocadherin 18	19.8
	410929	H47233	Hs.30643	ESTs	19.7
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	19.7
70	431555	AF016028	Hs.183428	sarcospan (Kras oncogene-associated gene	19.6
	409632	W74001	Hs.55279	serine (or cysteine) proteinase inhibitor	19.6
	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	19.6
	407118	AA156790	Hs.262036	ESTs, Weakly similar to Z223_HUMAN ZINC	19.5
	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypothe	19.4
75	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	19.4
	430187	AI799909	Hs.158989	ESTs	19.3
	420120	AL048610	Hs.95243	transcription elongation factor A (SII)-	19.3
	434423	NM_006769	Hs.3844	LIM domain only 4	19.2
80	417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	19.1
	409062	AL157468	Hs.50150	Homo sapiens mRNA; cDNA DKFZp564B182 (fr	19.0
	409038	T97490	Hs.50002	small inducible cytokine subfamily A (Cy	18.9
	436032	AA150797	Hs.109276	latexin protein	18.9
	431548	AI834273	Hs.9711	novel protein	18.9
	418565	AK001629	Hs.86149	phosphoinositol 3-phosphate-binding prot	18.9

5	445829	AI089660	Hs.323401	dpy-30-like protein	18.8
	453160	AI263307	Hs.239884	H2B histone family, member L	18.8
	439897	NM_015310	Hs.6763	KIAA0942 protein	18.8
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (vadulin)	18.8
	434987	AW975114	Hs.293273	ESTs	18.7
	407890	R47799	Hs.266957	hypothetical protein FLJ14281	18.7
	421913	AI934365	Hs.109439	osteoglycin (osteoblastic factor, mime	18.7
	418619	AA228776	Hs.191721	ESTs	18.7
10	450831	R37974	Hs.25255	ESTs	18.7
	415691	AW963979	Hs.24723	ESTs	18.7
	417124	BE122762	Hs.25338	ESTs	18.7
	445162	AB011131	Hs.12376	piccolo (presynaptic cytomatrix protein)	18.6
	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	18.5
15	410099	AA081630	Hs.169387	KIAA0036 gene product	18.5
	430722	AW968543	Hs.203270	ESTs, Weakly similar to ALU1_HUMAN ALU S	18.5
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	18.5
	436420	AA443968	Hs.31595	ESTs	18.4
	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	18.4
20	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	18.3
	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	18.3
	444931	AV652066	Hs.75113	general transcription factor IIIA	18.2
	437446	AA788946	Hs.16869	ESTs, Moderately similar to CA1C RAT COL	18.2
	439569	AW602165	Hs.222399	CEGP1 protein	18.1
25	417061	AI675944	Hs.186601	Homo sapiens cDNA FLJ12033 fis, clone HE	18.1
	424582	AW604804	Hs.161717	KIAA0437 protein	18.0
	432435	BE218886	Hs.282070	ESTs	17.9
	443547	AW271273	Hs.23767	hypothetical protein FLJ12866	17.8
30	431121	AW971167		gb:EST383245 MAGE resequences, MAGL Homo	17.8
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	17.7
	407110	AA018042	Hs.252085	Prader-Willi/Angelman syndrome-5	17.7
	440703	AL137663	Hs.7378	Homo sapiens mRNA; cDNA DKFZp434G227 (fr	17.7
	429925	NM_000786	Hs.226213	cytochrome P450, 51 (lanosterol 14-alpha	17.6
	427958	AA418000	Hs.98280	potassium intermediate/small conductance	17.6
35	421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	17.5
	430487	D87742	Hs.241552	KIAA0268 protein	17.4
	419355	AA428520	Hs.90061	progesterone binding protein	17.4
	417412	X16896	Hs.82112	interleukin 1 receptor, type I	17.3
40	423943	AF163570	Hs.135756	polymerase (DNA directed) kappa	17.3
	434217	AW014795	Hs.23349	ESTs	17.3
	439444	AI277852	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	17.2
	447603	AW207605	Hs.164230	ESTs, Highly similar to JC7266 3',5'-cyc	17.2
	430177	AW969233	Hs.302746	MSTP028 protein	17.2
	432473	AI202703	Hs.152414	ESTs	17.1
45	421823	N40850	Hs.28625	ESTs	17.1
	418522	AA605038	Hs.7149	Homo sapiens cDNA: FLJ21950 fis, clone H	17.0
	420092	AA814043	Hs.88045	ESTs	17.0
	414602	AW630088	Hs.76550	Homo sapiens mRNA; cDNA DKFZp554B1264 (f	17.0
	417426	NM_002291	Hs.82124	laminin, beta 1	17.0
50	400297	AI127076	Hs.334473	hypothetical protein DKFZp554O1278	17.0
	401747			Homo sapiens keratin 17 (KRT17)	17.0
	424181	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	17.0
	442369	AI565071	Hs.169983	ESTs	16.9
	432966	AA650114	Hs.325198	ESTs	16.9
55	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	16.8
	419536	AA603305		gb:np12d11.s1 NCL_CGAP_Pr3 Homo sapiens	16.8
	443745	AB039670	Hs.9728	ALEX1 protein	16.8
	438899	AF086833	Hs.135624	ESTs	16.8
	418555	AI417215	Hs.87159	hypothetical protein FLJ12577	16.8
60	442054	AI422867	Hs.88594	ESTs	16.8
	409385	AA071267		gb:zmf1g01.r1 Stratagene fibroblast (937	16.5
	453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocon	16.4
	443601	AW206942	Hs.253594	ESTs	16.3
	437536	X81221	Hs.144465	ESTs	16.3
65	409196	NM_001874	Hs.334873	carboxypeptidase M	16.3
	438337	AK002058	Hs.6166	hypothetical protein FLJ11196	16.3
	416239	AL038450	Hs.48948	ESTs	16.3
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	16.2
	407192	AA609200		gb:af12a02.s1 Soares_fas1s_NHT Homo sap	16.2
70	408050	AI815867	Hs.50130	necdin (mouse) homolog	16.1
	442571	C06338	Hs.165464	ESTs	16.1
	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked moi	16.1
	426125	X87241	Hs.166994	FAT tumor suppressor (Drosophila) homolo	16.0
	450164	AI239923	Hs.30098	ESTs	16.0
75	429653	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,	16.0
	408990	AL022395	Hs.49526	1-box and leucine-rich repeat protein 4	16.0
	417094	NM_006895	Hs.81182	histamine N-methyltransferase	16.0
	436024	AI800041	Hs.190555	ESTs	16.0
	412652	AI801777	Hs.6774	ESTs	16.0
80	456516	BE172704	Hs.222746	KIAA1610 protein	16.0
	452576	AB023177	Hs.29900	KIAA0960 protein	15.9
	430299	W28873	Hs.105747	serine carboxypeptidase 1 precursor prot	15.9
	434792	AA649253	Hs.132458	ESTs	15.9
	418036	Z37976	Hs.83337	latent transforming growth factor beta b	15.9

	442787	W93048	Hs.250723	hypothetical protein MGC2747	15.9
	448402	BE244226	Hs.21094	RAB18, member RAS oncogene family	15.9
	402812			NM_004930*:Homo sapiens capping protein	15.8
5	447313	U92981	Hs.18081	Homo sapiens clone DT1P1B6 mRNA, CAG rep	15.8
	413597	AW302885	Hs.117183	ESTs	15.7
	439677	R82331	Hs.164599	ESTs	15.7
	432527	AW975028	Hs.102754	ESTs	15.7
	413654	AA331881	Hs.75454	peroxiredoxin 3	15.7
10	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	15.7
	420501	AW043782	Hs.293616	ESTs	15.7
	435056	AW023337	Hs.5422	glycoprotein M6B	15.7
	414504	AW069181	Hs.115175	sterile-alpha motif and leucine zipper c	15.6
	443960	AJ093577	Hs.255416	hypothetical protein FLJ21986	15.6
	434988	AJ418055	Hs.161160	ESTs	15.6
15	435380	AA679001	Hs.192221	ESTs	15.6
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	15.6
	437252	AJ433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	15.6
	446377	AW014022	Hs.170953	ESTs	15.6
20	425009	X58288	Hs.154151	protein tyrosine phosphatase, receptor t	15.5
	415672	N53097	Hs.193579	ESTs	15.5
	450325	AJ935962	Hs.26289	ESTs	15.5
	400294	N95796	Hs.278695	Homo sapiens protein mRNA, complete cds	15.4
	443574	AJ081330	Hs.145008	ESTs	15.4
25	415263	AA948033	Hs.130853	ESTs	15.4
	442081	AA401863	Hs.22380	ESTs	15.3
	415788	AW628686	Hs.78851	KIAA0217 protein	15.3
	445457	AJ239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	15.3
	436299	AK000767	Hs.5111	hypothetical protein FLJ20729	15.3
30	418593	AJ750878	Hs.87409	thrombospondin 1	15.3
	422163	AF027208	Hs.112360	prominin (mouse)-like 1	15.3
	443180	R15875	Hs.258576	claudin 12	15.2
	432437	W07088	Hs.293685	ESTs	15.2
	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	15.2
35	446091	AW022192	Hs.200197	ESTs	15.2
	409341	AJ963376	Hs.12532	chromosome 1 open reading frame 21	15.2
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	15.1
	434096	AW662958	Hs.75825	pleiomorphic adenoma gene-like 1	15.1
	453698	AA037615	Hs.42746	ESTs	15.1
40	444805	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligase	15.1
	427707	NM_005578	Hs.180398	LIM domain-containing preferred transloc	15.1
	453308	AW959731	Hs.323099	ESTs	15.1
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	15.1
	433927	AJ557019	Hs.116467	small nuclear protein PRAC	15.0
45	443162	T49951	Hs.9029	DKFZP434G032 protein	15.0
	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fis, clone H	15.0
	424580	AA446539	Hs.339024	ESTs, Weakly similar to A46010 X-linked	15.0
	443912	R37257	Hs.164780	ESTs	15.0
	410297	AA148710	Hs.79914	lumican	15.0
50	431448	AL137517	Hs.334473	hypothetical protein DKFZp564O1278	14.9
	432305	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhib	14.9
	451652	AA018968	Hs.133536	ESTs	14.9
	406038	Y14443	Hs.88219	zinc finger protein 200	14.8
	408784	AW971350	Hs.63386	ESTs	14.8
55	453510	AJ699482	Hs.42151	ESTs	14.8
	407894	AJ278313	Hs.41143	phosphoinositide-specific phospholipase	14.8
	433908	AW298141	Hs.157975	ESTs	14.8
	440629	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	14.8
	413249	AF187160	Hs.75251	DEAD/H (Asp-Glu-Ala-Asp/His) box binding	14.8
60	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	14.7
	430665	BE350122	Hs.157367	ESTs, Weakly similar to I78885 serine/th	14.7
	447752	M73700	Hs.105938	lactotransferrin	14.7
	428044	AA502490	Hs.336895	ESTs	14.7
	403362			NM_001615*:Homo sapiens actin, gamma 2,	14.7
65	427982	NM_016156	Hs.161326	KIAA1073 protein	14.7
	407634	AW016569	Hs.136414	UDP-GlcNAc:betaGal beta-1,3-N-acetylgluc	14.7
	448362	AA641767	Hs.21015	hypothetical protein DKFZp564L0864 simi	14.7
	433226	AW503733	Hs.9414	KIAA148B protein	14.6
	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-I	14.6
70	453861	AJ028839	Hs.30120	ESTs, Weakly similar to NUCL_HUMAN NUCLE	14.6
	458082	AW978811	Hs.314451	ESTs, Weakly similar to ALU1_HUMAN ALU S	14.6
	409264	NM_014937	Hs.52463	KIAA0968 protein	14.6
	432729	AK000292	Hs.278732	hypothetical protein FLJ20285	14.5
	422270	AF114494	Hs.114062	protein tyrosine phosphatase-like (proti	14.5
75	410339	AJ916499	Hs.298258	ESTs	14.5
	431992	NM_002742	Hs.2891	protein kinase C, mu	14.5
	424432	AB037821	Hs.145858	protocadherin 10	14.5
	431933	AJ187057	Hs.132554	ESTs	14.5
	440749	W22335	Hs.7392	hypothetical protein MGC3199	14.5
80	416434	AW163045	Hs.78334	nuclear factor, interleukin 3 regulated	14.5
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	14.5
	407021	U52077		gb:Human mariner1 transposase gene, comp	14.5
	413788	AW613780	Hs.13500	ESTs	14.5
	437866	AA156781	Hs.74170	metallothionein 1E (functional)	14.5

	454078	AA601518	Hs.22209	secreted modular calcium-binding protein	14.4
	411990	AW963624	Hs.31707	ESTs, Weakly similar to YEW4_YEAST HYPOT	14.4
	443280	AA299688	Hs.24183	ESTs	14.4
5	416836	D54745	Hs.80247	cholecystokinin	14.4
	436860	H12751	Hs.5327	PRO1914 protein	14.3
	425174	D87450	Hs.154978	KIAA0261 protein	14.3
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	14.3
	443790	NM_003500	Hs.9795	acyl-Coenzyme A oxidase 2, branched chain	14.3
10	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecule)	14.2
	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11953 fis, clone HE	14.2
	437718	AI927288	Hs.196779	ESTs	14.2
	412828	AL133395	Hs.74821	prion protein (p27-30) (Creutzfeldt-Jakob)	14.2
	432712	AG016247	Hs.288031	sterol-C5-desaturase (fungal ERG3, delta)	14.2
15	433332	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	14.2
	451533	NM_004657	Hs.26530	serum deprivation response (phosphatidyl	14.2
	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	14.1
	446494	AA463278	Hs.288906	WW Domain-Containing Gene	14.1
	466508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	14.0
20	432261	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface	14.0
	426423	NM_012446	Hs.169833	single-stranded-DNA-binding protein	14.0
	442281	N34742	Hs.170065	Homo sapiens cDNA FLJ13492 fis, clone PL	14.0
	442145	AI022650	Hs.8117	erbB2-Interacting protein ERBIN	13.9
	418648	AI020951	Hs.193465	ESTs	13.9
25	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	13.9
	439518	W76326		gb:cd60d04.r1 Soares_fetal_heart_NbHH19W	13.9
	443967	AW294013	Hs.200942	ESTs	13.9
	424775	AB014540	Hs.153028	SWAP-70 protein	13.9
	411190	AA306342	Hs.69171	protein kinase C-like 2	13.9
30	447384	AI377221	Hs.40528	ESTs	13.9
	444880	AW118683	Hs.154150	ESTs	13.9
	433409	AI276802	Hs.25661	ESTs	13.9
	423201	NM_000163	Hs.125180	growth hormone receptor	13.9
	413724	AA131466	Hs.23767	hypothetical protein FLJ12666	13.9
35	464219	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	13.8
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	13.8
	430588	AK001764	Hs.247112	hypothetical protein FLJ10902	13.8
	444172	BE147740	Hs.104558	ESTs, Moderately similar to I38022 hypot	13.8
	416774	AI005169	Hs.28274	Homo sapiens cDNA: FLJ22049 fis, clone H	13.8
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	13.8
40	428738	NM_000380	Hs.192803	xeroderma pigmentosum, complementation g	13.8
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	13.8
	407839	W05608	Hs.312679	ESTs, Weakly similar to A49019 dynein he	13.8
	452261	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	13.7
45	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12165 fis, clone MA	13.7
	428054	AI948688	Hs.266619	ESTs	13.7
	444636	T96867	Hs.17877	ESTs	13.7
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	13.7
	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	13.7
50	462260	AA453208	Hs.28726	RAB9, member RAS oncogene family	13.7
	428966	AF069214	Hs.194687	cholesterol 25-hydroxylase	13.7
	450316	W84446	Hs.226434	hypothetical protein MGC4643	13.7
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	13.7
	443634	H73972	Hs.134460	ESTs	13.7
55	449474	AA019344	Hs.2055	ubiquitin-activating enzyme E1 (A1S9T an	13.7
	422278	AF072873	Hs.114218	frizzled (Drosophila) homolog 6	13.7
	445817	NM_003642	Hs.13340	histone acetyltransferase 1	13.7
	434629	AA789081	Hs.4029	glioma-amplified sequence-41	13.6
	416795	AI497778	Hs.20509	HBV pX associated protein-8	13.6
60	410001	AB041035	Hs.57771	kallikrein 11	13.6
	452242	R50956	Hs.159993	glycosyltransferase	13.6
	413231	D87461	Hs.75244	BCL2-like 2	13.6
	404641			NM_021965: Homo sapiens phosphoglucomuta	13.6
65	428648	AF052728	Hs.186021	potassium voltage-gated channel, subfam	13.6
	414279	AW021691	Hs.101067	GCNs (general control of amino-acid synt	13.6
	411573	AB029000	Hs.70823	KIAA1077 protein	13.5
	417632	R20855	Hs.5422	glycoprotein M6B	13.5
	431487	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	13.5
	450313	AK038989	Hs.332633	Bardet-Biedl syndrome 2	13.5
70	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	13.5
	419264	AA877104	Hs.293872	ESTs, Weakly similar to ALUB_HUMAN IIII	13.5
	418663	AK001100	Hs.41690	desmocollin 3	13.5
	452277	AL049013	Hs.28783	KIAA1223 protein	13.5
	447896	AI436124	Hs.294069	Homo sapiens cDNA FLJ13384 fis, clone PL	13.5
75	447082	T85314	Hs.42644	thioredoxin-like	13.5
	451468	AW503398	Hs.293863	ESTs, Moderately similar to I38022 hypot	13.4
	415443	T07353	Hs.7948	ESTs	13.4
	427212	AW293849	Hs.56279	ESTs, Weakly similar to ALU7_HUMAN ALU S	13.4
	442113	BE622187	Hs.99670	ESTs, Weakly similar to I38022 hypoteti	13.3
80	433517	AW022133	Hs.189838	ESTs	13.3
	430829	AW451999	Hs.194024	ESTs	13.3
	453111	AB014598	Hs.31720	hephaestin	13.3
	435839	AF249744	Hs.25951	Rho guanine nucleotide exchange factor (13.3
	429113	D28235	Hs.196384	prostaglandin-endoperoxide synthase 2 (p	13.3

5	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	13.3
	427286	AW732802	Hs.2132	epidermal growth factor receptor pathway	13.3
	437323	AA371146	Hs.226527	leptin receptor	13.2
	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	13.2
	433037	NM_014158	Hs.279938	HSPC067 protein	13.2
10	407538	AA905097	Hs.85050	phospholamban	13.2
	400860			Target Exon	13.2
	411031	W37943	Hs.34892	KIAA1323 protein	13.2
	436797	AA731491	Hs.336454	hypothetical protein MGC14879	13.2
	409277	T05558	Hs.166800	ESTs	13.2
15	434036	AI859131	Hs.197733	hypothetical protein MGC2849	13.2
	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	13.2
	450755	AA010984	Hs.159464	ESTs	13.1
	450649	NM_001429	Hs.25272	E1A binding protein p300	13.1
	408495	W68786	Hs.237731	ESTs	13.1
20	429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	13.1
	428639	AI767756	Hs.82302	Homo sapiens cDNA FLJ14814 fis, clone NT	13.1
	416987	D86957	Hs.80712	KIAA0202 protein	13.0
	453006	AI352575	Hs.167133	ESTs	13.0
	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	13.0
25	415752	BE314524	Hs.78776	putative transmembrane protein	13.0
	411529	AA430348	Hs.317596	Homo sapiens cDNA FLJ12927 fis, clone NT	13.0
	417318	AW953937	Hs.12891	ESTs	13.0
	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	12.9
	426034	AI276989	Hs.56123	Homo sapiens cDNA FLJ13443 fis, clone PL	12.9
30	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	12.9
	428218	AA424266	Hs.123642	EphA3	12.9
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	12.9
	448779	BE042877	Hs.177135	ESTs	12.8
	448944	AB014605	Hs.22599	atrophin-1 interacting protein 1; activi	12.8
35	417315	AK080042	Hs.336901	ribosomal protein S24	12.8
	429697	AW286451	Hs.24606	ESTs	12.8
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypotheti	12.8
	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	12.8
	451099	FS2795	Hs.25954	interleukin 13 receptor, alpha 2	12.8
40	424806	AA382523	Hs.105689	MSTP031 protein	12.7
	442343	AA592480	Hs.129874	ESTs	12.7
	432244	AI669973	Hs.200574	ESTs	12.7
	459513	AI032946		gbxx06g09.s1 Soares_fetal_liver_spleen_	12.7
	452512	AW363486	Hs.337635	ESTs	12.7
45	415079	R43179	Hs.22895	hypothetical protein FLJ23548	12.7
	422365	AF035537	Hs.115521	REV3 (yeast homolog)-like, catalytic sub	12.7
	411067	AI681006	Hs.71721	ESTs	12.7
	442501	AA315267	Hs.23128	ESTs	12.7
	434466	AB037829	Hs.3862	regulator of nonsense transcripts 2; DKF	12.7
50	437052	AA861697	Hs.120591	ESTs	12.7
	433234	AG040928	Hs.65306	KIAA1495 protein	12.6
	453830	AA534286	Hs.20953	ESTs	12.6
	409995	AW960597	Hs.30164	ESTs	12.6
	414290	AI588801	Hs.71721	ESTs	12.6
55	417248	AA329449	Hs.247302	twisted gastrulation	12.6
	418624	AI734080	Hs.104211	ESTs	12.6
	412654	AI093480	Hs.29263	hypothetical protein FLJ11896	12.6
	450253	AL133047	Hs.24716	Homo sapiens mRNA; cDNA DKFZp434D0215 (f	12.6
	446619	AU076643	Hs.313	secreted phosphoprotein 1 (osteopontin,	12.5
60	427078	AI676062	Hs.111902	ESTs	12.5
	420838	AW118210	Hs.5244	ESTs	12.5
	449784	AW161319	Hs.12915	ESTs	12.5
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	12.5
	415276	U88666	Hs.78353	SFRS protein kinase 2	12.5
65	426110	NM_002913	Hs.166563	replication factor C (activator 1) 1 (14	12.5
	400301	X03635	Hs.1657	estrogen receptor 1	12.5
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	12.5
	426316	NM_002430	Hs.268515	meningioma (disrupted in balanced trans	12.5
	420345	AW295230	Hs.25231	ESTs	12.4
70	432205	AI805583	Hs.125291	ESTs	12.4
	451893	AW192083	Hs.290855	ESTs	12.4
	435266	AK001942	Hs.4863	hypothetical protein DKFZp566A1524	12.4
	427003	U19487	Hs.2090	prostaglandin E receptor 2 (subtype EP2)	12.4
	404642			NM_021965~Homo sapiens phosphoglucoma	12.4
75	414241	AA425085	Hs.4007	Sarcolemmal-associated protein	12.4
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	12.4
	420871	AA702972	Hs.65300	ESTs	12.4
	448072	AI59306	Hs.24508	ESTs	12.4
	441269	AW015206	Hs.178784	ESTs	12.3
80	427761	AA412205	Hs.140996	ESTs	12.3
	425322	U63630	Hs.155637	protein kinase, DNA-activated, catalytic	12.3
	417733	AL048678	Hs.82503	H.sapiens mRNA for 3'UTR of unknown prot	12.3
	436521	AW203986	Hs.213003	ESTs	12.3
	408920	AL120071	Hs.48598	fibronectin leucine rich transmembrane p	12.3
	446332	AK001635	Hs.14838	hypothetical protein FLJ10773	12.2
	453994	BE180964	Hs.165580	ribosomal protein S13	12.2
	420397	NM_007018	Hs.97437	centrosomal protein 1	12.2

	447471	AF039843	Hs.18676	sprouty (Drosophila) homolog 2	12.2
	442562	BE379584	Hs.34789	dolichyl-diphosphooligosaccharide-prote	12.2
	400880			NM_000611: Homo sapiens CD69 antigen p18	12.2
5	425920	AL049977	Hs.162209	claudin 8	12.2
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	12.2
	414222	AL135173	Hs.878	sorbitol dehydrogenase	12.1
	427051	BE178110	Hs.173374	Homo sapiens cDNA FLJ10500 fis, clone NT	12.1
	452994	AW962597	Hs.31305	KIAA1547 protein	12.1
10	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	12.1
	437124	AA554458	Hs.197751	KIAA0666 protein	12.1
	411450	H49619	Hs.127301	ESTs	12.1
	421559	NM_014720	Hs.105751	Ste20-related serine/threonine kinase	12.1
	449525	NM_014253	Hs.23796	odc (odd Oz/ten-m, Drosophila) homolog 1	12.1
15	419459	AW291128	Hs.278422	DKFZP586G1122 protein	12.1
	426252	BE176980	Hs.28917	ESTs	12.1
	414171	AA360328	Hs.865	RAP1A, member of RAS oncogene family	12.1
	436169	AA888311	Hs.17602	Homo sapiens cDNA FLJ12381 fis, clone MA	12.0
	435047	AA454985	Hs.54973	cadherin-like protein VR20	12.0
20	417625	U59305	Hs.44708	Ser-Thr protein kinase related to the my	12.0
	439820	AL360204	Hs.283953	Homo sapiens mRNA full length insert cDN	12.0
	443846	AI085198	Hs.164226	ESTs	12.0
	434874	N62448	Hs.293970	methylmalonate-semialdehyde dehydrogenas	12.0
	443837	AI984525	Hs.9884	spindle pole body protein	12.0
25	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	12.0
	424232	AB015982	Hs.143460	protein kinase C, nu	11.9
	414555	N98569	Hs.76422	phospholipase A2, group IIA (platelets,	11.9
	446874	AW968304	Hs.56156	ESTs	11.9
	454119	BE549773	Hs.40510	uncoupling protein 4	11.9
30	436746	AA730046	Hs.187866	ESTs	11.9
	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	11.9
	416508	R39769	Hs.206086	ESTs, Moderately similar to ALUR_HUMAN A	11.8
	444758	AL044878	Hs.11899	3-hydroxy-3-methylglutaryl-Coenzyme A re	11.8
	413991	H44725	Hs.42653	ESTs	11.8
35	431645	AF078849	Hs.266483	dysmin light chain-A	11.8
	421406	AF179897	Hs.104105	Mels (mouse) homolog 2	11.8
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	11.8
	424903	T26477	Hs.22883	ESTs, Weakly similar to I38022 hypothesis	11.8
	412977	AA125910	Hs.191461	ESTs	11.8
40	428881	AL044675	Hs.173081	KIAA0530 protein	11.8
	410853	H04588	Hs.30469	ESTs	11.7
	444670	H58373	Hs.332938	hypothetical protein MGC5370	11.7
	444381	BE587335	Hs.283713	ESTs, Weakly similar to S64054 hypothesis	11.7
	434398	AA121098	Hs.3838	serum-inducible kinase	11.7
45	438032	BE045624	Hs.152992	ESTs	11.7
	433212	BE218049	Hs.121820	ESTs	11.6
	424330	AW073953	Hs.333396	Homo sapiens cDNA FLJ13596 fis, clone PL	11.6
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	11.6
	430929	AA489166	Hs.156933	ESTs	11.6
50	423782	AI472209	Hs.323117	ESTs	11.6
	425770	NM_014363	Hs.159492	spastic ataxia of Charlevoix-Saguenay (s	11.6
	437108	AA434054	Hs.80624	hypothetical protein MGC2560	11.6
	430200	BE613337	Hs.234896	geminin	11.5
	453957	AL080235	Hs.35861	DKFZP566E1621 protein	11.5
55	411096	U80034	Hs.68583	mitochondrial intermembrane peptidase	11.5
	422805	AA436989	Hs.121017	H2A histone family, member A	11.5
	422538	NM_006441	Hs.118131	5,10-methylenetetrahydrofolate synthetase	11.5
	412677	AW029608	Hs.17384	ESTs	11.5
	421896	N62293	Hs.45107	ESTs	11.5
60	453930	AA419466	Hs.36727	hypothetical protein FLJ10903	11.5
	443123	AA094538	Hs.272808	putative transcription regulation nuclea	11.5
	415293	R49462	Hs.106541	ESTs	11.5
	443161	AI039316		gb:cx48c08.x1 Soares_tota_fetus_Nb2HF8_	11.5
	420185	AL044056	Hs.158047	ESTs	11.5
65	445527	W39694	Hs.83286	ESTs, Weakly similar to S14747 sphingomy	11.5
	428529	R14050	Hs.194051	Homo sapiens mRNA; cDNA DKFZp566B213 (fr	11.5
	416852	AF283776	Hs.80285	Homo sapiens mRNA; cDNA DKFZp586C1723 (f	11.5
	449919	AI674685	Hs.200141	ESTs	11.5
	414844	AA296874	Hs.77494	deoxyguanosine kinase	11.5
70	449543	AF070632	Hs.23729	Homo sapiens clone 24405 mRNA sequence	11.4
	429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	11.4
	407786	AA687538	Hs.38972	tetraspan 1	11.4
	414407	AA147026	Hs.76704	ESTs	11.4
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoietin	11.4
75	456804	AI421645	Hs.139851	caveolin 2	11.4
	422546	AS007969	Hs.301478	KIAA0500 protein	11.4
	417350	U60928	Hs.82001	polycystic kidney disease 2 (autosomal d	11.4
	417683	AW566008	Hs.239154	ankyrin repeat, family A (RFXANK-like),	11.4
	424800	AL035588	Hs.153203	MyoD family inhibitor	11.4
80	433577	AW007080	Hs.8817	ESTs	11.4
	453935	AI633770	Hs.42572	ESTs	11.4
	415060	AJ223810	Hs.43213	ESTs, Weakly similar to IEF8_HUMAN TRANS	11.4
	425710	AF030880	Hs.159275	solute carrier family, member 4	11.3
	446768	AI473827	Hs.31793	ESTs	11.3

5	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	11.3
	410108	AA081659	Hs.318775	OSBP-related protein 6	11.3
	418450	R84397	Hs.193851	ESTs, Weakly similar to alternatively sp	11.3
	415457	AW081710	Hs.7369	ESTs, Weakly similar to ALU1_HUMAN ALU S	11.3
	452110	T47667	Hs.28005	Homo sapiens cDNA FLJ11309 fis, clone PL	11.3
10	414212	AA136569	Hs.10848	KIAA0187 gene product	11.3
	401519			C15000476-g[12737279]ref[XP_012163.1]	11.3
	458509	AA654650	Hs.282906	ESTs	11.2
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	11.2
	452784	BE463857	Hs.151258	hypothetical protein FLJ21062	11.2
15	436758	AW977167	Hs.155272	ESTs	11.2
	409401	AI201895	Hs.181309	proteasome (prosome, macropain) subunit,	11.2
	434715	BE005346	Hs.118410	ESTs	11.2
	427283	AL119795	Hs.174185	ectonucleotide pyrophosphatase/phosphodi	11.2
	428342	AI739168	Hs.131798	Homo sapiens cDNA FLJ13458 fis, clone PL	11.2
20	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	11.2
	430519	AF129534	Hs.49210	F-box only protein 4	11.2
	418838	AW385224	Hs.35198	ectonucleotide pyrophosphatase/phosphodi	11.1
	429163	AA894768		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	11.1
	434158	T06534	Hs.14372	ESTs	11.1
25	414341	D80004	Hs.75809	KIAA0182 protein	11.1
	414650	AA150435	Hs.72063	ESTs	11.1
	448475	BE613134	Hs.247474	hypothetical protein FLJ21032	11.1
	437575	AW954355	Hs.36529	hypothetical protein MGC11242	11.1
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	11.1
30	425289	AW139342	Hs.155630	Interferon, gamma-inducible protein 16	11.1
	452598	AI831594	Hs.68647	ESTs, Weakly similar to ALU7_HUMAN ALU S	11.1
	417433	BE270268	Hs.82128	5T4 oncofetal trophoblast glycoprotein	11.0
	438379	N23018	Hs.171391	C-terminal binding protein 2	11.0
	433230	AW136134	Hs.220277	ESTs	11.0
35	412622	AW864708	Hs.171959	ESTs	11.0
	450353	AI244661	Hs.103296	ESTs, Weakly similar to S65657 alpha-1C-	11.0
	434349	NM_015678	Hs.3821	neurobeachin	11.0
	430261	AA305127	Hs.237225	hypothetical protein HT023	11.0
	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	11.0
40	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	11.0
	442082	R41823	Hs.7413	ESTs	11.0
	422890	Z43784	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	11.0
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	11.0
	450244	AA007534	Hs.125062	ESTs	11.0
45	417189	R13550	Hs.246773	ESTs	11.0
	421481	AW391972	Hs.104695	KIAA1324 protein	10.9
	431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	10.9
	408988	AL119844	Hs.49476	Homo sapiens clone TUA8 Cri-du-chat regi	10.9
	439706	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	10.9
50	435133	AJ010482	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	10.9
	433658	L03678	Hs.158110	Immunoglobulin kappa constant	10.9
	428364	AA426565	Hs.311103	ESTs, Moderately similar to ALU1_HUMAN A	10.9
	441540	C01387	Hs.127128	ESTs	10.9
	431154	AW971228	Hs.290259	ESTs, Weakly similar to I38022 hypotheti	10.9
55	416777	AF146760	Hs.79844	DKFZP564M1416 protein	10.9
	439556	AI823752	Hs.163603	ESTs	10.9
	428280	H05541	Hs.183428	sarcomagen (Kras oncogene-associated gene	10.8
	453942	AW190920	Hs.19928	hypothetical protein SP329	10.8
	447982	H22853	Hs.137551	ESTs	10.8
60	422779	AA317036	Hs.118787	transforming growth factor, beta-induced	10.8
	447695	AW379130	Hs.18953	phospholipase 9A	10.8
	427115	AW972853	Hs.112237	ESTs	10.8
	448019	AW947164	Hs.195841	ESTs, Moderately similar to I38022 hypot	10.8
	419326	W94915	Hs.42419	ESTs	10.8
65	435163	AA668884	Hs.19155	ESTs	10.8
	417578	T91443	Hs.193963	ESTs	10.8
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	10.8
	450205	AI786460	Hs.201600	ESTs	10.8
	428413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	10.8
70	421977	W94187	Hs.110165	ribosomal protein L26 homolog	10.8
	437957	BE277414	Hs.5947	msl transforming oncogene (derived from	10.8
	408243	Y00787	Hs.624	interleukin 3	10.8
	439492	AF086310	Hs.103159	ESTs	10.8
	413492	D87470	Hs.75400	KIAA0280 protein	10.8
75	436962	AW377314	Hs.5364	DKFZP564I052 protein	10.8
	435572	AW975339	Hs.239828	ESTs, Weakly similar to GAG2_HUMAN RETRO	10.8
	422583	AA410506	Hs.27973	KIAA0874 protein	10.8
	417665	AW852858	Hs.22862	ESTs	10.7
	433285	AW976944	Hs.237396	ESTs	10.7
80	419693	AA133749	Hs.301350	FXD domain-containing ion transport reg	10.7
	424878	H57111	Hs.221132	ESTs	10.7
	449659	R60031	Hs.198899	eukaryotic translation initiation factor	10.7
	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	10.7
	433556	W55321	Hs.111460	calcium/calmodulin-dependent protein kin	10.7
	452241	AL050204	Hs.28540	Homo sapiens mRNA; cDNA DKFZp586F1223 (f	10.7
	450330	AW500775	Hs.24817	hypothetical protein FLJ20136	10.7
	430689	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	10.7

	433923	A1823453	Hs.146625	ESTs	10.7
	418186	A1745649	Hs.26549	KIAA1708 protein	10.7
	416155	A1807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheli	10.7
5	430057	AW450303	Hs.2534	bone morphogenetic protein receptor, typ	10.7
	429350	A1754634	Hs.131987	ESTs	10.7
	418601	AA279490	Hs.86368	calmagin	10.6
	437267	AW511443	Hs.258110	ESTs	10.6
	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	10.6
10	421982	AF206019	Hs.110347	REV1 (yeast homolog)- like	10.6
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	10.6
	418662	A1801098	Hs.151500	ESTs	10.6
	449685	AW296559	Hs.66095	ESTs	10.6
	441111	A1806867	Hs.126594	ESTs	10.6
	436671	AW137159	Hs.146151	ESTs	10.6
15	447974	R76886		gb:Y64b03.s1 Soares placenta NbZHP Homo	10.6
	417916	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic aci	10.6
	424562	A1420859	Hs.150657	basic transcription element binding prot	10.6
	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	10.6
20	443015	R33261	Hs.6614	ESTs, Weakly similar to A43932 mucin 2 p	10.6
	439584	AA838114	Hs.221612	ESTs	10.6
	426298	AW965059	Hs.111583	ESTs, Weakly similar to I38022 hypotheti	10.6
	420929	A1694143	Hs.296251	programmed cell death 4	10.6
	418318	U47732	Hs.84072	transmembrane 4 superfamily member 3	10.6
	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	10.6
25	418329	AW247430	Hs.84152	cystathionine-beta-synthase	10.6
	424433	H04607	Hs.9218	ESTs	10.6
	420230	AL034344	Hs.284186	forkhead box C1	10.6
	419441	AW023731	Hs.274368	MSTP032 protein	10.6
30	426011	AW980996	Hs.58924	ESTs, Weakly similar to JC5594 jerky gen	10.6
	461900	AB023199	Hs.27207	KIAA0882 protein	10.6
	424692	AA429834	Hs.151791	KIAA0092 gene product	10.6
	439999	AA115811	Hs.6838	ras homolog gene family, member E	10.5
	424368	AB037788	Hs.146085	KIAA1345 protein	10.5
35	402078			C50020Z:gil108287[pil]S55467 tropomy	10.5
	413886	AW958264	Hs.103832	similar to yeast Upf3, variant B	10.5
	445041	T64163	Hs.282952	solute carrier	10.5
	428927	AA441837	Hs.90250	ESTs	10.5
	414831	M31158	Hs.77439	protein kinase, cAMP-dependent, regulato	10.5
40	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	10.5
	426429	X73114	Hs.169849	myosin-binding protein C, slow-type	10.5
	452055	A1377431	Hs.141693	hypothetical protein MGC10858	10.5
	438913	A1380429	Hs.172445	ESTs	10.5
	443684	A1891307	Hs.55098	ESTs	10.5
45	429281	AA630858	Hs.29808	Homo sapiens cDNA: FLJ21122 fis, clone C	10.5
	421040	AA715026	Hs.135280	ESTs	10.5
	425277	NM_001241	Hs.155478	cydlin T2	10.5
	418564	AA631143	Hs.278695	Homo sapiens protein mRNA, complete cds	10.5
	440099	AL080058	Hs.6909	DKFZP564G202 protein	10.5
50	434958	T98949	Hs.303428	Homo sapiens cDNA FLJ14832 fis, clone OV	10.5
	419972	AL041465	Hs.182952	golgin-87	10.5
	416182	NM_004354	Hs.79089	cyclin G2	10.4
	418366	AW014345	Hs.161690	ESTs	10.4
	452286	A1368570	Hs.123933	ESTs, Weakly similar to ZN91_HUMAN ZINC	10.4
55	430361	A1033985	Hs.239926	sterol-C4-methyl oxidase-like	10.4
	446716	AA436575	Hs.16602	ESTs	10.4
	419544	A1908154		gb:QV-BT200-010499-007 BT200 Homo sapien	10.4
	433023	AW864793	Hs.87409	thrombospondin 1	10.4
	409151	AA306105	Hs.50785	SEC22, vesicle trafficking protein (S. c	10.4
60	449115	AW959952	Hs.37528	ESTs, Weakly similar to AF090944 1 PRO06	10.4
	445715	AB012958	Hs.13137	UV radiation resistance associated gene	10.4
	443228	W24781	Hs.293788	KIAA1710 protein	10.4
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp586J1922 (f	10.4
	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glu	10.4
65	452741	BE392914	Hs.30503	Homo sapiens cDNA FLJ11344 fis, clone PL	10.4
	428728	NM_016625	Hs.191381	hypothetical protein	10.4
	423905	AW578960	Hs.135160	lung type-I cell membrane-associated gly	10.4
	413328	Y15723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	10.3
	453020	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	10.3
70	411359	H86088	Hs.22635	ESTs	10.3
	420000	AB038063	Hs.94262	p53-inducible ribonucleotide reductase s	10.3
	412262	W26405	Hs.295923	seven in absentia (Drosophila) homolog 1	10.3
	419875	AA853410	Hs.93557	proenkephalin	10.3
	414422	AA147224	Hs.337232	Homeo box A13	10.3
	426581	AB040956	Hs.135890	KIAA1523 protein	10.3
75	424649	BE242035	Hs.151461	embryonic ectoderm development	10.3
	407317	AL204033	Hs.271461	ESTs, Weakly similar to I38022 hypotheti	10.3
	440426	A1158800	Hs.7181	Homo sapiens cDNA FLJ13663 fis, clone PL	10.3
	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	10.3
80	423250	BE061916	Hs.125849	chromosome B open reading frame 2	10.3
	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13855 fis, clone PL	10.3
	451593	AF151879	Hs.26708	CGI-121 protein	10.3
	435106	AA100847	Hs.193380	ESTs, Highly similar to AF174800 1 F-box	10.3
	438157	AW137011	Hs.49576	ESTs	10.3

5	443181	AI039201	Hs.283316	ESTs	10.3
	449125	AI671439	Hs.196029	Homo sapiens mRNA for KIAA1657 protein,	10.2
	411479	AW848047		gb:U3-CT0214-291299-052-A12 CT0214 Homo	10.2
	446553	AB021179	Hs.15299	HMBA-Inducible	10.2
	418278	AI088489	Hs.83937	hypothetical protein	10.2
10	419791	AI579909	Hs.105104	ESTs	10.2
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	10.2
	413753	U17760	Hs.75517	laminin, beta 3 (nicotin (125kD), kalinin	10.2
	445564	AB028957	Hs.12896	KIAA1034 protein	10.2
	435021	AA922192	Hs.54709	ESTs	10.2
15	457498	AI732230	Hs.191737	ESTs	10.2
	425828	NM_004476	Hs.1915	folate hydrolase (prostate-specific memb	10.2
	419589	AW973708	Hs.201925	Homo sapiens cDNA FLJ13446 fis, clone PL	10.2
	446162	AI631319	Hs.63841	hypothetical protein DKFZp434E2318	10.2
	414523	AJ076633	Hs.76353	serine (or cysteine) proteinase inhibitor	10.2
20	427393	AB029018	Hs.177635	KIAA1095 protein	10.1
	408741	M73720	Hs.846	carboxypeptidase A3 (mast cell)	10.1
	437743	AI383497	Hs.131811	ESTs, Weakly similar to ALU1_HUMAN ALU S	10.1
	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	10.1
	448172	N75276	Hs.135904	ESTs	10.1
25	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	10.1
	444518	AV653785	Hs.173334	ELL-RELATED RNA POLYMERASE II, ELONGATI	10.1
	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	10.1
	413431	AW248428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	10.1
	410150	AW382942	Hs.6774	ESTs	10.1
30	444100	AA383343	Hs.22115	CDC14 (cell division cycle 14, S. cerevi	10.1
	448148	NM_016878	Hs.20509	HBV pX associated protein-8	10.1
	443476	AW068594	Hs.133878	ESTs, Weakly similar to YCD1_HUMAN HYPOT	10.1
	433345	AI681545	Hs.152982	hypothetical protein FLJ13117	10.1
	423581	AB023215	Hs.131525	Homo sapiens mRNA; cDNA DKFZp434E199 (fr	10.1
35	450205	AI219748	Hs.11356	ESTs	10.1
	408374	AW025430	Hs.155591	forkhead box F1	10.0
	448035	NM_006558	Hs.13565	Sam68-like phosphotyrosine protein, T-ST	10.0
	432589	AL135726	Hs.131708	ESTs	10.0
	435604	AA625279	Hs.26892	uncharacterized bone marrow protein BM04	10.0
40	411997	AW673478	Hs.108323	ubiquitin-conjugating enzyme E2E 2 (homo	10.0
	419972	AA466113	Hs.23853	ESTs, Weakly similar to A34615 profilag	10.0
	444564	AI167877	Hs.143716	ESTs	10.0
	426931	NM_003416	Hs.2076	zinc finger protein 7 (KIX 4, clone HF.1	10.0
	451424	AI662026	Hs.302810	Novel human gene mapping to chromosome 20	10.0
45	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	10.0
	431616	AA508552	Hs.195839	ESTs, Weakly similar to I38022 hypotheti	10.0
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	10.0
	425833	AB037813	Hs.159200	hypothetical protein DKFZp762K222	10.0
	442760	BE075297	Hs.6814	ESTs, Weakly similar to A43932 mucin 2 p	10.0
50	418884	AA230228	Hs.59197	ESTs	10.0
	444821	AA063564	Hs.12040	STE20-like kinase	9.9
	451989	AF169797	Hs.27413	adaptor protein containing pH domain, PT	9.9
	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	9.9
	453127	AI696671	Hs.294110	ESTs	9.9
55	435706	W31254	Hs.7045	GL004 protein	9.9
	410748	BE383816	Hs.12532	chromosome 1 open reading frame 21	9.9
	418250	U29926	Hs.83918	adenosine monophosphate deaminase (ecto	9.9
	408832	AW086690	Hs.63428	ESTs, Weakly similar to Z195_HUMAN ZINC	9.9
	418339	AA639902	Hs.104215	ESTs, Moderately similar to SPCN_HUMAN S	9.9
60	452357	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	9.9
	432887	AI926047	Hs.162859	ESTs	9.9
	430291	AV660345	Hs.238126	CGI-49 protein	9.9
	440370	AA884000	Hs.8173	hypothetical protein FLJ10803	9.9
	412350	AI658308	Hs.73826	protein tyrosine phosphatase, non-recept	9.9
65	428825	AI084336	Hs.128783	ESTs, Weakly similar to I38022 hypotheti	9.9
	441054	AA913591	Hs.125480	ESTs	9.9
	416876	AA894876	Hs.5687	protein phosphatase 1B (formerly 2C), ma	9.9
	453078	AF053551	Hs.31504	metaxin 2	9.8
	409203	AA780473	Hs.687	cytochrome P450, subfamily IVB, polypept	9.8
70	446720	AI439136	Hs.140546	ESTs	9.8
	418475	AI658732	Hs.30443	senitin/SUMO-specific protease	9.8
	417708	N74392	Hs.50495	ESTs	9.8
	407870	AB032990	Hs.40719	hypothetical protein KIAA1184	9.8
	420568	F09247	Hs.247735	protocadherin alpha 10	9.8
75	418858	AW961605	Hs.21145	hypothetical protein RG083M05.2	9.8
	453548	AL079983	Hs.116774	integrin, alpha 1	9.8
	427308	D26067	Hs.174905	KIAA0033 protein	9.8
	434579	T55958		gb:yc35f05.r1 Stratagene fetal spleen (9	9.8
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	9.8
80	427528	AJ077143	Hs.179565	minichromosome maintenance deficient (S.	9.8
	413174	AA723564	Hs.191343	ESTs	9.8
	443250	AI041530	Hs.132107	ESTs	9.8
	451957	AI769320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL	9.8
	451406	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	9.8
	422299	AK000181	Hs.114556	hypothetical protein FLJ20174	9.8
	427635	BE397988	Hs.179962	tumor protein p53-binding protein	9.8
	416533	BE244053	Hs.79362	retinoblastoma-like 2 (p130)	9.8

	439091	AA830144	Hs.135613	ESTs, Moderately similar to I38022 hypot	9.8
	418575	AA225313	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	9.7
	432426	AW973152	Hs.31050	ESTs	9.7
	404571			NM_015902: Homo sapiens progesterone induce	9.7
5	444427	H25084	Hs.293663	ESTs, Moderately similar to I38022 hypot	9.7
	439183	AW970600	Hs.303261	ESTs	9.7
	432886	BE158028	Hs.279704	chromatin accessibility complex 1	9.7
	432689	AB018320	Hs.278526	Arg/Abi-interacting protein ArgBP2	9.7
10	417333	AL157545	Hs.42179	bromodomain and PHD finger containing, 3	9.7
	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	9.7
	412324	AW978439	Hs.69504	ESTs	9.7
	422072	AB018255	Hs.111138	KIAA0712 gene product	9.7
	431318	AA502700	Hs.293147	ESTs, Moderately similar to A48010 X-link	9.7
15	417171	BE613486	Hs.81412	tipin 1	9.7
	421709	AA159394	Hs.107056	CED-5 protein	9.7
	415156	X84908	Hs.78060	phosphorylase kinase, beta	9.7
	436446	AW016809	Hs.323795	ESTs	9.7
	447482	AB033059	Hs.18705	KIAA1233 protein	9.7
20	439726	AW445893	Hs.293707	ESTs, Weakly similar to I38598 zinc fing	9.7
	429525	N92540	Hs.205353	ectonucleoside triphosphate diphosphohyd	9.7
	409180	AU076536	Hs.50984	sarcoma amplified sequence	9.6
	419111	AA234172	Hs.137418	ESTs	9.6
	452487	AW207659	Hs.6630	Homo sapiens cDNA FLJ13329 fis, clone OV	9.6
25	416039	AA376989	Hs.78989	alcohol dehydrogenase 5 (class III), chi	9.6
	408239	AA053401	Hs.271827	ESTs, Moderately similar to ALU7_HUMAN A	9.6
	419241	AA523938	Hs.165258	ESTs	9.6
	409752	AW953990		gb:EST376063 MAGE resequences, MAGH Homo	9.6
	453894	AW937825	Hs.56847	Homo sapiens cDNA FLJ12874 fis, clone NT	9.6
30	439671	AW162840	Hs.6641	kinesin family member 5C	9.6
	407230	AA157857	Hs.182265	keratin 19	9.6
	426083	AW982712	Hs.126712	ESTs, Weakly similar to AF191020 1 E2IG5	9.6
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	9.6
	434263	N34895	Hs.44648	ESTs	9.6
	412766	BE544475	Hs.54347	ESTs	9.6
35	418723	AA504428	Hs.10487	Homo sapiens, clone IMAGE:3954132, mRNA,	9.6
	443970	AJ280341	Hs.166571	ESTs	9.6
	424534	DB7682	Hs.150275	KIAA0241 protein	9.6
	419407	AW410377	Hs.41502	hypothetical protein FLJ21276	9.6
40	447689	AW469180	Hs.170651	ESTs	9.5
	429504	X99133	Hs.204238	lipocalin 2 (oncogene 24p3)	9.5
	433165	AA578904	Hs.292437	ESTs	9.5
	418700	AJ933808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	9.5
	440282	BE262386	Hs.7137	clones 23667 and 23775 zinc finger prote	9.5
45	411830	U42349	Hs.71119	Putative prostate cancer tumor suppressor	9.5
	408915	NM_016651	Hs.48950	hepaticellular carcinoma novel gene-3 pro	9.5
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	9.5
	432682	AJ376400	Hs.159588	ESTs	9.5
	435803	Z44194	Hs.4994	transducer of ERBB2, 2	9.5
50	437444	H48008	Hs.31518	ESTs	9.5
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	9.5
	438497	AA808725	Hs.291712	ESTs, Weakly similar to I38022 hypotheti	9.5
	449226	AB002365	Hs.23311	KIAA0367 protein	9.4
	449465	NM_004380	Hs.23698	CREB binding protein (Rubinstein-Taybi s	9.4
55	420969	AJ636310	Hs.28310	ESTs	9.4
	449845	AW971183	Hs.96883	DnaJ (Hsp40) homolog, subfamily C, membe	9.4
	434415	BE177494		gb:RC6-HT0596-270300-011-C05 HT0596 Homo	9.4
	420805	L10333	Hs.99947	telomeron 1	9.4
	415083	AJ632683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	9.4
60	430987	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	9.4
	445280	AW055063	Hs.306088	v-crk avian sarcoma virus CT10 oncogene	9.4
	425657	T89839	Hs.119471	ESTs	9.4
	428260	AW809208	Hs.183297	DKFZP566F2124 protein	9.4
	453293	AA382267	Hs.10563	ESTs	9.4
65	412446	AJ768015	Hs.92127	ESTs	9.4
	441102	AA973905	Hs.331328	intermediate filament protein syncollin	9.4
	421689	N87820	Hs.106826	KIAA1696 protein	9.4
	448073	W19789	Hs.336635	Homo sapiens, clone IMAGE:4179482, mRNA	9.4
	422244	Y08890	Hs.113503	karyopherin (importin) beta 3	9.4
70	452323	W44358	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	9.4
	441499	AW298235	Hs.101689	ESTs	9.4
	420184	AA188408	Hs.95565	hypothetical protein	9.4
	420051	AW024837	Hs.29410	ESTs	9.4
	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	9.4
75	417407	AA823276	Hs.280905	ESTs, Weakly similar to protease [Hsap]	9.3
	450580	N40087	Hs.15248	ESTs	9.3
	419826	AW900992	Hs.93756	DKFZP586D2223 protein	9.3
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	9.3
	412639	AW961284	Hs.296235	ESTs	9.3
	429786	AL000232	Hs.220696	Homo sapiens mRNA; cDNA DKFZp586A061 (fr	9.3
80	446131	NM_000929	Hs.290	phospholipase A2, group V	9.3
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	9.3
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	9.3
	425139	AW630488	Hs.325820	protease, serine, 23	9.3

5	448807	AI571940	Hs.7549	ESTs	9.3
	412505	AA974491	Hs.21734	ESTs	9.3
	412314	AA825247	Hs.250899	heat shock factor binding protein 1	9.3
	445704	AI493742	Hs.166210	ESTs, Moderately similar to E38022 hypot	9.3
	402855			NM_001839*:Homo sapiens calponin 3, acid	9.3
10	428465	AW970976	Hs.293553	ESTs	9.3
	422664	AI148006	Hs.222120	ESTs	9.3
	430027	AB023197	Hs.227743	KIAA0980 protein	9.2
	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	9.2
	424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	9.2
15	433862	D86980	Hs.3610	KIAA0205 gene product	9.2
	429227	AI951456	Hs.21275	hypothetical protein FLJ11011	9.2
	401558			ENSP00000220478*:SECRETORANIN III.	9.2
	428634	AA811845	Hs.106290	Kelch motif containing protein	9.2
	437678	AA529860	Hs.122834	ESTs	9.2
20	416853	AA768553	Hs.74170	metallothionein 1E (functional)	9.2
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	9.2
	450606	NM_004460	Hs.418	fibroblast activation protein, alpha	9.2
	431187	AW971146	Hs.293187	ESTs	9.2
	421202	AF193339	Hs.102505	eukaryotic translation Initiation factor	9.1
25	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	9.1
	430669	AW969657	Hs.291029	ESTs	9.1
	435869	AF255910	Hs.54650	junctional adhesion molecule 2	9.1
	448822	BE149945	Hs.289038	hypothetical protein MGC4126	9.1
	456161	BE254845	Hs.282093	hypothetical protein FLJ21918	9.1
30	423800	AA331156		gb:EST35034 Embryo, 6 week, subtracted (9.1
	432189	AA527941		gbcnh30c04.s1 NCLCGAP_Pr3 Homo sapiens	9.1
	434361	AF129755	Hs.117772	ESTs	9.1
	443247	BE614387	Hs.333893	c-Myc target JPO1	9.1
	419879	Z17805	Hs.93564	Homer, neuronal immediate early gene, 2	9.1
35	411928	AA888624	Hs.197289	rab3 GTPase-activating protein, non-cata	9.1
	448704	AW090932	Hs.249247	heterogeneous nuclear protein similar to	9.1
	448430	AI500642	Hs.289067	Homo sapiens cDNA FLJ11404 fis, clone HE	9.1
	451246	AW189232	Hs.39140	cutaneous T-cell lymphoma tumor antigen	9.1
	418821	AA436002	Hs.183161	ESTs	9.1
40	427213	AW007211	Hs.18131	hypothetical protein FLJ12876	9.1
	419103	Z40229	Hs.95423	hypothetical protein FLJ23033	9.1
	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	9.1
	434194	AF119847	Hs.283940	Homo sapiens PRO1550 mRNA, partial cds	9.1
	447033	AI357412	Hs.157601	ESTs	9.0
45	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	9.0
	428593	AW207440	Hs.185973	degenerative spermatocyte (homolog Dros	9.0
	430223	NM_002514	Hs.235935	nephroblastoma overexpressed gene	9.0
	444984	H15474	Hs.132898	fatty acid desaturase 1	9.0
	445674	BE410347	Hs.13063	transcription factor CA150	9.0
50	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	9.0
	419852	AW503756	Hs.286184	hypothetical protein dJ551D2.5	9.0
	440349	AA884196	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone TH	9.0
	432161	AK000400	Hs.292807	ESTs, Weakly similar to envelope H1sapi	9.0
	405523			C8001409*:glj7441226 pir S31212 collage	9.0
55	416652	T25853	Hs.7538	ESTs	9.0
	422763	AA033639	Hs.83938	ESTs, Moderately similar to MAS2_HUMAN M	9.0
	446183	AA354991	Hs.14222	Homo sapiens mRNA; cDNA DKFZp761P019 (fr	9.0
	432897	AF155099	Hs.279780	NY-REN-18 antigen	9.0
	448988	Y09783	Hs.22785	gamma-aminobutyric acid (GABA) A recepto	8.9
60	448523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	8.9
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.9
	413554	AA319146	Hs.76426	secretogranin II (chromogranin C)	8.9
	414917	C04863	Hs.47191	ESTs	8.9
	434539	AW748078	Hs.214410	ESTs, Weakly similar to MUC2_HUMAN MUCIN	8.9
65	441805	AA285136	Hs.301914	neuronal specific transcription factor D	8.9
	412530	AA768268	Hs.265273	hypothetical protein FLJ13346	8.9
	424683	N87519	Hs.27196	ESTs	8.9
	426168	NM_001982	Hs.189087	v-erb-b2 avian erythroblastic leukemia v	8.9
	413132	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalyti	8.9
70	425490	NM_001821	Hs.170087	aryl hydrocarbon receptor	8.9
	445896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	8.9
	441079	AW150697	Hs.107418	ESTs	8.9
	437231	BE303000	Hs.288929	hypothetical protein FLJ13258 similar to	8.9
	431316	AA502683	Hs.145037	ESTs	8.9
75	403137			NM_005381*:Homo sapiens nucleolin (NCL),	8.9
	433628	AI821784	Hs.188578	ESTs	8.9
	418489	U76421	Hs.85302	adenosine deaminase, RNA-specific, B1 (h	8.9
	453344	BE349075	Hs.44571	ESTs	8.9
	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	8.9
80	417173	U61397	Hs.81424	ubiquitin-like 1 (senrin)	8.9
	408161	AW852912	Hs.300383	hypothetical protein MGC3032	8.9
	420495	AI338247	Hs.98314	Homo sapiens mRNA; cDNA DKFZp586L0120 (f	8.9
	433213	AW665130	Hs.137190	ESTs	8.9
	451573	AW130351	Hs.243549	ESTs	8.9
	408393	AW015318	Hs.23165	ESTs	8.8
	434725	AK000796	Hs.4104	hypothetical protein	8.8
	418876	AA740616		gb:ny9711.s1 NCLCGAP_GCB1 Homo sapiens	8.8

	444558	AW181975	Hs.165892	ESTs	8.8
	417365	D13168	Hs.82002	endothelin receptor type B	8.8
	424084	AI940676	Hs.20914	hypothetical protein FLJ23056	8.8
5	431706	AI816086	Hs.296341	adenylyl cyclase-associated protein 2	8.8
	424956	AW198103	Hs.158154	ESTs, Weakly similar to granule cell mar	8.8
	441866	BE464341	Hs.21201	nectin 3; DKFZP566B0846 protein	8.8
	444647	H14718	Hs.11506	Human clone 23589 mRNA sequence	8.8
	444858	AI199738	Hs.208275	ESTs, Weakly similar to ALUA_HUMAN !!!!	8.8
10	409643	AW450866	Hs.257359	ESTs	8.8
	428847	AA830050	Hs.124344	ESTs	8.8
	412330	NM_005100	Hs.788	A kinase (PRKA) anchor protein (gravin)	8.8
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	8.8
	425465	L18964	Hs.1904	protein kinase C, iota	8.8
15	424113	AJ743880	Hs.12876	ESTs	8.8
	459324	AW080953		gbxc28c12x1 NCI_CGAP_Co18 Homo sapiens	8.8
	451684	AF216751	Hs.26813	CDA14	8.8
	451244	AW008799	Hs.267448	hypothetical protein FLJ20039	8.8
	439170	AA332365	Hs.165539	ESTs, Weakly similar to I38022 hypotheti	8.8
20	424238	AA337401	Hs.137635	ESTs	8.8
	449686	AW072813	Hs.270868	ESTs, Moderately similar to ALUA_HUMAN A	8.8
	440658	H29142	Hs.143032	ESTs, Weakly similar to neuronal thread	8.8
	410870	U81599	Hs.66731	homeo box B13	8.8
	458229	AI929802	Hs.177	phosphatidylinositol glycan, class H	8.8
25	429831	AA584489	Hs.137526	ESTs	8.8
	453468	W00712	Hs.32980	DKFZP566F084 protein	8.8
	428340	AF261088	Hs.154721	aconitase 1, soluble	8.8
	453345	AA302862	Hs.90063	neurocalcin delta	8.8
	452208	AW340281	Hs.33074	Homo sapiens, clone IMAGE:3606518, mRNA,	8.8
30	440486	BE243513	Hs.7212	hypothetical protein PP1044	8.7
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	8.7
	408949	AF189011	Hs.49163	putative ribonuclease III	8.7
	424668	D83702	Hs.151573	cryptochrome 1 (photolyase-like)	8.7
	412719	AW016610	Hs.129911	ESTs	8.7
35	423872	AB020316	Hs.134015	uronyl 2-sulfotransferase	8.7
	408242	AA251694	Hs.43913	PIBF1 gene product	8.7
	430848	AW021726		gbcd27e02.y1 Morton Fetal Cochlea Homo	8.7
	421492	BE176990	Hs.104916	hypothetical protein FLJ21940	8.7
	449893	T97999	Hs.18214	ESTs, Weakly similar to B34087 hypotheti	8.7
40	410442	X73424	Hs.63768	propionyl Coenzyme A carboxylase, beta p	8.7
	425913	AA365799	Hs.50765	SEC22, vesicle trafficking protein [S. c	8.7
	425704	U79293	Hs.158264	Human clone 23948 mRNA sequence	8.7
	427723	AI355260	Hs.279789	histone deacetylase 3	8.7
	441683	BE564214	Hs.102946	ESTs	8.7
45	447335	BE617695	Hs.286192	hypothetical protein FLJ20940	8.7
	428259	AA424793	Hs.24144	ESTs	8.7
	433104	AL043002	Hs.128246	ESTs, Moderately similar to unnamed prot	8.7
	420041	AB005142	Hs.94592	Motho	8.7
	432432	AA541323	Hs.115831	ESTs	8.7
50	452335	AW188944	Hs.61272	ESTs	8.7
	412673	AL042957	Hs.31845	ESTs	8.7
	430335	D80007	Hs.239499	KIAA0185 protein	8.7
	419904	AA974411	Hs.18672	ESTs	8.6
	442402	NM_000954	Hs.8272	prostaglandin D2 synthase (21kD, brain)	8.6
55	433759	AA680003	Hs.108363	Homo sapiens cDNA: FLJ23603 fis, clone L	8.6
	434064	AL049045	Hs.180758	hypothetical protein PRO0082	8.6
	401785			NM_002276: Homo sapiens keratin 15 (KRT1	8.6
	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	8.6
	419647	AA348947	Hs.91816	hypothetical protein	8.6
60	425907	AA365752	Hs.155965	ESTs	8.6
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	8.6
	424434	H87028	Hs.146861	hypothetical protein FLJ20580	8.6
	400303	AA242758	Hs.79138	LIV-1 protein, estrogen regulated	8.6
	414680	AA743331	Hs.272572	hemoglobin, alpha 2	8.6
65	413992	W26276	Hs.136075	RNA, U2 small nuclear	8.6
	415071	AK002197	Hs.284270	Homo sapiens cDNA FLJ11335 fis, clone PL	8.6
	451230	BE546208	Hs.26090	hypothetical protein FLJ20272	8.6
	441790	AW294909	Hs.132208	ESTs	8.6
	441124	T97717	Hs.119553	ESTs	8.6
70	438160	AA779332	Hs.122671	ESTs	8.6
	433264	D85782	Hs.3229	cysteine dioxygenase, type I	8.6
	434951	AA808164	Hs.116502	ESTs	8.6
	420808	BE548277	Hs.103104	ESTs	8.6
	426535	AI077012	Hs.288582	ESTs, Weakly similar to ubiquitous TPR m	8.6
75	411667	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	8.5
	454058	AI273419	Hs.135148	hypothetical protein FLJ13984	8.5
	436614	R09718	Hs.20403	ESTs	8.5
	446585	T57448	Hs.15467	hypothetical protein FLJ20725	8.5
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	8.5
80	447894	AW204253	Hs.21912	ESTs	8.5
	452682	AA456193	Hs.9071	progesterone membrane binding protein	8.5
	418372	AA311833	Hs.84318	replication protein A1 (70kD)	8.5
	447231	AK001293	Hs.330208	crystallin, zeta (quinone reductase)-lik	8.5
	416208	AW206248	Hs.111092	hypothetical protein FLJ22332	8.5

5	434747	AA837085	Hs.220685	ESTs	8.5
	415938	BE383507	Hs.78921	A kinase (PKA) anchor protein 1	8.5
	450813	AI739625	Hs.203376	ESTs	8.5
	413956	AI821351	Hs.193133	ESTs, Weakly similar to ALU7_HUMAN ALU S	8.5
	408699	AA056614	Hs.106200	ESTs, Moderately similar to ZN91_HUMAN Z	8.5
	440840	AW629666	Hs.283713	ESTs, Weakly similar to S64054 hypothetical	8.5
	407891	AA486620	Hs.41135	endomucin-2	8.5
10	411019	AW993097	Hs.48617	Homo sapiens cDNA FLJ12540 fis, clone NT	8.5
	432620	AA777749	Hs.5978	LM domain only 7	8.5
	424511	BE300512	Hs.193557	ESTs, Moderately similar to ALU7_HUMAN A	8.5
	408170	AW204516	Hs.31835	ESTs	8.5
	452670	AF068227	Hs.30213	ceroid-lipofuscinosis, neuronal 5	8.5
	450516	AA902656	Hs.21943	NIF3 (Ngg1 interacting factor 3, S.pombe	8.5
15	417560	U73338	Hs.82283	5-methyltetrahydrofolate-homocysteine me	8.5
	430606	BE268026	Hs.31476	Homo sapiens cDNA FLJ13872 fis, clone TH	8.4
	436953	AW959074	Hs.23648	Homo sapiens cDNA FLJ13097 fis, clone NT	8.4
	418120	AA213437	Hs.192249	ESTs	8.4
	419436	AA991639	Hs.242413	hypothetical protein DKFZp434K1421	8.4
20	432600	AI821085		gb:ns95a12.y5 NCI_CGAP_Pc3 Homo sapiens	8.4
	448474	AI792014	Hs.13809	hypothetical protein FLJ10648	8.4
	434384	AA631910	Hs.162849	ESTs	8.4
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypotheti	8.4
	411562	AL050201	Hs.70769	hypothetical protein DKFZp586E1923	8.4
25	421622	AB037748	Hs.106204	KIAA1327 protein	8.4
	431160	AW971174	Hs.324330	ESTs	8.4
	449567	AI990790	Hs.188514	ESTs	8.4
	411088	BE247593	Hs.145053	ESTs	8.4
	452186	AA120761	Hs.28307	WW domain binding protein 4 (formin bind	8.3
30	437872	AK002015	Hs.5887	RNA binding motif protein 7	8.3
	429393	AA383024	Hs.201603	Homo sapiens mRNA; cDNA DKFZp434D0917 (f	8.3
	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	8.3
	438440	AA807228	Hs.225161	ESTs	8.3
	431952	AL049385	Hs.272251	Homo sapiens mRNA; cDNA DKFZp586M1418 (f	8.3
35	422295	AF051151	Hs.114408	tol-like receptor 5	8.3
	440145	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fis, clone K	8.3
	425242	D13635	Hs.155287	KIAA0010 gene product	8.3
	432769	AA620814	Hs.144959	ESTs	8.3
	433515	AA732982	Hs.269607	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.3
40	427229	AI799751	Hs.5635	ESTs	8.3
	446947	AF146747	Hs.232165	polycythemia rubra vera 1; cell surface	8.3
	403149			NM_001450:Homo sapiens four and a half L	8.3
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	8.3
	421991	NM_014918	Hs.110488	KIAA0990 protein	8.3
45	436476	AA326108	Hs.33829	bHLH protein DEC2	8.3
	434980	AW770553	Hs.14553	sterol O-acyltransferase (acyl-Coenzyme	8.3
	407385	AA510150	Hs.272072	ESTs, Weakly similar to I38022 hypotheti	8.3
	453121	AI968264	Hs.232286	ESTs	8.3
	420630	AL133101	Hs.99508	Homo sapiens mRNA; cDNA DKFZp434C0921 (f	8.3
50	426101	AL049987	Hs.186381	Homo sapiens mRNA; cDNA DKFZp564F112 (f	8.2
	419517	AF052107	Hs.90797	Homo sapiens clone 23620 mRNA sequence	8.2
	425707	AF115402	Hs.11713	E74-like factor 5 (els domain transcript	8.2
	440080	AW051597	Hs.143707	ESTs	8.2
	422049	W25760	Hs.77631	glycine cleavage system protein H (amino	8.2
55	430154	AW583058	Hs.234726	serine (or cysteine) proteinase inhibitor	8.2
	432695	D83480	Hs.278634	KIAA0146 protein	8.2
	407300	AA102616		gb:zn43e07.s1 Stralagene HeLa cell s3 S9	8.2
	408964	AF201468	Hs.49349	beta-site APP-cleaving enzyme	8.2
	418051	AW192535	Hs.19479	ESTs	8.2
60	412125	Y17114	Hs.73393	eyes absent (Drosophila) homolog 4	8.2
	441523	AW514263	Hs.301771	ESTs, Weakly similar to ALU7_HUMAN IIII	8.2
	417958	AA767382	Hs.193417	ESTs	8.2
	452040	AW973242	Hs.283690	ESTs, Weakly similar to I38022 hypotheti	8.2
	430468	NM_004673	Hs.241519	angiotensin-like 1	8.2
65	407802	D84145	Hs.39913	novel RGD-containing protein	8.2
	420556	AA278300	Hs.124292	Homo sapiens cDNA: FLJ23123 fis, clone L	8.2
	414138	AA135884	Hs.3772	ESTs	8.2
	438209	AL120659	Hs.6111	aryl-hydrocarbon receptor nuclear transi	8.2
	408267	AW380525	Hs.32675	tubulin-specific chaperone e	8.2
70	429692	N48422	Hs.9977	ESTs, Weakly similar to B34087 hypotheti	8.2
	408108	AI580492	Hs.42743	hypothetical protein	8.2
	408418	AW963897	Hs.44743	KIAA1435 protein	8.2
	430334	AI824719	Hs.328700	ESTs	8.2
75	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	8.2

TABLE 59B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accessions
409385	112523_1	AA071267 T65940 T64515 AA071334

	409752	115301_1	AW963990 AA078196 AW749462 AA077468 BE151571 AA376917
	411479	1247077_1	AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905
5	411667	1253334_1	BE160198 AW935898 T11520 AW935930 AW858073 AW861034
	416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE161005 AA190449 AW513465 BE161006 BE162499
	418866	179788_1	T66754 AA229857 AA229658
	418876	179960_1	AA740616 AA654854 AA229923
	419536	185688_1	AA603305 AA244095 AA244183
10	419544	185760_2	AI909154 AA526337 AA244193 AI909153
	423800	232161_1	AA331166 AA331157 AA331155
	426413	256650_1	AA377823 AW954494 AI022688
	429163	300543_1	AA884766 AW974271 AA592975 AA447312
	430848	324821_1	AW021726 AA487752 AA488085
	431121	328275_1	AW971157 AA492575 AA492520
15	432189	342819_1	AA527941 AI810608 AI620190 AA635266
	432600	350959_1	AI821085 AW973464 AA554802 AI821831 AA657438 AA640756 AA650339
	434415	385931_1	BE177494 AW276909 AA632849
	434579	38916_1	T55958 T57205 AF147346
	439518	47334_1	W76326 AF086341 W72300
20	443161	581305_1	AI038316 AI344631 AI261653
	447974	745643_1	R76886 AA63674 R77049

TABLE 59C

25	Pkey:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
30	Nt_position:	Indicates nucleotide positions of predicted exons.		
	Pkey	Ref	Strand	Nt_position
	400860	9757499	Minus	151830-162104,152649-152744
35	400880	9931121	Plus	29235-29336,36353-36580
	401197	9719705	Plus	176341-176452
	401424	8176894	Plus	24223-24428
	401519	6649315	Plus	157315-157950
	401558	7139678	Plus	103510-104090
40	401747	9789672	Minus	118586-118816,119119-119244,119609-119761,120422-120980,130161-130381,130468-130593,131097-131258,131866-131932,132451-132575,133580-134011
	401785	7249190	Minus	165776-165996,166169-166314,166408-166569,167112-167268,167387-167469,168634-168942
	402076	8117410	Plus	128316-128627
	402812	6010110	Plus	25026-25091,25844-25920
	402855	9662953	Minus	59763-59908
45	403047	3540153	Minus	59793-59968
	403137	9211494	Minus	92349-92572,92958-93084,93579-93712,93949-94072,94591-94748,95214-95337
	403149	9799833	Plus	25034-25185
	403362	8571772	Plus	64099-64260
	404210	5006246	Plus	168926-170121
50	404571	7249169	Minus	112450-112648
	404641	9788810	Minus	32247-32362
	404642	9796810	Plus	102999-103145
	405523	9454643	Plus	114550-114688,117265-117407,119490-119599,123237-123395,131140-131217

55	Table 60A lists about 1166 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" prostate cancer level was set to the 75 th percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 85 th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10 th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.			
60	TABLE 60A: ABOUT 1166 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES			

TABLE 60A: ABOUT 1166 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES					
65	Pkey:	Unique Eos probeset identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
70	R1:	Ratio of prostate tumor to normal adult body tissue			
	Pkey	ExAccn	Unigene ID	Unigene Title	R1
75	426747	AA535210	Hs.171995	kalikrein 3, (prostate specific antigen	56.6
	419526	AI821895	Hs.193481	ESTs	56.2
	420154	AI093165	Hs.95420	JM27 protein	44.0
	432441	AW292425	Hs.163484	ESTs	41.9
	414569	AF109298	Hs.118258	prostate cancer associated protein 1	39.9
	431616	AA508552	Hs.195839	ESTs, Weakly similar to I39022 hypotheti	37.9
80	400299	X07730	Hs.171995	kalikrein 3, (prostate specific antigen	36.0
	446057	AI420227	Hs.149358	ESTs, Weakly similar to A45010 X-linked	32.9
	425075	AA506324	Hs.1852	acid phosphatase, prostate	31.1
	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	30.0
	439176	AI446444	Hs.190394	ESTs, Weakly similar to B28096 linc-1 pr	29.8

	400302	N48056		folate hydrolase (prostate-specific memb	28.9
	431579	AW971082	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	27.9
	432101	A1918950	Hs.123642	EphA3	26.3
5	408369	R38438	Hs.182575	solute carrier family 15 (H7?? transport	26.2
	453096	AW294631	Hs.11325	ESTs	25.7
	400287	S39329	Hs.181350	kallikrein 2, prostatic	25.5
	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	24.6
	428819	AL135623	Hs.193914	KIAA0575 gene product	24.5
10	401424			NM_001172:Homo sapiens arginase, type II	24.5
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	22.4
	400292	AA250737	Hs.72472	BMP-R1B	22.3
	407202	N58172	Hs.109370	ESTs	22.3
	415989	AI267700		ESTs	20.2
15	407709	AA456135	Hs.23023	ESTs	20.0
	407168	R45175	Hs.117183	ESTs	19.6
	433444	AW975324	Hs.129816	ESTs	19.4
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	19.1
	428335	AA503115	Hs.183752	microsomal protein, beta-	18.7
20	410829	H47233	Hs.30643	ESTs	18.0
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	17.9
	418561	AW967646	Hs.23023	ESTs	17.7
	452792	AB037765	Hs.30652	KIAA1344 protein	17.5
	403047			NM_005656*:Homo sapiens transmembrane pr	17.3
25	433466	AA508353	Hs.105314	relaxin 1 (H1)	17.3
	418396	AI765805	Hs.26691	ESTs	17.1
	433647	AA603357	Hs.222294	ESTs	16.9
	432240	AI694767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL	16.7
	430487	D87742	Hs.241552	KIAA0268 protein	16.5
30	440260	AI972867	Hs.7130	copine IV	16.0
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	15.7
	425220	AW207206		ESTs	15.7
	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypothe	15.3
	418819	AA228776	Hs.191721	ESTs	14.8
35	421513	X00949	Hs.105314	relaxin 1 (H1)	14.8
	429918	AW873986	Hs.119383	ESTs	14.5
	420092	AA814043	Hs.88045	ESTs	14.5
	432473	AI202703	Hs.152414	ESTs	14.4
	450693	AW460461	Hs.203965	ESTs	14.4
40	431548	AI834273	Hs.9711	novel protein	14.4
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypothe	14.3
	430187	AI799909	Hs.158969	ESTs	14.3
	441690	R81733	Hs.33106	ESTs	14.3
	408621	AI970672	Hs.46638	chromosome 11 open reading frame 8	14.2
45	448899	AF179274	Hs.22791	transmembrane protein with EGF-like and	13.7
	450642	R39773	Hs.7130	copine IV	13.5
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	13.4
	432886	AA650114	Hs.325198	ESTs	13.4
	410330	AW023630	Hs.158425	ESTs	13.4
50	434666	AF151103	Hs.112259	T cell receptor gamma locus	13.1
	400297	AI127076	Hs.308201	hypothetical protein DKFZp56401278	13.0
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	12.8
	431474	AL133990	Hs.190642	ESTs	12.6
	418829	AA518531	Hs.55899	NK homeobox (Drosophila), family 3, A	12.5
55	453861	AK026838	Hs.30120	ESTs, Weakly similar to NUCL_HUMAN NUCLE	12.5
	434217	AW014795	Hs.23349	ESTs	12.3
	418432	M14156	Hs.65112	insulin-like growth factor 1 (somatomedi	12.3
	428398	AI249388	Hs.98558	ESTs	12.2
	421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	12.2
60	447313	U92981	Hs.18081	Homo sapiens clone D11P1B6 mRNA, CAG rep	12.2
	443960	AI093577	Hs.255416	hypothetical protein FLJ21986	12.1
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	12.1
	438032	AA150797	Hs.109276	relaxin protein	12.0
	432527	AW975028	Hs.102754	ESTs	12.0
65	434792	AA649253	Hs.132458	ESTs	12.0
	420424	AB033036	Hs.97594	KIAA1210 protein	11.9
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	11.9
	424846	AU077324	Hs.1832	neuropeptide Y	11.9
	448519	AW176665	Hs.278695	Homo sapiens protein mRNA, complete cds	11.9
70	418339	AA699902	Hs.104215	ESTs, Moderately similar to SPCN_HUMAN S	11.8
	432600	AI821085		gb:ns95a12y5 NCL_CGAP_P13 Homo sapiens	11.8
	413597	AW302885	Hs.117183	ESTs	11.8
	446100	AW967109	Hs.13804	hypothetical protein dJ462023.2	11.7
	431448	AL137517	Hs.306201	hypothetical protein DKFZp56401278	11.6
75	424701	NM_003923	Hs.151988	mitogen-activated protein kinase kinase	11.6
	432435	BE218866	Hs.282070	ESTs	11.5
	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	11.5
	410467	AF102546	Hs.83931	dachshund (Drosophila) homolog	11.5
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypothe	11.5
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	11.5
80	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	11.1
	417332	AW972717	Hs.288462	hypothetical protein FLJ21511	11.0
	407021	U52077		gb:Human mariner1 transposase gene, comp	11.0
	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HE	10.8

	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	10.6
	400301	X03635	Hs.1657	estrogen receptor 1	10.5
	419536	AA503305		gb:np12d11.s1 NCL_CGAP_Pr3 Homo sapiens	10.5
5	445472	AB006631	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	10.5
	415539	AI733881	Hs.72472	BMP-R1B	10.4
	419264	AA877104	Hs.293672	ESTs, Weakly similar to ALUB_HUMAN IIII	10.4
	424432	AB037821	Hs.146858	protocadherin 10	10.3
	439518	W76326		gb:zd80d04.r1 Soares_fetal_heart_AbHH19W	10.3
10	434036	AI659131	Hs.197733	hypothetical protein MGC2849	10.3
	415283	AA948033	Hs.130853	ESTs	10.2
	431217	NM_013427	Hs.250830	Rho GTPase activating protein 6	10.2
	444805	AB007899	Hs.12017	homolog of yeast ubiquitin-protein ligase	10.1
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	10.1
15	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	10.0
	418293	AI224483	Hs.16063	hypothetical protein FLJ21877	10.0
	432244	AI669973	Hs.200574	ESTs	10.0
	451640	AA195601	Hs.26771	Human DNA sequence from clone T47H23 on	9.9
	450164	AI239923	Hs.63931	ESTs	9.8
20	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	9.8
	415079	R43179	Hs.22895	hypothetical protein FLJ23548	9.7
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	9.6
	433234	AB040928	Hs.65366	KIAA1495 protein	9.5
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	9.5
25	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	9.5
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	9.4
	433927	AI557019	Hs.116467	small nuclear protein PRAC	9.4
	444670	H58373	Hs.332938	hypothetical protein MGC5370	9.4
	449625	NM_014253		odc (odd Oz/en-m, Drosophila) homolog 1	9.4
30	450325	AI935962	Hs.26289	ESTs	9.4
	427761	AA412205	Hs.140996	ESTs	9.4
	453930	AA419466	Hs.36727	hypothetical protein FLJ10903	9.4
	416785	AI497778	Hs.20509	HBV pX associated protein-8	9.3
	422805	AA436989	Hs.121017	H2A histone family, member A	9.3
35	418848	AI820961	Hs.193455	ESTs	9.2
	408430	S79876	Hs.44926	dipeptidylpeptidase IV (CD26, adenosine	9.2
	415788	AW528686	Hs.78851	KIAA0217 protein	9.2
	404641			NM_021955: Homo sapiens phosphoglucomuta	9.1
	432437	W07088	Hs.293685	ESTs	9.1
40	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	9.1
	436962	AW377314	Hs.5364	DKFZP564I052 protein	9.1
	410765	AI694972	Hs.66180	nucleosome assembly protein 1-like 2	9.0
	426342	AI739168		Homo sapiens cDNA FLJ13456 fis, clone PL	9.0
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	9.0
45	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	8.8
	442082	R41823	Hs.7413	ESTs	8.8
	436671	AW137159	Hs.146151	ESTs	8.7
	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	8.7
	440774	AI420611	Hs.153934	ESTs	8.7
50	420120	ALD49610	Hs.95243	transcription elongation factor A (SII)-	8.7
	427138	N77624	Hs.173717	phosphatidic acid phosphatase type 2B	8.7
	430722	AW958543	Hs.203270	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.6
	422487	AJ010901	Hs.198267	mucin 4, tracheobronchial	8.6
	443646	AI086198	Hs.164226	ESTs	8.6
55	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	8.5
	428728	NM_016625	Hs.191381	hypothetical protein	8.5
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	8.5
	437162	AW005605	Hs.5454	thyroid hormone receptor coactivating pr	8.5
	437866	AA156781		metallothionein 1E (functional)	8.5
60	453006	AI362575	Hs.303171	ESTs	8.4
	418723	AA504428	Hs.10487	Homo sapiens, clone IMAGE:3954132, mRNA,	8.3
	421040	AA715026	Hs.135280	ESTs	8.3
	414212	AA136569	Hs.10848	KIAA0187 gene product	8.3
65	417916	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic aci	8.2
	440749	W22335	Hs.7392	hypothetical protein MGC3199	8.2
	412715	NM_000947	Hs.74519	primase, polypeptide 2A (SBKID)	8.2
	426829	R14050	Hs.194051	Homo sapiens mRNA; cDNA DKFZp566B213 (fr	8.2
	447156	AW274731	Hs.157520	ESTs	8.1
	426330	L22624	Hs.2256	matrix metalloproteinase 7 (matrilysin,	8.1
70	417412	X16896	Hs.82112	interleukin 1 receptor, type I	8.0
	424592	AA429834	Hs.151781	KIAA0092 gene product	8.0
	435981	H74319	Hs.188620	ESTs	7.9
	442081	AA401863	Hs.22380	ESTs	7.9
	434988	AI418055	Hs.161160	ESTs	7.9
75	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	7.8
	420345	AW295230	Hs.25231	ESTs	7.8
	412324	AW978439	Hs.69504	ESTs	7.8
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	7.8
	408374	AW025430	Hs.155591	forkhead box F1	7.8
80	435604	AA625279	Hs.26892	uncharacterized bone marrow protein BM04	7.8
	453180	AI263307	Hs.239884	H2B histone family, member L	7.8
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp566J1922 (f	7.7
	416182	NM_004354	Hs.79069	cyclin G2	7.7
	452110	T47667	Hs.28005	Homo sapiens cDNA FLJ11309 fis, clone PL	7.6

	451099	R52795	Hs.25954	interleukin 13 receptor, alpha 2	7.6
	427003	U19487	Hs.2090	prostaglandin E receptor 2 (subtype EP2)	7.5
	443180	R15875	Hs.258576	claudin 12	7.5
5	454119	BE549773	Hs.40510	uncoupling protein 4	7.5
	418693	AI750878	Hs.87409	thrombospondin 1	7.5
	426581	AB040956	Hs.135890	KIAA1523 protein	7.5
	417683	AW566008	Hs.239154	ankyrin repeat, family A (RFXANK-like),	7.5
	439569	AW602166	Hs.222399	CEGP1 protein	7.4
10	416140	AI918035	Hs.301198	roundabout (axon guidance receptor, Dros	7.4
	451230	BE546208	Hs.26090	hypothetical protein FLJ20272	7.4
	400294	N95795	Hs.278695	Homo sapiens prostein mRNA, complete cds	7.4
	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	7.4
	419743	AW408762	Hs.5957	Homo sapiens clone 24416 mRNA sequence	7.3
15	428600	AW863261	Hs.242413	hypothetical protein DKFZp434K1421	7.3
	410252	AWB21182	Hs.61418	microfibrillar-associated protein 1	7.3
	424649	BE242035	Hs.151461	embryonic ectoderm development	7.3
	428218	AA424266	Hs.123642	EphA3	7.3
	434158	T86534	Hs.14372	ESTs	7.3
20	413249	AF167160	Hs.75251	DEAD/H (Asp-Glu-Ala-Asp/His) box binding	7.3
	430261	AA305127	Hs.237225	hypothetical protein HT023	7.3
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.3
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	7.2
	433556	W56321	Hs.111450	calcium/calmodulin-dependent protein kin	7.2
25	420871	AA702972	Hs.65300	ESTs	7.2
	418278	AI086489	Hs.83937	hypothetical protein	7.1
	456516	BE172704	Hs.222746	KIAA1610 protein	7.1
	417511	AL049176	Hs.82223	chordin-like	7.1
	411667	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	7.1
30	414422	AA147224	Hs.249195	Homo box A13	7.1
	407118	AA156790	Hs.262036	ESTs, Weakly similar to Z223_HUMAN ZINC	7.1
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20) (Drosop	7.0
	418564	AA631143	Hs.278695	Homo sapiens prostein mRNA, complete cds	7.0
	437872	AK002015	Hs.5887	RNA binding motif protein 7	7.0
35	448148	NM_016578	Hs.20509	HBV pX associated protein-8	7.0
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	6.9
	431657	AI345227	Hs.105448	ESTs, Weakly similar to B34087 hypotheti	6.9
	457728	AW974811		gb:EST386916 MAGE resequences, MAGN Homo	6.9
	415910	U20350	Hs.78913	chemokine (C-X3-C) receptor 1	6.9
40	421977	W94197	Hs.110165	ribosomal protein L26 homolog	6.9
	432161	AK000400	Hs.341181	ESTs, Weakly similar to envelope [H.sapi	6.9
	432887	AI926047	Hs.162859	ESTs	6.8
	444931	AV652066	Hs.75113	general transcription factor IIA	6.8
	421823	N40850	Hs.28625	ESTs	6.8
45	426981	AL044675	Hs.173081	KIAA0530 protein	6.8
	425170	AL077315	Hs.154970	transcription factor CP2	6.8
	411479	AW848047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	6.8
	420954	AA282074	Hs.237323	N-acetylglucosamine-phosphate mutase	6.8
	439492	AF086310	Hs.103169	ESTs	6.8
50	449919	AI674685	Hs.200141	ESTs	6.8
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	6.8
	431555	AI815470	Hs.280024	Cdc42 effector protein 3	6.7
	441111	AI806867	Hs.126594	ESTs	6.7
	457498	AI792230	Hs.191737	ESTs	6.7
55	415293	R49462	Hs.106541	ESTs	6.7
	429163	AA894766		gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	6.7
	433908	AW298141	Hs.157975	ESTs	6.7
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	6.7
	431770	BE221880	Hs.268556	5'-3' exonuclease 2	6.7
60	418575	AA225313	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	6.6
	443745	AB038670	Hs.9728	ALEX1 protein	6.6
	427858	AA418000	Hs.98280	potassium intermediate/small conductance	6.6
	447805	AW627932	Hs.302421	gemin4	6.6
	440995	T57773	Hs.10263	ESTs	6.6
65	422173	BE385828	Hs.250519	phorbol-like protein MDS019	6.6
	431992	NM_002742	Hs.2891	protein kinase C, mu	6.6
	437052	AAB51687	Hs.120691	ESTs	6.6
	444030	AW021254	Hs.135055	ESTs	6.6
	416836	D54745	Hs.80247	cholecystatidin	6.6
70	447033	AI367412	Hs.157601	ESTs	6.5
	428927	AA441837	Hs.90250	ESTs	6.5
	432189	AA527941		gb:nh30c04.s1 NCI_CGAP_Pr3 Homo sapiens	6.5
	448779	BE042877	Hs.177135	ESTs	6.4
	430598	AK001764	Hs.247112	hypothetical protein FLJ10502	6.4
75	411630	UA2349	Hs.71119	Putative prostate cancer tumor suppresso	6.4
	432682	AI376400	Hs.159588	ESTs	6.4
	441499	AW298235	Hs.101689	ESTs	6.4
	441676	BE564206	Hs.49889	ESTs	6.4
	421077	AK000061	Hs.101590	hypothetical protein	6.4
80	452784	BE463857	Hs.151258	hypothetical protein FLJ21052	6.4
	452055	AI377431	Hs.141693	hypothetical protein MGC10858	6.4
	431576	M76655	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	6.3
	418994	AA296520	Hs.89546	selectin E (endothelial adhesion molecu	6.3
	452277	AL049013	Hs.28783	KIAA1223 protein	6.3

	412953	Z45794	Hs.238809	ESTs	6.3
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoietin	6.3
	453350	AA862496	Hs.28482	ESTs	6.3
5	418450	R84397	Hs.193651	ESTs, Weakly similar to alternatively sp	6.3
	407829	AA045084	Hs.29725	hypothetical protein FLJ13197	6.3
	425704	U79293	Hs.159264	Human clone Z3948 mRNA sequence	6.3
	433510	AA806822	Hs.112547	ESTs	6.3
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	6.3
10	412977	AA125910	Hs.191461	ESTs	6.3
	441217	AB22183	Hs.213246	ESTs	6.3
	443912	R37257	Hs.184780	ESTs	6.3
	429281	AA830855	Hs.29808	Homo sapiens cDNA: FLJ21122 fs, clone C	6.2
	435021	AA922192	Hs.54709	ESTs	6.2
15	425466	L18964	Hs.1904	protein kinase C, iota	6.2
	418821	AA436002	Hs.183161	ESTs	6.2
	424511	BE300512	Hs.193557	ESTs, Moderately similar to ALU7_HUMAN A	6.2
	448106	AB00470	Hs.171941	ESTs	6.2
	408418	AW963897	Hs.44743	KIAA1435 protein	6.2
20	450728	AW162923	Hs.25363	presenilin 2 (Alzheimer disease 4)	6.2
	427078	AB76062	Hs.111902	ESTs	6.2
	426931	NM_003416	Hs.2076	zinc finger protein 7 (KQX 4, clone HF.1	6.2
	445907	AA004825	Hs.103281	ESTs	6.1
	458509	AA654650	Hs.282908	ESTs	6.1
25	437323	AA371145	Hs.194397	leptin receptor	6.1
	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	6.1
	429302	AB076674	Hs.198899	eukaryotic translation initiation factor	6.1
	412673	AL042957	Hs.31845	ESTs	6.0
	410150	AW382942	Hs.280024	ESTs	6.0
30	421863	AB952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	6.0
	446947	AF146747	Hs.232165	polycythemia rubra vera 1; cell surface	6.0
	408968	AB652236	Hs.49376	hypothetical protein FLJ20844	6.0
	408047	AW961434	Hs.31539	ESTs	6.0
	416601	AA279490	Hs.86368	calmagin	6.0
35	425710	AF030880	Hs.159275	solute carrier family, member 4	6.0
	439820	AL360204	Hs.283853	Homo sapiens mRNA full length insert cDN	6.0
	414905	HA0873	Hs.175971	ESTs	6.0
	450295	AB766732	Hs.210628	ESTs	6.0
	412505	AA974491	Hs.21734	ESTs	6.0
40	428730	AA625947	Hs.25750	ESTs	6.0
	445413	AA151342	Hs.12677	CGI-147 protein	6.0
	451424	AB62028	Hs.302810	Novel human gene mapping to chromosome 20	5.9
	425628	NM_004476	Hs.1915	folate hydrolase (prostate-specific memb	5.9
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	5.9
45	431359	AW993522	Hs.292934	ESTs	5.9
	404632			NM_022490:Homo sapiens hypothetical prot	5.9
	423748	AB149048	Hs.30211	hypothetical protein FLJ22313	5.9
	449118	R67477	Hs.23103	Bel1 (S. cerevisiae) homolog	5.9
	405523			C8001409*gil7441226[pil]S31212 collagen	5.9
50	448807	AB151940	Hs.7549	ESTs	5.8
	404642			NM_021965~Homo sapiens phosphoglucosula	5.8
	452598	AB31594		ESTs, Weakly similar to ALU7_HUMAN ALU S	5.8
	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	5.8
	435047	AA454985	Hs.54973	cadherin-like protein VR20	5.8
55	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fs, clone MA	5.8
	419038	AW134924	Hs.190325	ESTs	5.8
	416913	AW934714		gb:RC1-DT0001-031289-011-e11 DT0001 Homo	5.7
	432432	AA541323	Hs.115831	ESTs	5.7
	435937	AA830893	Hs.119769	ESTs	5.7
60	414628	AA148950	Hs.188836	ESTs	5.7
	432712	AB018247	Hs.288031	sterol-C5-desaturase (fungal ERG3, delta	5.7
	412783	BE276738	Hs.74578	DEAD/H (Asp-Glu-Ala-Asp/His) box polypep	5.7
	408828	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	5.7
	419083	AB79560	Hs.98613	Homo sapiens cDNA FLJ12292 fs, clone MA	5.7
65	420184	AA188408	Hs.95665	hypothetical protein	5.7
	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	5.7
	443250	AB041530	Hs.132107	ESTs	5.7
	443324	R44013	Hs.164225	ESTs	5.7
	448164	R61680	Hs.26904	ESTs, Moderately similar to Z195_HUMAN Z	5.7
70	448172	N75276	Hs.135904	ESTs	5.7
	433332	AB367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	5.6
	453455	AA063553	Hs.221931	ESTs, Weakly similar to JCI087 RNA helic	5.6
	452242	R50956	Hs.159993	glycosyltransferase	5.6
	410141	R07775	Hs.287657	Homo sapiens cDNA: FLJ21291 fs, clone C	5.6
75	418019	R68911	Hs.176275	ESTs	5.6
	450813	AB739625	Hs.203376	ESTs	5.6
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fs, clone C	5.6
	411096	U80034	Hs.68583	mitochondrial intermembrane peptidase	5.6
	451684	AF216751	Hs.26813	CDA14	5.6
80	427674	NM_003528	Hs.2178	H2B histone family, member Q	5.6
	407275	AB384186		gb:qw34h07.x1 NCI_CGAP_U4 Homo sapiens	5.6
	417958	AA767382	Hs.193417	ESTs	5.6
	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	5.6
	435176	AA744875	Hs.189413	ESTs	5.5

	428465	AW970876	Hs.293653	ESTs	5.5
	431316	AA502663	Hs.145037	ESTs	5.5
	434804	AA649530	Hs.348148	gb:ns44f05.s1 NCI_CGAP_Alv1 Homo sapiens	5.5
5	411990	AW963624	Hs.31707	ESTs, Weakly similar to YEW4_YEAST HYPOT	5.5
	416653	AA768553	Hs.193145	metallothionein 1E (functional)	5.5
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	5.5
	432169	Y00971	Hs.2970	phosphoribosyl pyrophosphate synthetase	5.5
	416239	AL038450	Hs.48948	ESTs	5.4
10	421470	R27496	Hs.1378	annexin A3	5.4
	408177	A1241733	Hs.43871	ESTs	5.4
	424084	A1940675	Hs.20914	hypothetical protein FLJ23056	5.4
	414171	AA360328	Hs.865	RAP1A, member of RAS oncogene family	5.4
	448072	AA59306	Hs.24908	ESTs	5.4
	420397	NM_007018	Hs.97437	centrosomal protein 1	5.4
15	429250	H56585	Hs.198308	tryptophan rich basic protein	5.4
	453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocon	5.4
	429165	AW008986	Hs.118258	prostate cancer associated protein 1	5.4
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	5.4
20	428364	AA426565	Hs.311103	ESTs, Moderately similar to ALU1_HUMAN A	5.4
	431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	5.4
	436679	A1127483	Hs.120451	ESTs, Weakly similar to unnamed protein	5.4
	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	5.4
	457211	AW972585	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	5.3
25	412677	AW029608	Hs.17384	ESTs	5.3
	430412	AW341754	Hs.189305	ESTs	5.3
	423250	BE061916	Hs.125849	chromosome 8 open reading frame 2	5.3
	421433	A1829192	Hs.22380	ESTs	5.3
	435572	AW975339	Hs.238828	ESTs, Weakly similar to GAG2_HUMAN RETRO	5.3
30	458571	AV653731	Hs.282829	ESTs, Moderately similar to PC4259 term	5.3
	441054	AA913591	Hs.126480	ESTs	5.3
	431725	X65724	Hs.2839	Norrie disease (pseudoglioma)	5.3
	433409	A1278802	Hs.25661	ESTs	5.3
	441102	AA973905		intermediate filament protein syncollin	5.3
35	453367	A1990741	Hs.252809	ESTs	5.3
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	5.3
	433923	A1823453	Hs.146625	ESTs	5.3
	426503	AA380153		gb:EST93093 Skin tumor 1 Homo sapiens cD	5.2
40	447574	AF162666	Hs.18895	taused-like kinase 1	5.2
	421896	N62293	Hs.45107	ESTs	5.2
	410870	U81599	Hs.66731	homeo box B13	5.2
	420729	AW964897	Hs.290825	ESTs	5.2
	425066	M82882	Hs.154365	ET4-like factor 1 (ets domain transcript	5.2
	429467	NM_004477	Hs.203772	F5HD region gene 1	5.2
45	447816	NM_007233	Hs.274329	TP53 target gene 1	5.2
	446553	AB021179	Hs.15299	HMBA-inducible	5.2
	453308	AW959731	Hs.323099	ESTs	5.2
	452576	AB023177	Hs.29900	KIAA0960 protein	5.2
	421437	AW821252	Hs.104336	hypothetical protein	5.2
50	422295	AF051151	Hs.114408	tol-like receptor 5	5.2
	453942	AW190820	Hs.19928	hypothetical protein SP329	5.2
	400424	AJ276316	Hs.287374	zinc finger protein 304	5.2
	430387	AW372894	Hs.240770	nuclear cap binding protein subunit 2, 2	5.2
	452688	AA889120	Hs.110537	homeo box A10	5.2
55	448944	AB014505	Hs.22599	abrophin-1 Interacting protein 1; activi	5.1
	413991	H44725	Hs.176090	ESTs	5.1
	444454	BE018316	Hs.11183	sorting nexin 2	5.1
	446785	A1797713	Hs.156471	ESTs	5.1
	407300	AA102816	Hs.120769	gb:zn43e07.s1 Stratagene HeLa cell s3 93	5.1
60	432340	AA534222		gb:nj21d02.s1 NCI_CGAP_AA1 Homo sapiens	5.1
	446469	BE094848	Hs.15113	homogentisate 1,2-dioxygenase (homogenti	5.1
	453293	AA362267	Hs.10653	ESTs	5.1
	408920	AL120071	Hs.48998	fibronectin leucine rich transmembrane p	5.1
	409543	AW450856	Hs.257359	ESTs	5.1
65	427723	A1365260	Hs.279789	histone deacetylase 3	5.1
	438157	AW137011	Hs.49576	ESTs	5.1
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	5.1
	432261	AW972983	Hs.232165	polycythemia rubra vera 1; cell surface	5.1
	418051	AW192535	Hs.19479	ESTs	5.1
70	419926	AW900992	Hs.93796	DKFZP586D2223 protein	5.1
	425843	BE313280	Hs.159627	death associated protein 3	5.1
	440594	AW445167	Hs.126036	ESTs	5.1
	452449	AW068558	Hs.20943	ESTs	5.1
	429769	NM_004917	Hs.218368	kallikrein 4 (protease, enamel matrix, p	5.1
75	428898	AB033070	Hs.194408	KIAA1244 protein	5.1
	415339	NM_015166	Hs.78398	KIAA0071 protein	5.1
	450671	A1356957	Hs.43086	ESTs, Weakly similar to A46010 X-linked	5.1
	444484	AK002126	Hs.11280	hypothetical protein FLJ11264	5.0
	433023	AW864793	Hs.87409	thrombospondin 1	5.0
80	433862	D86960	Hs.3610	KIAA0205 gene product	5.0
	451244	AW008796	Hs.343877	hypothetical protein FLJ20039	5.0
	418624	A1734080	Hs.104211	ESTs	5.0
	430291	AV660345	Hs.238126	CGI-49 protein	5.0
	432261	R42216	Hs.12342	Homo sapiens clone 24538 mRNA sequence	5.0

	429922	Z97630	Hs.226117	H1 histone family, member 0	5.0
	420218	AW958037	Hs.286	ribosomal protein L4	5.0
	425242	D13635	Hs.155287	KIAA0010 gene product	5.0
5	427176	AW381569	Hs.40334	ESTs	5.0
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	5.0
	439899	AF086534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	5.0
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	5.0
	450244	AA007534	Hs.125062	ESTs	5.0
10	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	5.0
	434237	AF119908	Hs.235516	hypothetical protein PRO2955	5.0
	416700	AI963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	5.0
	445865	H20899	Hs.13399	Homo sapiens clone 25032 mRNA sequence	4.9
	408331	NM_007240	Hs.44228	dual specificity phosphatase 12	4.9
15	417407	AA923278	Hs.290805	ESTs, Weakly similar to protease [Hsap]	4.9
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	4.9
	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	4.9
	401451			NM_004496*Homo sapiens hepatocyte nucle	4.9
	416434	AW163045	Hs.79334	nuclear factor, interleukin 3 regulated	4.9
20	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	4.9
	442281	N34742	Hs.170065	Homo sapiens cDNA FLJ13492 fis, clone PL	4.9
	420608	BE548277	Hs.103104	ESTs	4.9
	420911	U77413	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) tr	4.9
	424332	AA338919	Hs.101615	ESTs	4.9
25	430523	AW451385	Hs.161954	ESTs	4.9
	449300	AI656959	Hs.346514	ESTs	4.9
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	4.9
	422299	AK00181	Hs.114556	hypothetical protein FLJ20174	4.9
	438321	AA576635	Hs.6153	CGI-48 protein	4.9
30	452744	AI267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	4.9
	418618	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.8
	425174	D87450	Hs.154978	KIAA0261 protein	4.8
	430458	AA479300	Hs.225705	ESTs, Weakly similar to I38022 hypotheti	4.8
	455497	AA112573	Hs.278695	Homo sapiens protein mRNA, complete cds	4.8
35	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	4.8
	449539	W80363	Hs.58446	ESTs	4.8
	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	4.8
	434228	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	4.8
	407385	AA610150	Hs.272072	ESTs, Weakly similar to I38022 hypotheti	4.8
40	420210	AI557257	Hs.44811	ESTs	4.8
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	4.8
	428647	AA830050	Hs.124344	ESTs	4.8
	434015	AA644518	Hs.300876	hypothetical protein FLJ13386	4.8
	441879	AI521936	Hs.107149	novel protein similar to archaeal, yeast	4.8
45	408990	AL022395	Hs.49526	T-box and leucine-rich repeat protein 4	4.8
	416030	HI5261	Hs.21948	ESTs	4.8
	420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	4.8
	428749	U05848	Hs.132390	zinc finger protein 36 (KOX 18)	4.8
	410268	AA318181	Hs.81635	six transmembrane epithelial antigen of	4.7
50	452323	W44355	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	4.7
	443684	AI681307	Hs.55098	ESTs	4.7
	415821	AI648602	Hs.55468	ESTs	4.7
	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	4.7
	424433	H04607	Hs.9218	ESTs	4.7
55	438703	AW880614	Hs.146381	RNA binding motif protein, X chromosome	4.7
	451806	NM_003729	Hs.27076	RNA 3'-terminal phosphatase cyclase	4.7
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	4.7
	434973	AW449285	Hs.313636	EST	4.7
	433560	AI925195	Hs.130891	hypothetical protein MGC4400	4.7
60	431587	NM_016179	Hs.262960	transient receptor potential channel 4	4.7
	452260	AA463208		RAB9, member RAS oncogene family	4.7
	412846	AW961245	Hs.55896	Homo sapiens PAC clone RPS-978E18 from 7	4.7
	418836	AI855499	Hs.161712	ESTs	4.7
	401558			ENSP00000220478*SECRETOGNANIN III.	4.7
65	441647	AA534210	Hs.285280	Homo sapiens cDNA: FLJ22098 fis, clone H	4.7
	443881	R84512	Hs.237146	hypothetical protein FLJ12762	4.7
	417169	R13550	Hs.246773	ESTs	4.7
	423349	AF010258	Hs.127428	homeo box A9	4.7
	458611	AI268407	Hs.211458	OC-specific transmembrane protein	4.7
70	444961	AI783767	Hs.148635	ESTs, Moderately similar to ALU8_HUMAN I	4.6
	416774	AI005169	Hs.28274	Homo sapiens cDNA: FLJ22049 fis, clone H	4.6
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	4.6
	423242	AL039402	Hs.125783	DEME-6 protein	4.6
	452627	AI122843	Hs.184319	ESTs, Weakly similar to KIAA1006 protein	4.6
75	418005	T86358	Hs.193931	ESTs, Weakly similar to I54374 gene NF2	4.6
	403045			NM_005656*Homo sapiens transmembrane pr	4.6
	416602	NM_006159	Hs.79389	nel (chicken)-like 2	4.6
	407426	AF128533		gb:Homo sapiens F-box protein FB13b (FBL	4.6
	426011	AW986086	Hs.58924	ESTs, Weakly similar to JC5594 jerky gen	4.6
80	442138	AA445973	Hs.13303	Homo sapiens cDNA: FLJ21784 fis, clone H	4.6
	446015	T30968	Hs.13531	hypothetical protein FLJ10971	4.6
	452994	AW962597	Hs.31305	KIAA1547 protein	4.6
	446091	AW022192	Hs.200197	ESTs	4.6
	432908	AI861898	Hs.304505	ESTs	4.6

5	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	4.6
	431673	AW971302	Hs.293233	ESTs	4.6
	446183	AA364891	Hs.14222	Homo sapiens mRNA; cDNA DKFZp761P019 (fr	4.6
	452355	N54926	Hs.29202	G protein-coupled receptor 34	4.6
	432093	H28383		gb:yl52c03.r1 Scores breast 3NbHBst Homo	4.6
10	448402	BE244226	Hs.21094	RAB18, member RAS oncogene family	4.6
	409019	AW385412	Hs.9615	myosin regulatory light chain 2, smooth	4.6
	413812	AW188687	Hs.44748	ESTs	4.6
	414343	AL036166	Hs.323378	coated vesicle membrane protein	4.6
	434423	NM_006769	Hs.3844	LM domain only 4	4.5
15	407355	AA846203	Hs.193974	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.5
	421724	AB037832	Hs.107287	KIAA1411 protein	4.5
	412125	Y17114	Hs.73393	eyes absent (Drosophila) homolog 4	4.5
	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	4.5
	446720	AI439136	Hs.140646	ESTs	4.5
20	448664	AI879317	Hs.334691	splicing factor 3a, subunit 1, 120kD	4.5
	415083	AI632683	Hs.27179	Homo sapiens cDNA FLJ12933 fis, clone NT	4.5
	423412	AF109300		prostate cancer associated protein 5	4.5
	433507	AI817336	Hs.191791	ESTs	4.5
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	4.5
25	423782	AI472209	Hs.323117	ESTs	4.5
	456362	AW973003	Hs.175909	hypothetical protein FLJ22995	4.5
	415451	H19415	Hs.268720	ESTs, Moderately similar to ALU1_HUMAN A	4.5
	419745	AF042001	Hs.93005	slug (chicken homolog), zinc finger prot	4.5
	428715	AW283716	Hs.53126	ESTs	4.5
30	429857	AF089897	Hs.294020	topoisomerase-related function protein 4	4.5
	459681	AI547306		ESTs	4.5
	416155	AI807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	4.5
	414272	AI651603	Hs.46988	ESTs	4.5
	424890	BE538356	Hs.151777	eukaryotic translation initiation factor	4.5
35	417350	U50928	Hs.82001	polycystic kidney disease 2 (autosomal d	4.5
	450094	AI174047	Hs.295789	Homo sapiens mRNA; cDNA DKFZp564D1164 (f	4.5
	459324	AW880953		gb:xc28c12.x1 NCI_CGAP_Co18 Homo sapiens	4.5
	429784	M89796	Hs.30	membrane-spanning 4-domains, subfamily A	4.5
	401519			C15000476*:g[12737279]ref[XP_012163.1]	4.5
40	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	4.5
	427484	N32859	Hs.37288	nuclear receptor subfamily 1, group D, m	4.5
	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	4.4
	418958	AW961605	Hs.21145	hypothetical protein RG083M05.2	4.4
	433617	AW022133	Hs.189838	ESTs	4.4
45	429569	AI885345	Hs.26425	ESTs	4.4
	452338	AW506920	Hs.29159	zinc finger protein 75 (D8C6)	4.4
	409190	AU076536	Hs.50984	sarcoma amplified sequence	4.4
	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	4.4
	416547	H62914	Hs.268946	ESTs, Weakly similar to PC4259 ferritin	4.4
50	430320	BE245290	Hs.239218	uncharacterized hypothalamus protein HCD	4.4
	436953	AW959074	Hs.23648	Homo sapiens cDNA FLJ13097 fis, clone NT	4.4
	438497	AA808725	Hs.291712	ESTs, Weakly similar to I38022 hypotheti	4.4
	434384	AA631910	Hs.162849	ESTs	4.4
	444564	AI187677	Hs.143716	ESTs	4.4
55	447500	AI381900	Hs.159212	ESTs	4.4
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	4.4
	408380	AF123050	Hs.44532	dubiquitin	4.4
	448768	AI473827	Hs.31793	ESTs	4.4
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	4.4
60	432810	AA863400		ESTs	4.4
	437812	AI582291	Hs.16846	ESTs, Weakly similar to O4HUD1 debrisocu	4.4
	447247	AW369351	Hs.287965	Homo sapiens cDNA FLJ13090 fis, clone NT	4.4
	434022	R18374	Hs.117956	ESTs	4.4
	422385	AF035537	Hs.115621	REV3 (yeast homolog)-like, catalytic sub	4.4
65	417728	AW138437	Hs.24790	KIAA1573 protein	4.4
	420407	AA814732	Hs.145010	lipopolysaccharide-specific response 5-II	4.4
	425810	AI823627	Hs.31803	ESTs	4.4
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-II	4.3
	448560	AL161983	Hs.21415	Homo sapiens mRNA; cDNA DKFZp761K2024 (f	4.3
70	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	4.3
	417845	AL117461	Hs.82749	Homo sapiens mRNA; cDNA DKFZp586F1822 (f	4.3
	452335	AW188944	Hs.61272	ESTs	4.3
	429718	R25685	Hs.211933	collagen, type XII, alpha 1	4.3
	450316	W84446	Hs.226434	hypothetical protein MGC4643	4.3
75	408527	AL135018	Hs.33074	Homo sapiens, clone IMAGE:3606519, mRNA,	4.3
	419852	AW503756	Hs.286184	hypothetical protein cJ551D2.5	4.3
	424534	D87682	Hs.150275	KIAA0241 protein	4.3
	424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	4.3
	435023	AI692552		gb:wd73f12.x1 NCI_CGAP_Lu24 Homo sapiens	4.3
80	442914	AW188551	Hs.99519	hypothetical protein FLJ14007	4.3
	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	4.3
	421163	AA375974	Hs.32450	ESTs, Weakly similar to T23762 hypotheti	4.3
	420405	AA743396	Hs.189023	ESTs	4.3
	450330	AW500775	Hs.24817	hypothetical protein FLJ20136	4.3
	423998	H29138	Hs.157113	coenzyme Q, 7 (rat, yeast) homolog	4.3
	439764	T26536	Hs.22744	hypothetical protein MGC13105	4.3
	446351	AW444551	Hs.35380	x 001 protein	4.3

5	431583	AL042513	Hs.262476	S-adenosylmethionine decarboxylase 1	4.3
	414312	AA155594	Hs.191060	ESTs	4.3
	438379	N23018	Hs.171391	C-terminal binding protein 2	4.3
	411928	AA888524	Hs.197289	rab3 GTPase-activating protein, non-cata	4.3
	414680	AA743331		hemoglobin, alpha 2	4.3
10	423104	AJ005273	Hs.123647	antigenic determinant of recA protein (m	4.3
	440840	AW629686		ESTs, Weakly similar to S64054 hypotheti	4.3
	449802	AW901804	Hs.23984	hypothetical protein FLJ20147	4.3
	434574	N62448	Hs.293970	methylmalonate-semialdehyde dehydrogenas	4.2
	431429	AF072813		reticulation 3	4.2
15	413492	D87470	Hs.75400	KIAA0280 protein	4.2
	419929	U90268	Hs.93810	cerebral cavernous malformations 1	4.2
	435846	AA700870	Hs.14304	ESTs	4.2
	441623	AW514263	Hs.301771	ESTs, Weakly similar to ALUF_HUMAN IIII	4.2
	450546	AA010200	Hs.175551	ESTs	4.2
20	414222	AL135173	Hs.878	sorbitol dehydrogenase	4.2
	416445	AL043004	Hs.79337	KIAA0135 protein	4.2
	409151	AA306105	Hs.60785	SEC22, vesicle trafficking protein (S. c	4.2
	412707	AW206373	Hs.16443	Homo sapiens cDNA: FLJ21721 fls, clone C	4.2
	442891	BE281238	Hs.8886	hypothetical protein FLJ20424	4.2
25	447439	AA313565	Hs.146020	ESTs, Weakly similar to KIAA1205 protein	4.2
	449685	AW296669	Hs.66095	ESTs	4.2
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.2
	450377	AB033091	Hs.74313	KIAA1285 protein	4.2
	419847	AA348947	Hs.91816	hypothetical protein	4.2
30	442049	AA310393	Hs.190044	ESTs	4.2
	430669	AW989657	Hs.291029	ESTs	4.2
	424181	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	4.1
	443634	H73972	Hs.134460	ESTs	4.1
	426216	N77630	Hs.13895	Homo sapiens cDNA FLJ11654 fls, clone HE	4.1
35	422634	NM_016010	Hs.118821	CGI-62 protein	4.1
	445895	D29954	Hs.13421	KIAA0056 protein	4.1
	447669	AL049985	Hs.19180	Homo sapiens mRNA; cDNA DKFZp564E122 (fr	4.1
	407198	H91679		gbyyv04s07.s1 Soares fetal liver spleen	4.1
	447762	M73700	Hs.105938	lactoferrin	4.1
40	402855			NM_001839*:Homo sapiens calponin 3, acid	4.1
	443161	AI036316		gtxox48c08.x1 Soares fetal liver spleen	4.1
	415827	H17462	Hs.23079	ESTs	4.1
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	4.1
	418365	AW014345	Hs.161690	ESTs	4.1
45	429525	N92540	Hs.205353	ectonucleoside triphosphate diphosphohyd	4.1
	435401	R44477	Hs.10056	hypothetical protein FLJ14621	4.1
	446657	AI335191	Hs.280702	ESTs, Weakly similar to 2109260A B cell	4.1
	421141	AW117261	Hs.125914	ESTs	4.1
	430335	D80007	Hs.239409	KIAA0185 protein	4.1
50	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	4.1
	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	4.1
	443547	AW271273	Hs.23767	hypothetical protein FLJ12666	4.1
	410763	AF279145	Hs.8966	hypothetical protein FLJ21776	4.1
	410592	R94088	Hs.43569	ESTs	4.1
55	423698	AA329798	Hs.1098	DKFZp434J1813 protein	4.1
	426534	AA811845	Hs.106290	Kelch motif containing protein	4.1
	430253	AK001514	Hs.236844	hypothetical protein FLJ10652	4.1
	426211	M18667	Hs.1887	progastricsin (pepsinogen C)	4.0
	443273	AI042063	Hs.132156	ESTs	4.0
60	428055	AA420584	Hs.101760	ESTs	4.0
	425707	AF115402	Hs.11713	E74-like factor 5 (ets domain transcript	4.0
	451294	AI457338	Hs.29894	ESTs	4.0
	430519	AF129534	Hs.49210	F-box only protein 4	4.0
	441766	R53790	Hs.23294	hypothetical protein FLJ14393	4.0
65	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	4.0
	446354	AW449850	Hs.346335	ESTs	4.0
	451468	AW503389	Hs.293663	ESTs, Moderately similar to 138022 hypot	4.0
	409706	BE158773	Hs.213207	ESTs	4.0
	447082	T85314		thioredoxin-like	4.0
70	418594	AI732083	Hs.187619	ESTs	4.0
	426501	AW043782	Hs.293616	ESTs	4.0
	436797	AA731491	Hs.334477	hypothetical protein MGC14879	4.0
	418288	H51299		gbyyv07c06.s1 Soares breast 3Nb13st Homo	4.0
	419865	NM_007020	Hs.93502	U1-snRNP binding protein homolog (70kD)	4.0
75	425920	AL049977	Hs.162209	claudin 8	4.0
	416658	U03272	Hs.79432	fibillin 2 (congenital contractual ara	4.0
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	4.0
	433209	AB040907	Hs.278436	KIAA1474 protein	4.0
	428801	AW227121	Hs.254881	ESTs	4.0
80	419629	AB020695	Hs.91662	KIAA0888 protein	4.0
	451061	AW291487	Hs.213659	ESTs, Weakly similar to KIAA1357 protein	3.9
	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	3.9
	400895			C11002514*gi11280151 p E82756 beta-	3.9
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	3.9
	419985	H66373	Hs.5856	ESTs, Highly similar to bA393J16.3 [Hsa	3.9
	429340	N35938	Hs.199429	Homo sapiens mRNA; cDNA DKFZp434M2216 (f	3.9
	433759	AA680003	Hs.109363	Homo sapiens cDNA: FLJ23603 fls, clone L	3.9

	428862	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	3.9
	413450	Z99716	Hs.75372	N-acetylglucosaminidase, alpha-	3.9
	427615	BE410107	Hs.179817	CGI-82 protein	3.9
5	450649	NM_001429	Hs.25272	E1A binding protein p300	3.9
	445796	NM_012421	Hs.13321	rearranged L-myc fusion sequence	3.9
	416198	H27332	Hs.99598	hypothetical protein MGC5338	3.9
	431147	AI767751	Hs.20300	ESTs	3.9
	439192	AW970536	Hs.105413	ESTs	3.9
10	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	3.9
	451900	AB023199	Hs.27207	KIAA0882 protein	3.9
	420802	U22376	Hs.1334	v-myb avian myeloblastosis viral oncogen	3.9
	425083	AW962712	Hs.126712	ESTs, Weakly similar to AF191020.1 E2G5	3.9
	442320	AI287817	Hs.129636	ESTs	3.9
	447541	AK000288	Hs.18800	hypothetical protein FLJ20281	3.9
15	444636	T96667	Hs.17877	ESTs	3.9
	432103	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), cat	3.9
	412676	AA447718	Hs.107057	ESTs	3.9
	423852	AW877787	Hs.136102	KIAA0853 protein	3.9
20	437916	BE566249	Hs.20899	hypothetical protein FLJ23142	3.9
	442242	AV647908	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	3.9
	447280	BE617907	Hs.97635	ESTs	3.9
	421750	AK000768	Hs.107872	hypothetical protein FLJ20761	3.8
	450580	NA0087		ESTs	3.8
25	432359	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	3.8
	429323	NM_001649	Hs.2391	apical protein, <i>Xenopus laevis</i> -like	3.8
	407332	AI801565	Hs.200113	Homo sapiens cDNA FLJ11379 fis, clone HE	3.8
	426413	AA377823		gb:EST90805 Synovial sarcoma Homo sapien	3.8
	412652	AI801777	Hs.260024	ESTs	3.8
30	426226	AA769045		gb:aa80h07.s1 NC1_CGAP_GCB1 Homo sapiens	3.8
	437816	AI823445	Hs.280698	ESTs	3.8
	444534	AW271828	Hs.42294	ESTs	3.8
	459241	AA032276	Hs.99010	ESTs, Moderately similar to T14342 NSD1	3.8
	408242	AA251594	Hs.43913	PIBF1 gene product	3.8
	443484	AI091458	Hs.134559	ESTs	3.8
35	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	3.8
	428043	T92248	Hs.2240	uteroglobin	3.8
	407192	AA609200		gb:af12e02.s1 Soares_testis_NHT Homo sap	3.8
	421590	AF004716	Hs.105940	jerky (mouse) homolog-like	3.8
40	453020	AL162039	Hs.31422	Homo sapiens mRNA; cDNA DKFZp434M229 (fr	3.8
	437372	AA323968	Hs.283531	hypothetical protein DKFZp547G183	3.8
	432278	AL137508	Hs.274256	hypothetical protein FLJ23563	3.8
	407917	U63139	Hs.41587	RAD50 (S. cerevisiae) homolog	3.8
	408547	AA574291	Hs.57837	ESTs	3.8
45	427636	BE397988	Hs.179962	tumor protein p53-binding protein	3.8
	430968	AW872830		gb:EST384925 MAGE resequences, MAGL Homo	3.8
	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypotheti	3.8
	453696	AA037615	Hs.42746	ESTs	3.8
	408875	NM_015434	Hs.48604	DKFZP434B188 protein	3.8
50	431197	AL036596	Hs.250745	polymerase (RNA) III (DNA directed) (62k	3.8
	434072	H70854	Hs.283069	Homo sapiens PRO1082 mRNA, complete cds	3.8
	438138	R98299	Hs.177602	ESTs	3.8
	447906	AL050062	Hs.19999	DKFZP566K023 protein	3.8
	415992	C05837	Hs.145807	hypothetical protein FLJ13593	3.7
55	435655	AW106863	Hs.6947	HSPC069 protein	3.7
	430607	AW973521	Hs.247324	mitochondrial ribosomal protein S14	3.7
	439398	AA284267	Hs.221504	ESTs	3.7
	448515	H68443	Hs.13528	hypothetical protein FLJ14054	3.7
	445242	BE156478	Hs.21108	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
60	418576	AW968159	Hs.289104	Epithelial calcium channel 2, CaT-like A	3.7
	436024	AI800041	Hs.190555	ESTs	3.7
	407783	AW996872	Hs.172028	a disintegrin and metalloproteinase doma	3.7
	436207	AA334774	Hs.12845	hypothetical protein MGC13159	3.7
	442861	AA243837	Hs.57787	ESTs	3.7
65	448207	AM75490	Hs.170577	ESTs	3.7
	450628	AW382884	Hs.204715	ESTs	3.7
	432506	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	3.7
	438613	C05569	Hs.243122	hypothetical protein FLJ13057 similar to	3.7
	443031	AW134696	Hs.49418	ESTs	3.7
70	447608	AW205042	Hs.18956	Homo sapiens cDNA FLJ20657 fis, clone KA	3.7
	408312	AF263813	Hs.44198	intracellular membrane-associated calci	3.7
	412777	AI335773	Hs.270123	ESTs	3.7
	424602	AK002055	Hs.151048	hypothetical protein FLJ11193	3.7
	424882	AI379481	Hs.153636	far upstream element (FUSE) binding prot	3.7
75	425898	AA366649	Hs.269478	ESTs, Weakly similar to PC4259 ferritin	3.7
	443323	BE560621	Hs.9222	estrogen receptor binding site associate	3.7
	452129	AW291379	Hs.212827	ESTs	3.7
	453927	AA082465	Hs.125031	choline/ethanolaminephosphotransferase	3.7
	432336	NM_002759	Hs.274382	protein kinase, interferon-inducible dou	3.7
80	425988	BE045897	Hs.274454	ESTs, Weakly similar to I38022 hypotheti	3.7
	443123	AA094538	Hs.272808	putative transcription regulation nuclea	3.7
	445467	AI239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.7
	423855	AA331761	Hs.254859	ESTs	3.7
	403790			NM_001334*:Homo sapiens cathepsin O (CTS	3.7

	434470	AA634818	Hs.298138	ESTs	3.7
	452032	BE244005	Hs.27610	retinoic acid- and interferon-inducible	3.7
	420026	AJ831190	Hs.166676	ESTs	3.7
5	421838	AW881089	Hs.108806	Homo sapiens mRNA; cDNA DKFZp566M0947 (f	3.7
	449916	T60525	Hs.299221	pyruvate dehydrogenase kinase, isoenzyme	3.7
	452270	AW975014	Hs.26	femochelataase (protoporphyrin)	3.7
	445941	AJ267371	Hs.172635	ESTs	3.6
	416882	AI633044		tryptophanyl tRNA synthetase 2 (mitochond	3.6
10	412533	AA679863	Hs.69606	ESTs	3.6
	431740	N75450	Hs.183412	ESTs, Moderately similar to AF116721.67	3.6
	442710	AJ015631	Hs.23210	ESTs	3.6
	448212	AI475858		gb:tc87d07.x1 NCL CGAP CLL1 Homo sapiens	3.6
	413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	3.6
15	453038	AW292415	Hs.20509	HBV pX associated protein-B	3.6
	427661	AA410292	Hs.104761	ESTs	3.6
	420923	AF097021	Hs.273321	differentially expressed in hematopoietic	3.6
	414844	AA296874	Hs.77494	deoxyguanosine kinase	3.6
	441866	BE464341	Hs.21201	nectin 3; DKFZP566B0846 protein	3.6
20	406815	AA833930	Hs.288036	IRNA isopentenylpyrophosphate transferase	3.6
	423482	BE280172	Hs.129228	galactokinase 2	3.6
	424677	U09414	Hs.151689	zinc finger protein 137 (clone pHZ-30)	3.6
	430160	AW968210	Hs.293957	ESTs, Weakly similar to ALUC_HUMAN III	3.6
	433672	BE281165	Hs.288038	TLS-associated serine-arginine protein 1	3.6
25	433887	AW204232	Hs.279522	ESTs	3.6
	452670	AF068227	Hs.30213	ceroid-lipofuscinosis, neuronal 5	3.6
	411890	H92738	Hs.75811	N-acylsphingosine amidohydrolase (acid c	3.6
	432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	3.6
	431724	AA514535	Hs.283704	ESTs	3.6
30	435703	AW630133	Hs.83313	GK003 protein	3.6
	445874	BE410347	Hs.13083	transcription factor CA150	3.6
	414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypotheti	3.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (3.6
	432840	AK001403	Hs.279621	hypothetical protein FLJ20530	3.6
35	439726	AW448893	Hs.293707	ESTs, Weakly similar to I38598 zinc fing	3.6
	445704	AI493742	Hs.167700	ESTs, Moderately similar to I38022 hypoth	3.6
	449115	AW959952	Hs.37528	ESTs, Weakly similar to AF090944.1 PRO06	3.6
	439379	AA835002	Hs.125611	ESTs	3.6
	414646	AA353776	Hs.901	CD48 antigen (B-cell membrane protein)	3.6
40	434579	T55858		gbyb35f05.r1 Stratagene fetal spleen (9	3.6
	451367	AA923729	Hs.26322	cell cycle related kinase	3.6
	420285	AA258124	Hs.293878	ESTs, Moderately similar to ZN91_HUMAN Z	3.6
	431253	AW129203	Hs.322915	ESTs	3.6
	431952	Z70696	Hs.272240	Homo sapiens cDNA FLJ11086 fis, clone PL	3.6
45	439092	AA830149		gb:acc44f08.s1 NCL CGAP_GCB1 Homo sapiens	3.6
	411562	AL050201	Hs.70769	hypothetical protein DKFZp586E1923	3.5
	417771	AA804698	Hs.82547	retinoic acid receptor responder (tazaro	3.5
	419440	AB020889	Hs.90419	KIAA0882 protein	3.5
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	3.5
50	419241	AA523939	Hs.165258	ESTs	3.5
	410782	AF228053	Hs.56170	HSKM-B protein	3.5
	413364	NM_000401	Hs.75334	exostoses (multiple) 2	3.5
	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	3.5
	428004	AA449583	Hs.161393	glutamate-cysteine ligase, catalytic sub	3.5
55	420380	AA330047	Hs.191187	ESTs	3.5
	418662	T25853	Hs.7538	ESTs	3.5
	433280	AA581404	Hs.289037	Homo sapiens cDNA FLJ14135 fis, clone MA	3.5
	433285	AW975944	Hs.237396	ESTs	3.5
	421991	NM_014918	Hs.110488	KIAA0980 protein	3.5
60	413950	AA240096	Hs.32783	ESTs	3.5
	431318	AA502700	Hs.293147	ESTs, Moderately similar to A48010 X-fin	3.5
	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	3.5
	411149	N68715	Hs.289128	ESTs	3.5
	417601	NM_014735	Hs.82292	KIAA0215 gene product	3.5
65	418334	AA319233	Hs.5521	ESTs	3.5
	422583	AA410606	Hs.27973	KIAA0874 protein	3.5
	425717	X07282	Hs.171495	retinoic acid receptor, beta	3.5
	425856	AA364908	Hs.88927	hypothetical protein FLJ13993	3.5
	434569	AI311295	Hs.344478	KIAA0196 gene product	3.5
70	419438	AA591639	Hs.242413	hypothetical protein DKFZp434K1421	3.5
	437296	AA350994	Hs.20281	KIAA1700	3.5
	432697	AW975050	Hs.293892	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.5
	439605	AF088431	Hs.22380	ESTs	3.5
	442145	AI022650	Hs.8117	erbB2-interacting protein ERBIN	3.5
75	432589	AL135725	Hs.131708	ESTs	3.5
	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	3.5
	412095	AI824707	Hs.5921	Homo sapiens cDNA: FLJ21592 fis, clone C	3.5
	421129	BE438899	Hs.89271	ESTs	3.5
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	3.5
80	434839	AI743069	Hs.134736	ESTs	3.5
	435166	AL391470	Hs.158818	ESTs	3.5
	448966	AW372914	Hs.86149	phosphoinositide 3-phosphate-binding prot	3.5
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	3.5
	453311	AW104911	Hs.126707	hypothetical protein FLJ11457	3.5

5	456497	AW967966	Hs.123648	ESTs, Weakly similar to AF108460.1 ubl1n	3.5
	413786	AW613780	Hs.13500	ESTs	3.5
	430935	AW072916		zinc finger protein 131 (clone pHZ-10)	3.5
	439904	AW892676		gb:CM3-NN0004-280300-131-c12 NN0004 Homo	3.5
	449909	AA004681	Hs.59432	ESTs	3.5
10	445817	NM_003642	Hs.13340	histone acetyltransferase 1	3.5
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	3.5
	417251	AW015242	Hs.99488	ESTs, Weakly similar to YK64_YEAST HYPOT	3.5
	423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	3.5
	438527	AJ969251	Hs.115325	RAB7, member RAS oncogene family-like 1	3.5
15	453916	AW974874	Hs.75212	ornithine decarboxylase 1	3.5
	430200	BEG13337	Hs.234896	geminin	3.4
	437187	AL080208	Hs.306325	Homo sapiens mRNA; cDNA DKFZp586C1523 (f	3.4
	423645	AI215632	Hs.147487	ESTs	3.4
	432370	AA308334	Hs.274424	N-acetylneuraminic acid phosphate synth	3.4
20	434866	AA657494		gb:nt66004.s1 NCI_CGAP_Pr3 Homo sapiens	3.4
	404571			NM_015902*:Homo sapiens progesterone induce	3.4
	418727	AA227609	Hs.94834	ESTs	3.4
	436374	AA400709	Hs.96716	ESTs, Weakly similar to T17210 hypotheti	3.4
	452721	AJ269629	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.4
25	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-I	3.4
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	3.4
	402031			ENSP00000251056*:Plasma membrane calcium	3.4
	407137	T97307		gb:ye53h05.s1 Soares fetal liver spleen	3.4
	449603	AJ656882	Hs.197698	ESTs	3.4
30	425692	D90041	Hs.155856	N-acetyltransferase 1 (arylamine N-acety	3.4
	436905	AA731533	Hs.270751	ESTs	3.4
	437357	AA749316	Hs.271879	ESTs, Moderately similar to ALU1_HUMAN A	3.4
	407908	BE379758	Hs.110853	uncharacterized hemopoietic stem/proge	3.4
	430144	AJ732722	Hs.187894	ERGL protein; ERGLC-53-like protein	3.4
35	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	3.4
	423800	AA331153		gb:EST35034 Embryo, 6 week, subtracted (3.4
	439375	AA689526	Hs.344249	steroid dehydrogenase homolog	3.4
	429084	AJ001443	Hs.185614	splicing factor 3b, subunit 3, 130kD	3.4
	432886	BE169028	Hs.279704	chromatin accessibility complex 1	3.4
40	408267	AW380626	Hs.343564	tubulin-specific chaperone a	3.4
	408632	AW085690	Hs.63428	ESTs, Weakly similar to Z195_HUMAN ZINC	3.4
	422564	AJ148006	Hs.222120	ESTs	3.4
	424842	AA034127	Hs.153487	signal transducing adaptor molecule (SH3	3.4
	429984	AL050102	Hs.227209	hypothetical protein FLJ21617	3.4
45	435256	AF193766	Hs.13872	cytokine-like protein C17	3.4
	436137	AI056769	Hs.133512	ESTs	3.4
	440348	AW015802	Hs.47023	ESTs	3.4
	442910	AJ365130	Hs.11307	ESTs, Weakly similar to T19326 hypotheti	3.4
	443242	BE243910	Hs.9082	nucleoporin p54	3.4
50	445469	AW288370	Hs.153714	complement-c1q tumor necrosis factor-rel	3.4
	449517	AW500106	Hs.23643	serine/threonine protein kinase MASK	3.4
	425354	U62027	Hs.166936	complement component 3a receptor 1	3.4
	433037	NM_014156	Hs.279938	HSPC067 protein	3.4
	423044	AA320828	Hs.97266	protocadherin 18	3.4
55	434128	W93170	Hs.284164	protein x 0004	3.4
	449845	AW971183	Hs.9683	DnaJ (Hsp40) homolog, subfamily C, membe	3.4
	423590	AW952412	Hs.65874	ESTs, Weakly similar to A40348 Elav/Sex-	3.4
	440370	AA884000	Hs.8173	hypothetical protein FLJ10803	3.4
	438825	BE327427	Hs.79953	ESTs	3.4
60	446874	AW966304	Hs.56156	ESTs	3.4
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	3.4
	419131	AA408293	Hs.41167	ESTs	3.4
	423178	AI033140	Hs.124883	Homo sapiens mRNA; cDNA DKFZp564C142 (fr	3.4
	433764	AW753676	Hs.39982	ESTs	3.4
65	440658	H29142	Hs.143032	ESTs, Weakly similar to neuronal thread	3.4
	411558	AA102570	Hs.70725	gamma-aminobutyric acid (GABA) A recepto	3.3
	452815	AA418841		gb:zw01e11.s1 Soares_NhHMPu_S1 Homo sapit	3.3
	421234	AA907153	Hs.190060	ESTs	3.3
	424075	AI807320	Hs.227630	RE1-silencing transcription factor	3.3
70	412045	AA099802	Hs.83883	transmembrane, prostate androgen induced	3.3
	420041	AB005142	Hs.94592	klotho	3.3
	426174	AA547959	Hs.115838	ESTs	3.3
	427083	NM_006363	Hs.173497	Sec23 (S. cerevisiae) homolog B	3.3
	441021	AW578716	Hs.7644	H1 histone family, member 2	3.3
75	436654	AW197887	Hs.253353	ESTs	3.3
	441124	T97717	Hs.119563	ESTs	3.3
	444169	AV648170	Hs.58756	ESTs	3.3
	421476	AW953805	Hs.21887	ESTs	3.3
	422165	AL041199	Hs.1481	histidine decarboxylase	3.3
80	455100	BE160198		gb:QV1-HT0413-010200-059-h03 HT0413 Homo	3.3
	450747	AI064821	Hs.318535	ESTs, Highly similar to 1818357A EWS gen	3.3
	401197			ENSP00000229263*:HSPC213.	3.3
	433404	T32982	Hs.102720	ESTs	3.3
	422546	AB007969	Hs.301478	KIAA0500 protein	3.3
	443894	N20517	Hs.194397	leptin receptor	3.3
	414341	D80004	Hs.75909	KIAA0182 protein	3.3
	425292	NM_005824	Hs.155545	37 kDa leucine-rich repeat (LRR) protein	3.3

	414407	AA147026	Hs.76704	ESTs	3.3
	420324	AF163474	Hs.96744	prostate androgen-regulated transcript 1	3.3
	423453	AW450737	Hs.128791	CGI-09 protein	3.3
5	444170	AW613879	Hs.102408	ESTs	3.3
	445474	AI240014	Hs.259558	ESTs	3.3
	450682	AI339732		G-rich RNA sequence binding factor 1	3.3
	451246	AW189232	Hs.39140	cutaneous T-cell lymphoma tumor antigen	3.3
	434194	AF119847	Hs.283940	Homo sapiens PRO1550 mRNA, partial cds	3.3
10	444324	AI301330	Hs.143638	ESTs	3.3
	427581	NM_014788	Hs.179703	KIAA0129 gene product	3.3
	429258	AA448765		gb:zx10e09.r1 Soares_total_fetus_Nb2HF8_	3.3
	400880			NM_000611*:Homo sapiens CD59 antigen p18	3.3
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.3
15	451968	H66196	Hs.26409	Homo sapiens mRNA; cDNA DKFZp547K204 (tr	3.3
	411190	AA306342	Hs.69171	protein kinase C-like 2	3.3
	410860	AI061118	Hs.66328	Fanconi anemia, complementation group F	3.3
	420493	AI635113	Hs.270366	ESTs, Weakly similar to I78885 serine/thr	3.3
	423740	Y07701	Hs.293007	aminopeptidase puromycin sensitive	3.3
20	428523	AW974540	Hs.98626	ESTs	3.3
	428743	AI080060	Hs.301549	Homo sapiens mRNA; cDNA DKFZp564H172 (tr	3.3
	432363	AA534489		gb:nf76g11.s1 NCLCGAP_Co3 Homo sapiens	3.3
	435102	AW889053	Hs.76917	F-box only protein 8	3.3
	438147	AW250553		H-2K binding factor-2	3.3
25	445808	AV655234		ESTs, Moderately similar to PC4259 ferri	3.3
	453058	AW612293	Hs.288884	Homo sapiens cDNA FLJ11750 fis, clone HE	3.3
	453286	AA034319	Hs.29041	Homo sapiens cDNA FLJ14177 fis, clone NT	3.3
	453802	AL134767		gb:DKFZp547G109D_r1 547 (synonym: hfor1)	3.3
	422017	NM_003877	Hs.110778	STAT induced STAT inhibitor-2	3.3
30	411373	BE325276	Hs.8861	ESTs	3.3
	435114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	3.3
	443674	AI081330	Hs.145008	ESTs	3.3
	427528	AU077143	Hs.179565	minichromosome maintenance deficient (S.	3.3
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	3.3
35	420969	AI636310	Hs.28310	ESTs	3.3
	421654	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	3.3
	409542	AA503020	Hs.36563	hypothetical protein FLJ22418	3.3
	410119	F07841	Hs.13926	ESTs	3.3
	417379	AA196390		gb:zp99b10.s1 Stratagene muscle 937209 H	3.3
40	423201	NM_000163	Hs.125180	growth hormone receptor	3.3
	442787	W93048	Hs.250723	hypothetical protein MG2747	3.3
	407930	AA045847	Hs.188361	Homo sapiens cDNA FLJ12807 fis, clone NT	3.3
	423427	AL137612	Hs.285848	KIAA1454 protein	3.3
	424903	T26477	Hs.22883	ESTs, Weakly similar to I38022 hypotheti	3.3
45	426776	AA384564		ESTs	3.3
	432378	AI493046	Hs.146133	ESTs	3.3
	438875	AA827640	Hs.189059	ESTs	3.3
	452959	AI933416	Hs.189674	ESTs	3.3
	453124	AI139058	Hs.125790	leucine-rich repeat-containing 2	3.3
50	417560	U73338	Hs.82283	5-methyltetrahydrofolate-homocysteine me	3.2
	433002	AF048730	Hs.279908	cyclin T1	3.2
	430929	AA489166	Hs.156933	ESTs	3.2
	437444	H46008	Hs.31518	ESTs	3.2
	446297	AI346930	Hs.149728	ESTs	3.2
55	407870	AB032990	Hs.40719	hypothetical protein KIAA1164	3.2
	429377	AA813192	Hs.200588	KIAA0547 gene product	3.2
	426030	BE243933	Hs.108642	zinc finger protein 22 (KIX 15)	3.2
	420583	H77859	Hs.65450	reticulon 4	3.2
	425264	AA353953	Hs.20389	ESTs, Weakly similar to gonadotropin ind	3.2
60	442662	BE379584		dolichyl-diphosphooligosaccharide-prote	3.2
	418871	NM_001608	Hs.1209	acyl-Coenzyme A dehydrogenase, long chal	3.2
	421029	AW067782	Hs.293053	ESTs	3.2
	452997	N64777	Hs.44666	ESTs	3.2
	435035	BE568487	Hs.47668	x 006 protein	3.2
65	408412	AW193033	Hs.124436	ESTs	3.2
	421684	BE281591	Hs.106768	hypothetical protein FLJ10511	3.2
	421887	AW161450	Hs.109201	CGI-86 protein	3.2
	432409	AA806538	Hs.130732	KIAA1575 protein	3.2
	434378	AA631739	Hs.335440	EST	3.2
70	409401	AI201895	Hs.181309	proteasome (prosome, macropain) subunit,	3.2
	420195	N44348	Hs.26243	Homo sapiens cDNA FLJ11177 fis, clone PL	3.2
	410264	AK001863	Hs.61508	Homo sapiens cDNA FLJ10991 fis, clone PL	3.2
	410296	AW630675	Hs.271946	ESTs	3.2
	413838	AV661185	Hs.76574	mitochondrial ribosomal protein L19	3.2
75	414342	AA742181	Hs.75912	KIAA0257 protein	3.2
	414709	AA704703	Hs.77031	Sp2 transcription factor	3.2
	425475	W56339	Hs.107057	ESTs	3.2
	437814	AI088192	Hs.135474	ESTs, Weakly similar to DDX9_HUMAN ATP-D	3.2
	449897	AW819642	Hs.24135	transmembrane protein veszelin; hypotheti	3.2
80	452295	BE379836	Hs.28866	programmed cell death 10	3.2
	437517	AI927675	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	3.2
	432960	AW150945	Hs.144758	ESTs	3.2
	452498	AK000101	Hs.29700	hypothetical protein FLJ20094	3.2
	427299	AA830210	Hs.214283	ESTs, Moderately similar to ALU1_HUMAN A	3.2

	421645	AA974127	Hs.129777	ESTs	3.2
	457489	AI693815	Hs.127179	cryptic gene	3.2
	415691	AW963979	Hs.24723	ESTs	3.2
5	433852	AI378329	Hs.126629	ESTs	3.2
	439735	AI636386	Hs.142845	hypothetical protein	3.2
	428279	AA425310	Hs.155766	ESTs, Weakly similar to A47582 B-cell gr	3.2
	427715	BE245274	Hs.180428	KIAA1181 protein	3.2
	408699	AA056614	Hs.105200	ESTs, Moderately similar to ZN91_HUMAN Z	3.2
10	415715	F30364	Hs.302204	ESTs	3.2
	426172	AA371307	Hs.125056	ESTs	3.2
	434825	N87549	Hs.125287	zinc finger protein ZNF140-like protein	3.2
	436246	AW450963	Hs.119991	ESTs	3.2
	436401	AI087958	Hs.29088	ESTs	3.2
15	408784	AW971350	Hs.63386	ESTs	3.2
	432125	AW972667		Homo sapiens cDNA FLJ12300 fis, clone MA	3.2
	426716	NM_006379	Hs.171921	same domain, immunoglobulin domain (Ig),	3.2
	405658			Target Exon	3.2
	434747	AA837085	Hs.220585	ESTs	3.2
20	414591	AI888490	Hs.55902	ESTs, Weakly similar to ALU8_HUMAN ALU S	3.2
	426991	AK001535		Homo sapiens cDNA FLJ10674 fis, clone NT	3.2
	426171	AI128606	Hs.6557	zinc finger protein 161	3.2
	402802			NM_001397:Homo sapiens endothelin conver	3.2
	412530	AA766268	Hs.266273	hypothetical protein FLJ13346	3.2
25	433050	AI093930	Hs.163440	Homo sapiens cDNA: FLJ21000 fis, clone C	3.2
	439221	AA737106	Hs.32250	ESTs, Moderately similar to I78886 serin	3.2
	440351	AFD30933	Hs.7179	RAD1 (S. pombe) homolog	3.2
	445218	T79971	Hs.12432	Homo sapiens clone 24407 mRNA sequence	3.2
	448568	AA149121	Hs.71947	ESTs	3.2
30	420131	F08266	Hs.95262	nuclear factor related to kappa B bindin	3.1
	429299	AI620463	Hs.347408	hypothetical protein MGC13102	3.1
	407913	BE393767	Hs.41569	phosphatidic acid phosphatase type 2A	3.1
	415009	C75253	Hs.220650	ESTs	3.1
	406827	T64904	Hs.163780	ESTs	3.1
35	438666	AW014493	Hs.126727	ESTs	3.1
	419875	AA853410	Hs.93557	proenkephalin	3.1
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	3.1
	416701	AA814948	Hs.95343	ESTs, Weakly similar to ALUC_HUMAN !!!	3.1
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	3.1
40	440300	N39760	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	3.1
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	3.1
	431416	AA532718	Hs.178604	ESTs	3.1
	422662	BE274778	Hs.119007	RAB4, member RAS oncogene family	3.1
	449543	AF070632	Hs.23729	Homo sapiens clone 24405 mRNA sequence	3.1
45	437083	AW082697	Hs.244662	ESTs	3.1
	430294	AI538226	Hs.32976	guanine nucleotide binding protein 4	3.1
	417380	T06809	Hs.332086	ESTs	3.1
	410905	H16382	Hs.70258	ESTs	3.1
	430039	BE253012	Hs.153400	ESTs, Weakly similar to ALU1_HUMAN ALU B	3.1
50	430188	AL049242	Hs.234794	Homo sapiens mRNA; cDNA DKFZp5648083 (fr	3.1
	446146	AI287539	Hs.148078	ESTs	3.1
	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	3.1
	418555	AI417215	Hs.87159	hypothetical protein FLJ12577	3.1
	453496	AA442103	Hs.33084	solute carrier family 2 (facilitated glx	3.1
55	423847	AW451954	Hs.135941	KIAA1048 protein	3.1
	451893	AW192083	Hs.290855	ESTs	3.1
	447728	AL137838	Hs.19368	matrilin 2	3.1
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	3.1
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	3.1
60	443331	AI052026	Hs.149995	ESTs	3.1
	410340	AW182833	Hs.112188	hypothetical protein FLJ13149	3.1
	414372	AA143654		gb2665a02.r1 Stratagene pancreas (93720	3.1
	427421	AA402414	Hs.3059	coatomer protein complex, subunit beta	3.1
	429399	AA452244	Hs.16727	ESTs	3.1
65	430092	AI821399	Hs.16514	ESTs	3.1
	433577	AW007080	Hs.284192	ESTs	3.1
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	3.1
	436894	HB0696	Hs.233313	ESTs	3.1
	437756	AA767637	Hs.197098	ESTs	3.1
70	438979	AW976218	Hs.32565	ESTs	3.1
	441791	AW372449	Hs.61271	hypothetical protein FLJ21159	3.1
	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.1
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	3.1
	419030	T79957	Hs.188466	ESTs	3.1
75	438308	AI343469	Hs.127685	KIAA1527 protein	3.1
	433571	AA765256	Hs.135191	ESTs, Weakly similar to unnamed protein	3.1
	421685	AF189723	Hs.106778	ATPase, Ca transporting, type 2C, member	3.1
	428878	AA436884	Hs.48926	ESTs	3.1
	432205	AI806583	Hs.125291	ESTs	3.1
80	440093	AL080058	Hs.6909	DKFZP564G202 protein	3.1
	428259	AA424793	Hs.24144	ESTs	3.1
	434614	AI249502	Hs.29689	ESTs	3.1
	420380	AA640891	Hs.102406	ESTs	3.1
	433323	AA805132	Hs.159142	ESTs	3.1

	439544	W26354	Hs.28891	hypothetical protein FLJ11360; artemis p	3.1
	412086	A1699496	Hs.108932	ESTs	3.1
	434361	AF129755	Hs.88474	ESTs	3.1
5	400684			NM_002425:Homo sapiens matrix metallopro	3.1
	436354	A1879252	Hs.5151	RAN binding protein 7	3.1
	449474	AA019344	Hs.2055	ubiquitin-activating enzyme E1 (A1S9T an	3.1
	410595	AW629223	Hs.64794	zinc finger protein 183 (RING finger, C3	3.1
	415245	N59650	Hs.27252	ESTs	3.1
10	418647	AA226198		gb:nc28a07.s1 NCL CGAP_Pr1 Homo sapiens	3.1
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	3.1
	453716	AA037675	Hs.152875	ESTs	3.1
	432952	AA813887	Hs.188173	Homo sapiens cDNA FLJ12187 fis, clone MA	3.0
	408705	AA312135	Hs.46967	HSPC034 protein	3.0
15	430280	AA361258	Hs.237868	interleukin 7 receptor	3.0
	445819	T53519	Hs.334692	hypothetical protein MGC14141	3.0
	441790	AW294908	Hs.132208	ESTs	3.0
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	3.0
	452619	AW298597	Hs.61884	Homo sapiens, clone IMAGE:4298026, mRNA,	3.0
20	422788	AL117352	Hs.77196	Human DNA sequence from clone RP5-876810	3.0
	439703	AF086538	Hs.196245	ESTs	3.0
	444489	AI151010	Hs.157774	ESTs	3.0
	453878	AW964440	Hs.19025	DC32	3.0
	440193	AW902312	Hs.7037	Homo sapiens clone 24923 mRNA sequence	3.0
25	433680	A1805366	Hs.199945	ESTs	3.0
	426363	M58524	Hs.2025	transforming growth factor, beta 3	3.0
	447595	AW379130	Hs.18953	phosphodiesterase 9A	3.0
	426044	AA502490	Hs.170290	ESTs	3.0
	431862	AL049385	Hs.272251	Homo sapiens mRNA; cDNA DKFZp586M1418 (f	3.0
30	445084	H38914	Hs.250848	hypothetical protein FLJ14761	3.0
	452737	AK001680	Hs.30488	DKFZP434F091 protein	3.0
	458229	A1929602	Hs.177	phosphatidylinositol glycan, class H	3.0
	435712	AA694607	Hs.176956	ESTs	3.0
	407378	AA298264	Hs.57776	ESTs, Moderately similar to I38022 hypot	3.0
35	414993	AW619403	Hs.77724	KIAA0586 gene product	3.0
	419459	AW291128	Hs.278422	DKFZP586G1122 protein	3.0
	421988	AW450481	Hs.161333	ESTs	3.0
	432833	N51075	Hs.110028	ESTs	3.0
	445210	H08323	Hs.27133	ESTs	3.0
40	447620	AW290951	Hs.224965	ESTs	3.0
	449375	R07114	Hs.271224	ESTs	3.0
	428695	A1356647	Hs.189999	purinergic receptor (family A group 5)	3.0
	443667	AW294013	Hs.200942	ESTs	3.0
	441224	AU076964	Hs.7753	calumenin	3.0
45	448822	BE149845	Hs.289038	hypothetical protein MGC4126	3.0
	435688	H72286	Hs.128367	ESTs	3.0
	441889	A1090455	Hs.268371	hypothetical protein FLJ20274	3.0
	411704	A1499220	Hs.71573	hypothetical protein FLJ10074	3.0
	419564	AA171850	Hs.42251	ESTs	3.0
50	419544	A1909154		gb:QV-BT200-010499-007 BT200 Homo sapien	3.0
	420077	AW512260	Hs.87767	ESTs	3.0
	443475	A1066470	Hs.132809	ESTs	3.0
	447231	AK001293	Hs.330206	crystallin, zeta (quinone reductase)-lik	3.0
	438436	AA807168	Hs.271552	ESTs	3.0
55	427871	AW992405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	3.0
	443280	AA299668	Hs.24183	ESTs	3.0
	448264	A1478933	Hs.188260	ESTs	3.0
	428673	AW601325	Hs.337757	Homo sapiens mRNA; cDNA DKFZp566M063 (fr	3.0
	453843	D25215	Hs.35804	hect domain and RLD 3	3.0
60	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	3.0
	445943	AW896533	Hs.181574	ESTs	3.0
	432286	AW327432	Hs.255843	ESTs	3.0
	431707	R21326	Hs.267905	hypothetical protein FLJ10422	3.0
	432675	A1791855	Hs.105884	ESTs	3.0
65	443162	T49951	Hs.9029	DKFZP434G032 protein	3.0
	448073	W19789	Hs.338635	Homo sapiens, clone IMAGE:4179482, mRNA	3.0
	419713	AW968058	Hs.92381	nudix (nucleoside diphosphate linked mol	3.0
	447968	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	3.0
	423583	AL122055	Hs.129836	KIAA1028 protein	3.0
70	418304	AA215702		gb:zr97g10.r1 NCL CGAP_GCB1 Homo sapiens	3.0
	417206	AA291183	Hs.81648	hypothetical protein FLJ11021 similar to	3.0
	410011	AB020641	Hs.57856	PFTAIIE protein kinase 1	3.0
	411850	AK002033	Hs.72782	hypothetical protein FLJ11171	3.0
	436986	AF085888	Hs.269307	ESTs	3.0
75	445921	AW015211	Hs.146181	ESTs	3.0
	447124	AW976438	Hs.17428	RBP1-like protein	3.0
	452953	A1932884	Hs.271741	ESTs, Weakly similar to A46010 X-linked	3.0

80

TABLE 60B

Pkey: Unique Eos probeset identifier number

CAT number: Gene cluster number
Accession: Genbank accession numbers

	Pkey	CAT Number	Accessions
5	411479	1247077_1	AW848047 AW848202 AW848631 AW848142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069 AW848905 AW848214
10	411667	1253334_1	BE160198 AW935898 T11520 AW935930 AW856073 AW861034
	414372	143909_1	AA143554 AW753140 AA213770 AW970865 AA569075 AA492132
	414680	147525_1	AA743331 AA837388 AW684540 AA775711 AA150965 BE465475 AA968994 AA886905 A1141054 AW194991 AA252147 AA319500 A1184288 AA708749 AA644620 AA652769 AA242975 AA151074 T19890
15	415989	156454_1	A1267700 A1720344 AA191424 A1023543 A1469633 AA172056 AW958465 AA172236 AW953397 AA355086
	416268	1585983_1	H51299 H44619 H46391 RB6024 H51892 T72744
	416982	162718_1	A1633044 AW016212 AW241143 AA769058 R43272 AW068956 AA210918 AA293774 A1748815 A1763294 A1333114 A1277384 A1088297 A1468477 A1824624 AW189606 A1631751 Z40749 A1984673 A1671316 AA189024 AW235412 BE178426 R24677 R40635 H05100 R40597
20	416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
	417379	167238_1	AA196390 AA507837 AA196468
	418304	173658_2	AA215702 AA368006 AA215703 BE068555 BE068676
	418547	177521_1	AA226198 AA226513 AA383773
	418866	179788_1	T65754 AA229857 AA229658
	419536	185688_1	AA803305 AA244095 AA244183
	419544	185780_2	A1909154 AA526337 AA244183 A1909153
	423412	228001_1	AF109300 A1299378 A1202654
25	423800	232161_1	AA331156 AA331157 AA331155
	426226	262918_1	AA769045 AA372590 AW963633
	426413	266850_1	AA377823 AW954494 A1026868
	426503	268283_1	AA380153 AA380233 AW963529
	426775	271683_1	AA384564 AW966475 H02121 N41297 D63213 AA886888 A1922414 AW044240 AW196808 A1076736 AA599294 A1954433 AW117617 A1640323 H98134
30	426991	27415_1	AK001536 AA191092 AW510354 A1554256 AL353958 AA134266
	428342	290035_2	A1739168 AA426249 A1199536 AW505198 AW977291 AA824583 AA863419 AA724079 A1015524 A1377728 AW293682 A1928140 AA731438 A1092404 A1085630 AA731340
35	429163	300543_1	AA884766 AW974271 AA592975 AA447312
	429220	301384_1	AW207206 AW341473 AA448195 A1951341
	429258	301917_1	AA48765 C04967 C03045 AA658293
	430935	325772_1	AW072916 A1184913 AA489195 AW466994 AW469044 N59350 A1819642 A1280239 A1220572 AA789302 A1473611 AW841126 D60937
	430968	326269_1	AW972830 AA527647 AA489620 AA570382
	431429	33313_1	AF072813 AF119297 AA362885 AF059524 NM_006054 AA157365 AW163623 AA058148 AA227062 AA418057 AA227076 AA078753 AA233594 D58629 AA232373 AA233577 T35956 BE18035 AA354497 AA359082 T32010 AA134519 BE299901 BE268096 BE396826 AA324268 A120308 A1187561 AA311680
40	432093	341283_1	H28383 AW972670 H28359 AA525808
	432125	341776_1	AW972667 AA526539 A1057032 AW167842
	432169	342819_1	AA527941 A1810608 A1620190 AA635266
	432340	345248_1	AA534222 AA632632 T81234
45	432363	345469_1	AA534469 AW970240 AW970323
	432600	350959_1	A1821085 AW973464 AA554802 A1821831 AA657438 AA640756 AA850339
	432810	354376_1	AA863400 A1991439 AW018017 AW014704 A1367512 H17550 AA744752 R46187 AW471324 A1126670 AA826033 A1276287 A1094253 A1286003 A1147163 A1911443 AW512612 AA972102 AA999975 A1684428 A1335035 D63102 A1524234 A1539156 AA565542
50	434579	38916_1	T65958 T57205 AF147346
	434966	396504_1	AA657494 A1582663 A1581639
	435023	398093_1	A1892552 A1393343 A1800510 A1377711 F24263 AA681876
	437668	44433_2	AA156781 AW293839 U52054 AA024953 AA778446 BE073977 AW444904 AW602574 BE164040 BE164012 BE163972 BE163974 BE163992 AA837481 AW468444 BE185091 AW468002 AA687333 AAB11830 AA581806 A1866886 A1572124 AA043777 AA040926 D20160 A1536733 AA812489 AW874142 A147188
55	438147	45074_1	AW250553 L07876 Z36843 R30593 A1190097 AW966317
	439092	468554_1	AA830149 AW978407 M85983 AW503637
	439518	47334_1	W76328 AF086341 W72300
	439904	479942_1	AW892676 AA853877 D44747
	440840	50357_2	AW629666 AW969831 AW205739 BE620243 AA412367 AW300025 AW051920 A1288591 AW236114 A1302852 A1038548 AA534496 A1797207 AA921877
60	441102	509804_1	AA973905 A1299888 AA917019 H63235 T90771
	442562	54500_2	BE379584 R34211 BE544788 AW973709 A1653056 A1653173 A1286043 A1658750 H74180 A1492830 A1376090 A1472184 D58940 AW170056 A1082443 AW021142 A1167921 A1348677 A1278577 AW130865 AA761517 A1698203 AA115535 A1264790 R34328 D59939 AW205074 AA554902 D52102 A10007
65	443161	561305_1	A1088316 A1344831 A1261653
	445808	65133_1	AV655234 AW966332 AA340239
	447082	707248_1	T85314 A1360584 T85528 T91254
	448212	755099_1	A1475858 AW966013
70	449625	8113_1	NM_014253 AF100772 BE088769 A1022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW296554 AA323193 AA235370 AW779760 N48674 A1375997 R45432 D59344 A1203107 F07491 R35360 R25094 A1913631 A1498402 T61382 A1016320 N45528 T61415 AA331486 N40087 H12925 AA460779 AA095372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816888 AW816889 AW816940 AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW887764 AW023805 AW022095 AA164518 AA730973 W00417 W65303
75	450582	83933_1	A1339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878
	452280	9074_1	AA453208 NM_004421 U44103 A1671547 N57463 AW007621 A1479232 T82809 R67109 AW796099 A1833027 A1765395 A1763029 A1758228 BE326331 A1934576 A1922378 AW276431 A1718468 N36566 AA904753 BE464245 A1338752 A1659875 AW272338 A1423136 A1089270 A1160804 AA664354 BE1
80	452598	92338_2	A1831594 AW970667 AW027959 A1129800 A1927949 A1650270 A1625105 AW514661 A1708393 A1138076 BE180510 A1926721 A1399955 AA749139 A1862160 AW874011 A1242763 AA262795 AA039864 H73499 A1093249 BE245661 A1816834 N25206 AA828301 A1084565 A1020816 AA026905 AA77255
	452815	93255_1	AA418841 A1452657 A1768876 AA028973 BE179873 C00215 AA418930
	453802	981589_1	AL134757 AW079131
	455100	1253334_1	BE160198 AW935898 T11520 AW935930 AW856073 AW861034

457728 393853_1 AW974811 AA651534 AA650072

5 TABLE 60C

10 Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham 1. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham 1. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 NL_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
400664	8118495	Plus	13558-13721,13842-14090,14554-14679
400695	7249150	Plus	160456-160567,164757-164873
400880	9931121	Plus	29235-29336,36363-36580
401197	9719705	Plus	176341-176452
401424	8176894	Plus	24223-24428
401451	8834068	Minus	119928-121272
401519	6649315	Plus	157315-157950
401558	7139678	Plus	103510-104090
402031	7656761	Plus	33080-33263,33939-34094,36103-36507
402802	3287156	Minus	53242-53432
402855	9662953	Minus	59763-59909
403046	3540153	Minus	55707-55859,56369-56511
403047	3540153	Minus	59793-59938
403790	8084957	Minus	67826-67947,60835-90002
404571	7249169	Minus	112450-112648
404632	9796668	Plus	45096-45229
404641	9796810	Minus	32247-32362
404642	9796810	Plus	102959-103145
405523	9454643	Plus	114550-114688,117265-117407,119490-119599,123237-123395,131140-131217
405558	1621110	Plus	4502-4644,5983-6083

35 Table 61A lists about 440 genes up-regulated in prostate cancer compared to normal prostate and normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" prostate cancer to "average" normal prostate tissue was greater than or equal to 2.0 and the ratio to normal adult tissues was greater than or equal to 2.0. The "average" prostate cancer level was set to the 75th percentile amongst prostate cancers. The "average" normal prostate tissue level was set to the 95th percentile amongst prostate tissues. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

40 TABLE 61A: ABOUT 440 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL PROSTATE AND NORMAL ADULT TISSUES

45 Pkey: Unique Eos probeset identifier number
 ExAccn: Exonmap Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of prostate tumor to normal adult body tissue
 R2: Ratio of prostate tumor to normal prostate tissue

Pkey	ExAccn	UnigeneID	Unigene Title	R1	R2
444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	42.2	42.2
421566	NM_000390	Hs.1395	early growth response 2 (Krox-20) (Drosop)	3.2	26.5
420729	AW964897	Hs.290825	ESTs	3.7	15.8
401197			ENSP00000229263*HSPC213.	3.0	12.6
450096	AI682068	Hs.79375	holocarboxylase synthetase (biotin-prop	12.4	12.4
449156	AF103907	Hs.171353	prostate cancer antigen 3, non-coding DD	12.3	12.3
443271	BE568568	Hs.195704	ESTs	11.6	11.6
434078	AW880709	Hs.283683	chromosome 8 open reading frame 4	2.1	11.2
431117	AF003522	Hs.250500	delta (Drosophila)-like 1	9.4	9.4
417315	AI080042	Hs.180450	ribosomal protein S24	2.3	9.0
416182	NM_004354	Hs.79089	cyclin G2	8.4	8.4
421913	AI934355	Hs.109439	osteoglycin (osteoblast-inductive factor, mime	2.2	8.4
434217	AW014795	Hs.23349	ESTs	8.3	8.3
425782	U68468	Hs.159625	cell growth regulatory with EF-hand doma	8.3	8.3
442501	AA315267	Hs.23128	ESTs	2.0	8.3
429584	AL050102	Hs.227209	hypothetical protein FLJ21617	8.1	8.1
445048	Z45051	Hs.22920	similar to 868401 (cattle) glucose induc	3.1	8.0
417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	34.0	7.9
402120	AL049610	Hs.95243	transcription elongation factor A (SII)-	7.5	7.5
419078	M93119	Hs.89584	insulinoma-associated 1	7.4	7.4
425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	9.4	7.3
425018	BE245277	Hs.154195	E4F transcription factor 1	7.2	7.2
452221	C21322	Hs.288057	hypothetical protein FLJ22242	7.0	7.0
421552	AF026592	Hs.105700	secreted frizzled-related protein 4	4.0	6.6
409799	D11928	Hs.76845	phosphoserine phosphatase-like	6.3	6.3
411373	BE326276	Hs.8861	ESTs	3.2	6.3
423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	6.7	6.2
422583	AA410506	Hs.27973	KIAA0874 protein	2.3	6.2
438209	AL120559	Hs.6111	aryl-hydrocarbon receptor nuclear transl	6.1	6.1
437147	AL049964	Hs.8358	hypothetical protein FLJ20366	2.6	6.0

5	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	6.0	6.0
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	6.2	6.0
	449118	R67477	Hs.23103	Bett1 (S. cerevisiae) homolog	5.9	5.9
	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-1	3.3	5.9
	431548	AI834273	Hs.9711	novel protein	15.7	5.8
10	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	4.2	5.8
	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	3.5	5.8
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.9	5.8
	422538	NM_006441	Hs.118131	5,10-methylenetetrahydrofolate synthetase	5.7	5.7
	414812	X72755	Hs.77367	monokine induced by gamma interferon	2.5	5.6
15	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	5.6	5.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A {	5.5	5.5
	414516	AI037802	Hs.135560	ESTs, Weakly similar to T43458 hypotheti	2.7	5.5
	414343	AL036166	Hs.323378	coated vesicle membrane protein	5.4	5.4
	451684	AF216751	Hs.26813	CDA14	3.9	5.4
20	421470	R27496	Hs.1378	annexin A3	5.3	5.3
	426350	NM_003245	Hs.2022	transglutaminase 3 [E polypeptide, prote	5.3	5.3
	436476	AA326108	Hs.33829	bHLH protein DEC2	2.8	5.3
	437571	AA760894	Hs.153023	ESTs	5.2	5.2
	447072	D81594	Hs.17279	tyrosylprotein sulfotransferase 1	5.2	5.2
25	444917	R68651	Hs.144997	ESTs	5.1	5.1
	417318	AW953937	Hs.240845	ESTs	4.6	5.1
	434170	AA826509	Hs.122329	ESTs	5.1	5.0
	432697	AF155099	Hs.279760	NY-REN-18 antigen	3.3	5.0
	433660	AI925195	Hs.130891	hypothetical protein MGC4400	4.8	5.0
30	421823	N40850	Hs.28625	ESTs	5.0	5.0
	451244	AW008798	Hs.343877	hypothetical protein FLJ20039	4.9	4.9
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	29.8	4.9
	425242	D13635	Hs.155287	KIAA0010 gene product	2.2	4.8
	439024	R96696	Hs.35598	ESTs	5.4	4.8
35	407235	D20569	Hs.168407	SAC2 (suppressor of actin mutations 2, y	4.8	4.8
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (tr	4.7	4.7
	437916	BE566249	Hs.20999	hypothetical protein FLJ23142	3.6	4.7
	451952	AL120173	Hs.301663	ESTs	4.7	4.7
	431676	AI685464	Hs.159993	gbc188f04.x1 NCL_CGAP_Pt28 Homo sapiens	9.1	4.7
40	452242	RS0956	Hs.159993	glycosyltransferase	4.7	4.7
	401519			G16000476.g[12737279]ref[XP_012163.1]	4.6	4.6
	414342	AA742181	Hs.75912	KIAA0257 protein	3.4	4.6
	426197	AA004410	Hs.100009	acyl-Coenzyme A oxidase 1, palmitoyl	3.3	4.6
	429467	NM_004477	Hs.203772	FSHD region gene 1	2.1	4.6
45	406380	AF123050	Hs.44532	ubiquitin	4.2	4.6
	425907	AA365752	Hs.155965	ESTs	2.2	4.6
	427078	AI676062	Hs.111902	ESTs	4.8	4.5
	419455	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	2.7	4.5
	429250	H56585	Hs.198308	tryptophan rich basic protein	4.5	4.5
50	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	2.5	4.5
	443250	AI041530	Hs.132107	ESTs	8.1	4.4
	423545	AP000692	Hs.129781	chromosome 21 open reading frame 5	4.4	4.4
	423698	AA329796	Hs.1098	DKFZp434J1813 protein	4.4	4.4
	442281	N84742	Hs.170065	Homo sapiens cDNA FLJ13492 fis, clone PL	4.4	4.4
55	428826	ALB48842	Hs.194019	aktactin	2.0	4.3
	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	4.3	4.3
	416701	AA814948	Hs.98343	ESTs, Weakly similar to ALUC_HUMAN IIII	4.2	4.2
	429900	AA460421	Hs.30875	ESTs	4.2	4.2
	439518	W76326		gbczd60d04.r1 Soares_fetal_heart_NbHH19W	2.2	4.2
60	409151	AA305105	Hs.50785	SEC22, vesicle trafficking protein (S. c	3.5	4.2
	420544	AA677577	Hs.98732	Homo sapiens Chromosome 16 BAC clone CIT	10.0	4.2
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	2.8	4.2
	443622	AI911627	Hs.11805	ESTs	2.2	4.1
	410037	AB020725	Hs.68009	KIAA0918 protein	4.1	4.1
65	421129	BE439899	Hs.89271	ESTs	4.1	4.1
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	3.9	4.1
	448664	AI879317	Hs.334691	splicing factor 3a, subunit 1, 120kD	2.8	4.1
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	2.0	4.1
	433867	AW204232	Hs.279522	ESTs	4.1	4.1
70	436556	AI354997	Hs.7572	ESTs	4.1	4.1
	400301	X03635	Hs.1657	estrogen receptor 1	4.1	4.1
	443846	AI085198	Hs.164226	ESTs	4.1	4.1
	430389	AL117429	Hs.240845	DKFZP434D146 protein	2.2	4.0
	418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	4.0	4.0
75	433409	AI278802	Hs.25661	ESTs	4.0	4.0
	447247	AW359351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	4.0	4.0
	423749	U09848	Hs.132390	zinc finger protein 36 (KIX 18)	3.9	3.9
	444765	AA431791	Hs.113823	ClpX (caseinolytic protease X, E. coli)	3.9	3.9
	431912	AI660552	Hs.76549	ESTs, Weakly similar to A56154 Abl subst	2.2	3.9
80	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	3.3	3.9
	447482	AB033059	Hs.18705	KIAA1233 protein	2.2	3.9
	460203	AF097994	Hs.301528	L-tyrosine/alpha-aminoadipate aminotra	3.9	3.9
	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	3.4	3.8
	452588	AA889120	Hs.110637	homeo box A10	6.5	3.8
	422601	NM_014700	Hs.119004	KIAA0665 gene product	3.8	3.8
	407317	AI204033	Hs.271451	ESTs, Weakly similar to I38022 hypotheti	2.3	3.8
	410330	AW023630	Hs.159425	ESTs	6.2	3.8

	117357	N24829		gb:yx98h12.s1 Soares melanocyte 2NbHM Ho	5.6
	120827	AA382525	Hs.132967	Human EST clone 122887 mariner transpos	5.6
	123494	AW179019	Hs.112110	mitochondrial ribosomal protein L42	5.5
5	100438	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	5.5
	126165	AI741816	Hs.125897	ESTs	5.5
	125934	AA193325	Hs.32646	hypothetical protein FLJ21901	5.5
	124370	AI243499	Hs.170652	ESTs	5.5
	106135	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	5.5
10	106668	R49390	Hs.254129	KIAA1678	5.4
	132967	AA316181	Hs.61635	six transmembrane epithelial antigen of	5.4
	109608	Z43371	Hs.7012	ESTs	5.4
	115816	BE042915	Hs.22572	Homo sapiens cDNA FLJ13575 fis, clone P1	5.4
	125186	AA610620	Hs.181165	major histocompatibility complex, class	5.4
15	131185	BE280074	Hs.23960	cyclin B1	5.4
	111227	T06701	Hs.12268	ESTs	5.4
	106516	AK001269	Hs.30738	hypothetical protein FLJ10407	5.4
	103409	NM_004454	Hs.43697	ets variant gene 5 (ets-related molecule	5.4
	116008	T79153	Hs.48599	zinc finger protein 228	5.3
20	106394	Z42993	Hs.25320	Homo sapiens clone 25142 mRNA sequence	5.3
	115121	AI634549	Hs.325422	ESTs	5.3
	125464	N71807		gb:yz29d09.r1 Soares_multiple_sclerosis_	5.3
	115596	AW296587	Hs.61884	Homo sapiens, clone IMAGE4298026, mRNA,	5.3
	119040	R02394	Hs.269438	ESTs, Moderately similar to PCA259 ferri	5.3
25	128040	AW500486	Hs.180610	splicing factor proline/glutamine rich (5.3
	110151	H18835	Hs.31608	hypothetical protein FLJ20041	5.3
	105539	AB040884	Hs.109894	KIAA1451 protein	5.2
	130567	AA383092	Hs.1608	replication protein A3 (14kD)	5.2
	111077	N41367	Hs.173002	ESTs, Weakly similar to I38022 hypothet	5.2
30	120830	AI568170	Hs.96886	ESTs	5.2
	106516	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (5.2
	103318	X83301	Hs.324728	SMA5	5.2
	116129	AF189011	Hs.49183	putative ribonuclease III	5.2
	131253	R71802	Hs.24853	ESTs	5.2
35	116880	AW902848	Hs.273829	ESTs	5.2
	123949	AA621665	Hs.208957	EST	5.2
	105511	AB037829	Hs.3862	regulator of nonsense transcripts 2; DKF	5.2
	125847	AW161835	Hs.269745	ESTs	5.1
40	108301	AA069728	Hs.184582	ribosomal protein L24	5.1
	110799	AK089660	Hs.323401	dpy-30-like protein	5.1
	104899	AA054726	Hs.285574	ESTs	5.1
	125972	AI927475	Hs.35406	ESTs, Highly similar to unnamed protein	5.1
	107869	AW976998	Hs.58595	ESTs, Weakly similar to I38022 hypothet	5.1
	121309	AA293834	Hs.97312	ESTs	5.1
45	125321	T86652	Hs.178294	ESTs	5.1
	102827	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	5.1
	104448	AF084555	Hs.7351	cyclic AMP phosphoprotein, 19 kD	5.0
	126020	H79863	Hs.114243	ESTs	5.0
	118814	H50934	Hs.77899	gb:yp88a10.s1 Soares fetal liver spleen	5.0
50	130622	AI682291	Hs.16848	ESTs, Weakly similar to O44H01 debrisocu	5.0
	110818	AL157503	Hs.27652	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	4.9
	127785	AA871146	Hs.129074	ESTs, Moderately similar to MEG1 MOUSE M	4.9
	108768	AF181721	Hs.61345	RU25	4.9
	120484	AA253170	Hs.98473	EST	4.9
55	114518	AW163267	Hs.106469	suppressor of var1 (S.cerevisiae) 3-like	4.9
	129012	R81936		ribosomal protein L44	4.9
	124973	AI476956	Hs.102243	ESTs, Weakly similar to I78885 sarine/th	4.9
	124648	AA249086	Hs.125034	hypothetical protein FLJ13340	4.9
	126904	AA948033	Hs.130853	ESTs	4.9
60	131526	AI005169	Hs.28274	Homo sapiens cDNA: FLJ22049 fis, clone H	4.9
	130637	AA356784	Hs.17109	Integral membrane protein 2A	4.8
	126769	AA083458		gb:zn09g06.r1 Stratagene hNT neuron (937	4.8
	128098	H75881		gb:yl77g01.r1 Soares fetal liver spleen	4.8
	100169	AL037228	Hs.82043	D123 gene product	4.8
65	130262	D63216	Hs.153684	frizzled-related protein	4.8
	109260	AW978515	Hs.131915	KIAA0963 protein	4.8
	103120	BE410731	Hs.74050	follicular lymphoma variant translocatio	4.8
	111099	R15337	Hs.21958	Homo sapiens mRNA; cDNA DKFZp547D086 (fr	4.8
	126142	H86261	Hs.40568	ESTs	4.8
70	126802	AW806510	Hs.97056	hypothetical protein FLJ21834	4.8
	105848	AW954064	Hs.24851	ESTs	4.7
	127987	AI022103	Hs.124511	ESTs	4.7
	129708	AA443241		ribosomal protein L44	4.7
	128598	N30436	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	4.7
75	126529	AL096739	Hs.107260	hypothetical protein DKFZp588H0623	4.7
	111348	AA034922	Hs.9565	ESTs	4.7
	100448	AF234887	Hs.57652	cadherin, EGF LAG seven-pass G-type rece	4.7
	127542	AA703684	Hs.179833	ESTs, Moderately similar to ALU5_HUMAN A	4.7
	132452	AW973521	Hs.247324	mitochondrial ribosomal protein S14	4.7
80	123778	AW352149	Hs.102314	ESTs	4.7
	128521	AI475110	Hs.203933	ESTs	4.7
	110343	AW136703	Hs.17268	ESTs	4.6
	102963	X02404	Hs.274534	calcitonin-related polypeptide, beta	4.6
	127207	AA377165	Hs.44833	ESTs	4.6

	420297	AI626272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.9	2.9
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (hls	2.9	2.9
	437812	AS82291	Hs.16846	ESTs, Weakly similar to C4HUD1 debrisou	2.9	2.9
5	445808	AV655234		ESTs, Moderately similar to PC4259 ferri	2.9	2.9
	428600	AW863261	Hs.242413	hypothetical protein DKFZp434K1421	4.7	2.9
	442320	AI287817	Hs.129636	ESTs	3.7	2.9
	418407	AL044818	Hs.84928	nuclear transcription factor Y, beta	2.4	2.9
	433050	AI093930	Hs.163440	Homo sapiens cDNA: FLJ21000 fis, clone C	2.9	2.9
10	451786	AL133019	Hs.27038	Homo sapiens mRNA; cDNA DKFZp434G2127 (f	2.9	2.9
	407783	AW996872	Hs.172026	a disintegrin and metalloproteinase doma	3.0	2.9
	459029	AA131376	Hs.343809	fibroblast growth factor 12B	2.9	2.9
	441676	BE564206	Hs.49889	ESTs	4.4	2.9
	439352	BE614347	Hs.169615	hypothetical protein FLJ20989	2.1	2.9
15	463628	AW243307	Hs.83937	hypothetical protein	2.9	2.9
	412324	AW978439	Hs.69504	ESTs	2.0	2.8
	408063	BE086548	Hs.42346	calcineurin-binding protein calcardin-1	5.0	2.8
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	6.4	2.8
	421247	BE391727	Hs.102910	general transcription factor IIH, polype	2.8	2.8
20	433865	N29862	Hs.44104	ESTs	2.8	2.8
	423201	NM_000163	Hs.125180	growth hormone receptor	6.3	2.8
	450832	AW970602	Hs.105421	ESTs	2.1	2.8
	416913	AW934714		gb:RC1-DT0001-031299-011-a11 DT0001 Homo	2.8	2.8
	417251	AW015242	Hs.99488	ESTs, Weakly similar to YK54_YEAST HYPOT	2.8	2.8
25	427144	X95097	Hs.2126	vasoactive intestinal peptide receptor 2	2.8	2.8
	444668	AA654850	Hs.282905	ESTs	2.2	2.8
	434015	AA844518	Hs.300876	hypothetical protein FLJ13386	3.2	2.8
	432689	AB018320		Arg/Abi-interacting protein ArgBP2	2.1	2.8
	423482	BE280172	Hs.129228	galactokinase 2	2.4	2.8
30	448206	BE522585	Hs.3731	ESTs, Moderately similar to I38022 hypot	2.8	2.8
	450546	AA010200	Hs.175551	ESTs	2.2	2.7
	452270	AW975014	Hs.26	ferrochelatase (protoporphyrin)	3.6	2.7
	458332	AK000341	Hs.220491	ESTs	4.9	2.7
	436109	AA922153	Hs.132760	hypothetical protein MGC15729	2.7	2.7
	422867	L32137	Hs.1584	cartilage oligomeric matrix protein (pse	2.1	2.7
35	412576	AA447718	Hs.107057	ESTs	2.7	2.7
	413336	AI569936	Hs.295178	hypothetical protein FLJ22637	2.7	2.7
	433577	AW007080	Hs.284192	ESTs	2.7	2.7
	439093	AA634163	Hs.5476	Homo sapiens, clone IMAGE:3530123, mRNA,	2.7	2.7
40	442833	AA328153	Hs.88201	ESTs, Weakly similar to A Chain A, Cryst	2.7	2.7
	447401	BE618582	Hs.97661	ESTs	2.7	2.7
	409619	AK001015	Hs.55220	BCL2-associated atlanogene 2	2.7	2.7
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	2.2	2.7
	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.2	2.7
45	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	9.0	2.7
	409205	AI952884	Hs.14832	ESTs, Moderately similar to unnamed prot	2.4	2.7
	422805	AA436989	Hs.121017	H2A histone family, member A	13.6	2.7
	448238	T95143	Hs.14511	SCO (cytochrome oxidase deficient, yeast	2.1	2.7
	447313	U92981	Hs.18081	Homo sapiens clone DT1P186 mRNA, CAG rep	8.1	2.7
50	411630	U42349	Hs.71119	Putative prostate cancer tumor suppresso	6.2	2.6
	410592	R94088	Hs.43569	ESTs	2.6	2.6
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	2.6	2.6
	417601	NM_014736	Hs.82292	KIAA0215 gene product	2.6	2.6
	433419	AI830342	Hs.211272	ESTs	2.9	2.6
55	447509	AF107454	Hs.107637	chromosome 7 open reading frame 2	2.0	2.6
	424580	AA446539	Hs.339024	ESTs, Weakly similar to A46010 X-linked	2.4	2.6
	407252	AA659037	Hs.163780	ESTs	2.6	2.6
	420061	AW024937	Hs.29410	ESTs	2.4	2.6
	424432	AB037821	Hs.146858	protocadherin 10	7.9	2.6
60	417683	AW566008	Hs.239154	ankyrin repeat, family A (RFXANK-like),	2.7	2.6
	414312	AA155694	Hs.191080	ESTs	2.6	2.6
	417135	AA422067	Hs.50547	ESTs	2.6	2.6
	437748	AF234882	Hs.5814	suppression of tumorigenicity 7	2.6	2.6
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	9.0	2.6
65	453070	AK001465	Hs.31575	SEC63, endoplasmic reticulum translocon	2.2	2.6
	406627	T64904	Hs.163780	ESTs	6.7	2.6
	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown [Hs	2.4	2.6
	425815	R94023	Hs.94580	ESTs, Moderately similar to I38022 hypot	2.6	2.6
	433805	AA706910	Hs.112742	ESTs	2.6	2.6
70	431474	AL133990	Hs.190642	ESTs	9.3	2.5
	436204	AK002014	Hs.47546	Homo sapiens cDNA FLJ11458 fis, clone HE	2.2	2.5
	439328	W07411	Hs.118212	ESTs, Moderately similar to ALU3_HUMAN A	3.3	2.5
	449115	AW959952	Hs.37528	ESTs, Weakly similar to AF090944 1 PRO08	2.3	2.5
	437531	AI400752	Hs.112259	T cell receptor gamma locus	2.6	2.5
75	445424	AB028945	Hs.12696	cortactin SH3 domain-binding protein	3.4	2.5
	403047			NM_005656-Homo sapiens transmembrane pr	21.1	2.5
	416198	H27332	Hs.99598	hypothetical protein MGC5336	2.5	2.5
	417576	AA339449	Hs.82285	phosphoribosylglycinamide formyltransfer	2.5	2.5
	430607	AW973521	Hs.247324	mitochondrial ribosomal protein S14	2.5	2.5
80	436401	AI087958	Hs.29088	ESTs	2.5	2.5
	450654	AJ245587	Hs.25275	Kruppel-type zinc finger protein	2.5	2.5
	426216	N77630	Hs.13895	Homo sapiens cDNA FLJ11654 fis, clone HE	3.0	2.5
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	11.9	2.5
	410102	AW248508	Hs.279727	Homo sapiens cDNA FLJ14035 fis, clone HE	2.5	2.5

	446791	AI632278	Hs.195922	ESTs	2.5	2.5
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	2.5	2.5
	419791	AI579909	Hs.105104	ESTs	2.7	2.5
5	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipase	3.0	2.5
	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	2.1	2.5
	452741	BE392914	Hs.30503	Homo sapiens cDNA FLJ11344 fis, clone PL	2.5	2.5
	447702	AI420256	Hs.161271	ESTs	2.1	2.4
	412043	BE156622	Hs.333371	Homo sapiens clone TA40 untranslated mRNA	2.4	2.4
10	421413	AI826128	Hs.57637	ESTs, Weakly similar to A49364 59 protei	2.4	2.4
	429128	AA446869	Hs.119316	ESTs	2.0	2.4
	429258	AA446765		gb:zx10e09.r1 Soares fetal_fetus_Nb2HF8_	2.4	2.4
	435102	AW899053	Hs.76917	F-box only protein 8	2.4	2.4
	456161	BE264645	Hs.282093	hypothetical protein FLJ21918	3.1	2.4
15	407021	U52077		gb:Human mariner1 transposase gene, comp	7.3	2.4
	437517	AI927675	Hs.244482	Homo sapiens, clone IMAGE:3611719, mRNA,	2.1	2.4
	408267	AW380525	Hs.343564	tubulin-specific chaperone a	4.3	2.4
	447713	AI420733	Hs.207083	ESTs	2.4	2.4
	456848	AL121087	Hs.296406	KIAA0885 gene product	2.2	2.4
20	437617	AI026701	Hs.5716	KIAA0310 gene product	2.6	2.4
	432378	AM93046	Hs.146133	ESTs	5.2	2.4
	443180	R15875	Hs.258578	claudin 12	10.1	2.4
	445929	AI089660	Hs.323401	dpy-30-like protein	2.2	2.4
	424701	NM_005923	Hs.151988	mitogen-activated protein kinase kinase	2.3	2.4
25	445255	NM_014841	Hs.12477	synaptoosomal-associated protein, 91 kDa	2.5	2.4
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	27.5	2.4
	421709	AA159394	Hs.107055	CED-6 protein	2.3	2.4
	412707	AW206373	Hs.16443	Homo sapiens cDNA: FLJ21721 fis, clone C	4.7	2.4
	418882	NM_004996	Hs.89433	ATP-binding cassette, sub-family C (CFTR	2.4	2.4
30	451071	AW138807	Hs.204939	ESTs, Highly similar to A54677 homeotic	2.4	2.4
	420344	BE463721	Hs.97101	putative G protein-coupled receptor	3.1	2.3
	433037	NM_014158	Hs.279938	HSPC067 protein	2.4	2.3
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	4.1	2.3
	419544	AI909154		gb:CV-BT200-010499-007 BT200 Homo sapien	2.3	2.3
35	424502	AK002055	Hs.151045	hypothetical protein FLJ11193	2.1	2.3
	450693	AW460461	Hs.203965	ESTs	2.3	2.3
	462387	AI680772	Hs.308094	trinucleotide repeat containing 12	2.3	2.3
	412045	AA099802	Hs.83883	transmembrane, prostate androgen induced	4.1	2.3
	428180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	2.0	2.3
40	419438	AA406400	Hs.12482	glycerophosphate O-acyltransferase	2.7	2.3
	443194	AI954968	Hs.279009	matrix Gla protein	2.1	2.3
	414869	AA157291	Hs.21479	ubiquitin 1	2.5	2.3
	407300	AA102616	Hs.120769	gb:zn43a07.s1 Stratagene HeLa cell s3 S3	2.3	2.3
	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	2.3	2.3
45	439221	AA737106	Hs.32250	ESTs, Moderately similar to I78885 serin	2.3	2.3
	453802	AL134767		gb:DKFZp547G1080_r1 547 (synonym: hibr1)	4.1	2.3
	421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	7.9	2.3
	426413	AA377823		gb:EST190805 Synovial sarcoma Homo sapien	2.2	2.3
	431147	AI767751	Hs.20300	ESTs	5.8	2.3
50	442677	AI557914		peroxisomal acyl-CoA thioesterase	2.5	2.3
	446091	AW022192	Hs.200197	ESTs	4.0	2.3
	431563	AK027643	Hs.120912	ESTs	2.2	2.3
	439478	AF049460	Hs.6574	deformed epidermal autoregulatory factor	2.1	2.3
	413049	NM_002151	Hs.823	hepsin (transmembrane protease, serine 1	3.5	2.3
55	405685			C2002829:gil4507689[ra]NP_003296.1] tra	2.3	2.3
	407917	U63139	Hs.41687	RAD50 (S. cerevisiae) homolog	2.3	2.3
	450378	AW240181	Hs.19954	ESTs, Weakly similar to T19873 hypotheti	2.3	2.3
	429303	AW137635	Hs.44238	ESTs, Weakly similar to S65657 alpha-1C-	2.3	2.3
	417248	AA329449	Hs.247302	twisted gastrulation	2.3	2.2
60	429277	AW452018	Hs.127863	ESTs, Weakly similar to SFR4_HUMAN SPUC	2.6	2.2
	431555	AI815470	Hs.260024	Odc42 effector protein 3	4.5	2.2
	440098	AL080058	Hs.6909	DKFZP564G202 protein	2.9	2.2
	416653	AA768553	Hs.193145	metallothionein 1E (functional)	3.4	2.2
	431542	H63010	Hs.5740	ESTs	7.0	2.2
65	401558			ENSP00000220478::SECRETORANIN III.	2.2	2.2
	418281	U09550	Hs.1154	oviductal glycoprotein 1, 120kD (mucin 9	2.2	2.2
	422295	AF051151	Hs.114408	tol-like receptor 5	2.2	2.2
	432453	AI885537	Hs.27172	ESTs, Moderately similar to PC4259 fami	2.2	2.2
	447499	AW262580	Hs.147674	protocadherin beta 16	2.2	2.2
70	452994	AW962597	Hs.31305	KIAA1547 protein	4.0	2.2
	450325	AI935952	Hs.26289	ESTs	11.9	2.2
	422390	AW450893	Hs.121830	ESTs, Weakly similar to T42682 hypotheti	2.1	2.2
	448789	BE539108	Hs.22051	hypothetical protein MGC15548	2.6	2.2
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	11.8	2.2
75	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	3.2	2.2
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	13.6	2.2
	410252	AW821182	Hs.61418	microfibrillar-associated protein 1	4.2	2.2
	439699	AF068534	Hs.187561	ESTs, Moderately similar to ALU1_HUMAN A	4.8	2.2
	422576	BE548555	Hs.118554	CGI-83 protein	2.1	2.2
80	433293	AF007835	Hs.32417	hypothetical protein MGC4309	11.0	2.2
	410733	D84284	Hs.66062	CD38 antigen (p45)	3.1	2.2
	421379	Y15221	Hs.103982	small inducible cytokine subfamily B (Cy	2.1	2.2
	442995	AA532511	Hs.288455	Homo sapiens cDNA: FLJ23270 fis, clone C	2.2	2.2
	408833	AW612232	Hs.254835	ESTs	3.0	2.2

	422424	AI186431	Hs.296638	prostate differentiation factor	4.4	2.2
	433444	AW975324	Hs.129816	ESTs	11.7	2.2
	446354	AW449650	Hs.346335	ESTs	2.6	2.2
	438869	AF075009		gb:Homo sapiens full length insert cDNA	6.9	2.2
5	425628	NM_004476	Hs.1915	folate hydrolase (prostate-specific memb	12.8	2.2
	424036	AA770888		H2A histone family, member L	3.8	2.2
	440146	AW014231	Hs.90790	Homo sapiens cDNA: FLJ22930 fig, clone K	4.8	2.2
	404541			NM_021965*-Homo sapiens phosphoglucomuta	2.2	2.2
10	407253	AA411175	Hs.141939	ESTs, Moderately similar to S65657 alpha	2.2	2.2
	406068			C2002008.gij7303957[gb]AAFS9000.11 (AE00	3.1	2.1
	415162	AF035718	Hs.78061	transcription factor 21	2.1	2.1
	423349	AF010258	Hs.127428	homeo box A9	5.9	2.1
	424534	D87682	Hs.150275	KIAA0241 protein	2.3	2.1
	407756	AA116021	Hs.38260	ubiquitin specific protease 18	2.5	2.1
15	440658	H29142	Hs.143032	ESTs, Weakly similar to neuronal thread	2.5	2.1
	416547	H62914	Hs.268946	ESTs, Weakly similar to PC4259 ferritin	2.1	2.1
	432281	AK001239	Hs.274263	hypothetical protein FLJ10377	2.1	2.1
	447533	NM_004786	Hs.18792	thioredoxin-like, 32kD	2.1	2.1
20	448956	AW372914	Hs.86149	phosphoinositol 3-phosphate-binding prot	2.1	2.1
	449897	AW819542	Hs.24135	transmembrane protein vezatin; hypotheti	2.1	2.1
	452959	AI933416	Hs.189574	ESTs	2.1	2.1
	427083	NM_006363	Hs.173497	Sec23 (S. cerevisiae) homolog B	2.8	2.1
	408291	AB023191	Hs.44131	KIAA0974 protein	2.1	2.1
25	418727	AA227609	Hs.94834	ESTs	2.1	2.1
	440491	R35252	Hs.130558	ESTs, Weakly similar to 2109260A B cell	2.1	2.1
	433466	AA508353	Hs.105314	relaxin 1 (H1)	17.3	2.1
	432695	D63480	Hs.278634	KIAA0146 protein	2.3	2.1
	427982	NM_016156	Hs.181326	KIAA1073 protein	3.2	2.1
30	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I	2.5	2.1
	434569	AI311295	Hs.344478	KIAA0196 gene product	2.1	2.1
	441791	AW372449	Hs.61271	hypothetical protein FLJ21159	2.1	2.1
	438520	AA706319	Hs.98416	ESTs	2.7	2.1
	414289	AA298489	Hs.303171	olfactory receptor, family 51, subfamily	17.3	2.1
35	410660	AI061118	Hs.65328	Fanconi anemia, complementation group F	3.5	2.1
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	7.4	2.1
	450861	AI523898	Hs.17617	ESTs	2.4	2.1
	419193	D29843	Hs.34789	dolichyl-diphosphooligosaccharide-protei	2.1	2.1
	423784	AK000039	Hs.132826	Homo sapiens cDNA FLJ14913 fig, clone PL	3.2	2.1
40	416208	AW291168	Hs.41295	ESTs, Weakly similar to MUC2_HUMAN MUCIN	6.4	2.1
	407182	AA312551	Hs.230157	ESTs	2.1	2.1
	421689	N87820	Hs.106826	KIAA1696 protein	2.1	2.1
	432833	N51075	Hs.110028	ESTs	2.1	2.1
	425170	AB077315	Hs.154970	transcription factor CP2	2.6	2.0
45	436278	BE396290	Hs.5097	synaptogyrin 2	2.8	2.0
	438719	AA357129	Hs.239625	integral membrane protein 2B	2.3	2.0
	432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	3.6	2.0
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	2.0	2.0
	429716	R25685	Hs.211933	collagen, type XII, alpha 1	3.6	2.0
50	424081	NM_006413	Hs.139120	ribonuclease P (30kD)	2.0	2.0
	433800	AI034361	Hs.135150	lung type-I cell membrane-associated gly	2.0	2.0
	413627	BE182082	Hs.246873	ESTs	3.3	2.0
	414133	AW022188	Hs.41167	ESTs	2.3	2.0
	411096	U80034	Hs.69583	mitochondrial intermediate peptidase	14.7	2.0
55	450244	AA007534	Hs.125062	ESTs	3.1	2.0
	422493	AW474183	Hs.250173	hypothetical protein FLJ13158	2.6	2.0
	408219	AA393383	Hs.133331	ESTs	2.1	2.0
	419986	AI345455	Hs.78915	GA-binding protein transcription factor,	2.0	2.0
	421969	AF052217	Hs.110099	core-binding factor, runt domain, alpha	2.0	2.0
60	434128	W93170	Hs.284164	protein x 0004	2.7	2.0
	434503	T36231	Hs.17762	ESTs	2.0	2.0
	443292	AK000213	Hs.9195	hypothetical protein	2.0	2.0
	443555	N71710	Hs.21398	ESTs, Moderately similar to A Chain A, H	2.0	2.0
	448172	N75276	Hs.135904	ESTs	6.0	2.0
65	452039	AI922988	Hs.172510	ESTs	2.0	2.0
	400290	H18836	Hs.31608	hypothetical protein FLJ20041	6.2	2.0
	449625	NM_014253		odx (odd Oz/ten-in, Drosophila) homolog 1	10.1	2.0
	441406	Z45957	Hs.7837	phosphoprotein regulated by mitogenic pa	2.3	2.0
	451369	AA017321	Hs.269691	ESTs	2.1	2.0
70	434011	AW953437	Hs.5486	clone FLB5214	2.1	2.0
	408808	AW847814	Hs.289005	Homo sapiens cDNA: FLJ21532 fig, clone C	5.4	2.0
	433388	AI432872	Hs.288539	hypothetical protein FLJ22191	2.7	2.0
	432653	N52096	Hs.293185	ESTs, Weakly similar to JC7328 amino ac	5.5	2.0
	446783	AW138343	Hs.141867	ESTs	4.4	2.0
75	437323	AA371145	Hs.194397	leptin receptor	2.6	2.0
	410076	T05387	Hs.7991	ESTs	2.9	2.0
	421501	M29971	Hs.1384	O-6-methylguanine-DNA methyltransferase	2.1	2.0
80	419733	AW362955		Homo sapiens cDNA FLJ14415 fig, clone HE	2.5	2.0

TABLE 61B

Pkey: Unique Eos probe/identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

5	Pkey	CAT Number	Accession
	414680	147525_1	AA743331 AA837388 AW664540 AA775711 AA150955 BE465475 AA968994 AA886905 AI141054 AW194991 AA252147 AA319500 AI184288 AA708749 AA644620 AA652769 AA242975 AA151074 T19890
	416882	162718_1	AI633044 AW016212 AW241143 AA769058 R43272 AW068958 AA210918 AA293774 AI748815 AI763294 AI333114 AI277384 AI088297 AI468477 AI824624 AW165606 AI631751 Z40749 AI984673 AI671316 AA189024 AW235412 BE1784
10	416913	163001_1	AW934714 BE161007 BE162500 AW749902 AW749864 BE162498 BE161005 AA190449 AW513465 BE161006 BE162499
	419544	185760_2	AI909164 AA526337 AA244193 AI909153
	419733	187589_1	AW362955 H59486 AI040666 W60958 W94209 H27231 T84625 H75715 W04957 W63676 AA659693 AA514302 W63789 BE046412 T91396 AI951970 AW044233 N20018 AW563548 T90114 AI139947 AA809643 AA846232 AA581566 AA789002
15	424036	23460_1	AA770588 H15373 AW161070 BE304523 BE378517 AA969300 AA904029 BE254211 AA449148 AI268420 AI300495 AI215637 AI300494 AI268551 AA928971 AA179427 AA947684 BE393792 H98018 AI885781 AI188567 AI290658 C15404
	426413	266650_1	AA377823 AW954494 AI022688
	429258	301917_1	AA448765 C04957 C03045 AA668293
	431676	336411_1	AI685464 AW971336 AA513587 AA525142
20	432689	35275_1	AB018320 H55457 AA247916 N83488 N87920 AA095653 T19858 AL134279 AA094167 AI673378 AI000340 R47500 W16595 AW152297 AI625937 AA002027 AI814851 AA902666 AI039729 AW975053 BE302243 AI240793 AI193203 N5581
	438569	46651_1	AF075009 R63109 R63068
	439518	47334_1	W76326 AF06341 W72300
	442677	548626_1	AI557914 W81031 AW473764 AI814081 W81068 AW182826 AW173295 AI376594 AI220500 BE257195 BE246486 R55637 C20788 AI014407 AI248353 AW028015
25	445808	65133_1	AV666234 AW966332 AA340239
	449625	8113_1	NM_014253 AF100772 BE088769 AL022718 BE161779 AW863569 BE161640 AL039060 BE168542 AW295554 AA323193 AA235370 AW779760 N48674 AI375997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T613
	450580	83929_1	N40087 H12925 AA460779 AA095372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816869 AW816940 AW816892 AW816891 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW8
30	453802	981589_1	AL134757 AW079131

TABLE 61C

35

Play:

Ref:

Strand:

Nt position:

Unique number corresponding to an Eos probe/

Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Indicates DNA strand from which exons were predicted.

Indicates nucleotide positions of predicted exons.

40

Play

Ref

Strand

Nt position

401197

9719706

Plus

176341-176452

401519

6649315

Plus

157315-157950

401558

7139678

Plus

103510-104090

402802

3287156

Minus

53242-53432

403047

3540153

Minus

59793-59958

404641

9796810

Minus

32247-32382

405685

4508129

Minus

37956-38097

406068

9114084

Plus

382-543

45

50

Table 62A lists about 600 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 3.0. The "average" prostate cancer level was set to the 75th percentile amongst prostate cancers. The "average" normal prostate tissue level was set to the 95th percentile amongst normal prostate tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 62A: ABOUT 600 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL PROSTATE TISSUES

60

Pkey: Unique Eos probe/identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of prostate tumor to normal prostate tissue

65

Pkey	ExAccn	UnigeneID	Unigene Title	R1
444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	42.2
421566	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	26.5
427274	NM_006211	Hs.174142	colony stimulating factor 1 receptor, fo	16.0
420729	AW964897	Hs.290825	ESTs	16.8
412326	R07566	Hs.73817	small inducible cytokine A3 (homologous	14.7
416188	BE157280	Hs.79070	v-myo avian myelocytomatosis viral oncog	13.6
417696	BE241624	Hs.82401	CD69 antigen (p60, early T-cell activat	13.1
424247	X14008	Hs.234734	lysozyme (renal amyloidosis)	12.6
401197			ENSP00000229263~HSPC213.	12.6
426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	12.6
450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-prop	12.4
449156	AF103907	Hs.171363	prostate cancer antigen 3, non-coding DD	12.3
443271	BE568568	Hs.195704	ESTs	11.6
434078	AW880709	Hs.283683	chromosome 8 open reading frame 4	11.2
423396	AI382555	Hs.127950	bromodomain-containing 1	11.2

70

75

80

	406038	Y14443		zinc finger protein 200	11.1
	426559	AB001914	Hs.170414	paired basic amino acid cleaving system	10.6
	419563	N34145	Hs.10177	ESTs, Moderately similar to ZN91_HUMAN Z	10.4
5	418036	Z37976	Hs.83337	latent transforming growth factor beta b	10.3
	410023	AB017169	Hs.57929	sit (Drosophila) homolog 3	10.1
	421684	BE281591	Hs.106768	hypothetical protein FLJ10511	9.9
	426490	NM_001621	Hs.170087	aryl hydrocarbon receptor	9.9
	437866	AA156781		metallothionein 1E (functional)	9.5
	440274	R24595	Hs.7122	scrapie responsive protein 1	9.4
10	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	9.4
	405141	Y14443		zinc finger protein 200	9.2
	448520	AB002367	Hs.21355	doublecortin and CaM kinase-like 1	9.2
	417315	AI080042	Hs.180450	ribosomal protein S24	9.0
	433332	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	9.0
15	456614	AV553110	Hs.106650	hypothetical protein FLJ20533	8.9
	427019	AA001732	Hs.173233	hypothetical protein FLJ10970	8.9
	432606	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	8.8
	417381	AF164142	Hs.82042	solute carrier family 23 (nucleobase tra	8.6
	425174	D87450	Hs.154978	KIAA0261 protein	8.6
20	445701	AF055681	Hs.13131	lymphocyte adaptor protein	8.5
	416182	NM_004354	Hs.79069	cyclin G2	8.4
	445230	U97018	Hs.12451	echinoderm microtubule-associated protel	8.4
	421913	AI934365	Hs.109439	osteoglycin (osteoclast-inductive factor, mime	8.4
	434217	AW014795	Hs.23349	ESTs	8.3
25	417363	AW129357	Hs.328700	ESTs	8.3
	425782	U86468	Hs.159525	cell growth regulatory with EF-hand doma	8.3
	442501	AA315267	Hs.23128	ESTs	8.3
	429503	AA394183	Hs.26873	ESTs	8.2
30	429984	AL050102	Hs.227209	hypothetical protein FLJ21617	8.1
	443837	AI954625	Hs.9884	spindle pole body protein	8.0
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	8.0
	444880	AW118683	Hs.154150	ESTs	7.9
	417407	AA923278	Hs.290905	ESTs, Weakly similar to protease [H.sapi	7.9
	436962	AW377314	Hs.5364	DKFZP564I052 protein	7.9
35	450313	AI038989	Hs.332633	Bardet-Biedl syndrome 2	7.6
	420120	AL049510	Hs.95243	transcription elongation factor A (SII)-	7.5
	438613	C05569	Hs.243122	hypothetical protein FLJ13057 similar to	7.4
	419078	M93119	Hs.89584	insulinoma-associated 1	7.4
40	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	7.3
	451900	AB023199	Hs.27207	KIAA0862 protein	7.3
	447769	AW873704	Hs.320831	Homo sapiens cDNA FLJ14597 fis, clone NT	7.3
	452436	BE077546	Hs.31447	ESTs, Moderately similar to A46010 X-in	7.3
	452359	BE167229	Hs.29206	hypothetical protein MGC14376	7.2
45	425018	BE245277	Hs.154196	E4F transcription factor 1	7.2
	447737	AK000543	Hs.19404	DKFZP564L0862 protein	7.2
	424897	D63216	Hs.153684	frizzled-related protein	7.1
	433867	AK000596	Hs.3618	hippocampal-like 1	7.1
	427308	D26067	Hs.174905	KIAA0033 protein	7.1
50	432359	AA078049	Hs.274415	Homo sapiens cDNA FLJ10229 fis, clone HE	7.0
	452221	C21322	Hs.288057	hypothetical protein FLJ22242	7.0
	416051	AA835868	Hs.25253	mannosidase, alpha, class 1A, member 1	6.9
	421181	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	6.9
	448076	AJ133123	Hs.20198	adenylate cyclase 9	6.9
55	426769	AI580401	Hs.21213	ESTs	6.8
	416292	AA178233	Hs.42390	nasopharyngeal carcinoma susceptibility	6.8
	417302	BE245812	Hs.8941	ESTs	6.8
	417022	NM_014737	Hs.80905	Ras association (RelGDS/AF-6) domain fam	6.7
	451957	AI786320	Hs.10299	Homo sapiens cDNA FLJ13545 fis, clone PL	6.7
60	452859	AI300555	Hs.288158	hypothetical protein FLJ23591	6.7
	413431	AW246428	Hs.75355	ubiquitin-conjugating enzyme E2N (homolo	6.7
	408405	AK001332	Hs.44672	hypothetical protein FLJ10470	6.7
	421552	AF026692	Hs.105700	secreted frizzled-related protein 4	6.6
	426108	AA822037	Hs.166468	programmed cell death 5	6.6
65	429490	AI971131	Hs.23889	ESTs, Weakly similar to ALU7_HUMAN ALU S	6.6
	454219	X75042	Hs.44313	v-rel avian reticuloendotheliosis viral	6.5
	443020	AI350058	Hs.106129	ESTs	6.5
	415762	BE314524	Hs.78776	putative transmembrane protein	6.4
	412482	AI499930	Hs.334885	mitochondrial GTP binding protein	6.4
70	417880	BE241595	Hs.82848	selectin L (lymphocyte adhesion molecule	6.4
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	6.4
	448019	AW947164	Hs.196641	ESTs, Moderately similar to I38022 hypot	6.3
	408799	D11928	Hs.76845	phosphoserine phosphatase-like	6.3
	424308	AW975531	Hs.154443	mitochondrion maintenance deficient (S.	6.3
75	411373	BE326276	Hs.8861	ESTs	6.3
	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	6.2
	422583	AA410506	Hs.27973	KIAA0674 protein	6.2
	418196	AI745649	Hs.26549	KIAA1708 protein	6.1
	438209	AL120859	Hs.6111	aryl-hydrocarbon receptor nuclear transi	6.1
80	437147	AL049964	Hs.8358	hypothetical protein FLJ20366	6.0
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	6.0
	446896	T15767	Hs.22452	Homo sapiens mRNA for KIAA1737 protein,	6.0
	408242	AA251594	Hs.43913	PIBF1 gene product	5.9
	447985	AW292577	Hs.94446	ESTs	5.9

5	449118	R67477	Hs.23103	Bel1 (S. cerevisiae) homolog	5.9
	427472	AA522539	Hs.131250	transposon-derived Buster3 transposase-1	5.9
	431548	A1834273	Hs.9711	novel protein	5.8
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	5.8
	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	5.8
10	414734	AA151712	Hs.82572	ESTs	5.8
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	5.8
	419047	AW952771	Hs.90043	ESTs	5.8
	435080	A1831760	Hs.155111	hypothetical protein FLJ14428	5.8
	445715	AB012958	Hs.13137	UV radiation resistance associated gene	5.8
15	422538	NM_006441	Hs.118131	5,10-methylenetetrahydrofolate synthetase	5.7
	431055	AL157845	Hs.48783	sialyltransferase 6 (N-acetylglucosaminid	5.7
	434540	NM_016045	Hs.3945	CGI-107 protein	5.7
	452144	AA032197	Hs.102558	Homo sapiens, clone MGC:5352, mRNA, comp	5.7
	407938	AA050597	Hs.85050	phospholamban	5.7
20	445467	A1239832	Hs.15617	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.6
	414812	X72755	Hs.77367	monokine induced by gamma interferon	5.6
	448552	AW973653	Hs.20104	hypothetical protein FLJ00052	5.6
	408672	M26041	Hs.198253	major histocompatibility complex, class	5.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (5.6
25	453942	AW190920	Hs.19928	hypothetical protein SP329	5.5
	416619	AF013168	Hs.79393	tuberous sclerosis 1	5.5
	432485	N90865	Hs.276770	CDW52 antigen (CAMPATH-1 antigen)	5.5
	414516	A1307802	Hs.135660	ESTs, Weakly similar to T43458 hypotheti	5.5
	414343	AL036166	Hs.323378	coated vesicle membrane protein	5.4
30	412490	AW803564	Hs.288850	Homo sapiens cDNA: FLJ22528 fls, clone H	5.4
	416384	AU076903	Hs.79283	selectin P ligand	5.4
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (undulin)	5.4
	458079	A1798870	Hs.54277	DNA segment on chromosome X (unique) 992	5.4
	451684	AF216751	Hs.26813	CDA14	5.4
35	418758	AW859311	Hs.172012	hypothetical protein DKFZp434J037	5.4
	445757	AW449065	Hs.13264	KIAA0856 protein	5.4
	449807	AA004825	Hs.103281	ESTs	5.4
	419159	AW874945	Hs.268049	hypothetical protein	5.3
	421470	R27496	Hs.1378	annexin A3	5.3
40	411486	N85785	Hs.181165	eukaryotic translation elongation factor	5.3
	429568	A088591	Hs.208414	Homo sapiens mRNA; cDNA DKFZp564D0472 (f	5.3
	403851			C5002154*.gij7289015[gb]AA54217.1 (AEO	5.3
	428839	A1767756	Hs.82302	Homo sapiens cDNA FLJ14814 fls, clone NT	5.3
	417426	NM_002291	Hs.82124	laminin, beta 1	5.3
45	424624	AB032947	Hs.151301	Ca2+-dependent activator protein for secr	5.3
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	5.3
	436476	AA326108	Hs.33829	bHLH protein DEC2	5.3
	422746	NM_004484	Hs.119651	glypican 3	5.2
	437571	AA760894	Hs.163023	ESTs	5.2
50	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	5.2
	446985	AL038704	Hs.156827	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	447072	D61594	Hs.17279	tyrosylprotein sulfotransferase 1	5.2
	449969	AW295142	Hs.180187	Homo sapiens cDNA FLJ14337 fls, clone PL	5.2
	453204	R10799	Hs.191990	ESTs	5.2
55	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	5.1
	438510	AL080220	Hs.6265	DKFZP586P0123 protein	5.1
	444917	R68651	Hs.144997	ESTs	5.1
	414212	AA136589	Hs.10848	KIAA0187 gene product	5.1
	451593	AF151879	Hs.26706	CGI-121 protein	5.1
60	417318	AW953837	Hs.240845	ESTs	5.1
	444172	BE147740	Hs.104558	ESTs, Moderately similar to I38022 hypot	5.1
	433600	R42833	Hs.22232	ESTs	5.0
	434170	AA826509	Hs.122329	ESTs	5.0
	424090	X99699	Hs.139262	XIAP associated factor-1	5.0
65	408331	NM_007240	Hs.44229	dual specificity phosphatase 12	5.0
	435706	W31254	Hs.7045	GL004 protein	5.0
	417421	AL138201	Hs.82120	nuclear receptor subfamily 4, group A, m	5.0
	432897	AF155089	Hs.279780	NY-REN-18 antigen	5.0
	433560	A1925195	Hs.130891	hypothetical protein MGC4400	5.0
70	410762	AF228053	Hs.86170	HSKM-B protein	5.0
	421823	N40850	Hs.28626	ESTs	5.0
	417094	NM_006895	Hs.81182	histamine N-methyltransferase	4.9
	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	4.9
	451244	AW008798	Hs.343877	hypothetical protein FLJ20039	4.9
75	453370	A1470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	4.9
	424259	AK001776	Hs.143954	hypothetical protein FLJ10814	4.9
	434094	AA305599	Hs.238205	hypothetical protein PRO2013	4.9
	452323	W44358	Hs.292812	ESTs, Weakly similar to T33468 hypotheti	4.9
	437446	AA788946	Hs.101302	ESTs, Moderately similar to CA1C RAT COL	4.9
80	411352	NM_002890	Hs.758	RAS p21 protein activator (GTPase activa	4.8
	443062	N77999	Hs.8963	Homo sapiens mRNA full length insert cDN	4.8
	425242	D13635	Hs.155287	KIAA0010 gene product	4.8
	445800	AA128419	Hs.32944	inositol polyphosphate-4-phosphatase, ty	4.8
	439024	R96696	Hs.35598	ESTs	4.8
	407235	D20569	Hs.169407	SAC2 (suppressor of actin mutations 2, y	4.8
	430835	AW072916		zinc finger protein 131 (clone p12-10)	4.7
	412953	Z45794	Hs.238809	ESTs	4.7

	413450	Z99716	Hs.75372	N-acetylgalactosaminidase, alpha-	4.7
	421863	A952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	4.7
	437916	BE568249	Hs.20899	hypothetical protein FLJ23142	4.7
5	451952	AL120173	Hs.301863	ESTs	4.7
	416155	AJ807264	Hs.205442	ESTs, Weakly similar to T34036 hypotheti	4.7
	451831	NM_001674	Hs.460	activating transcription factor 3	4.7
	414522	AW518944	Hs.76325	step II splicing factor SLU7	4.7
	427176	AW381569	Hs.40334	ESTs	4.7
10	441390	A1692560	Hs.131175	ESTs	4.7
	447382	AW027790	Hs.182261	ESTs	4.7
	431676	A1685464		gb:188104.x1 NCL_CGAP_Py28 Homo sapiens	4.7
	422241	Y00062	Hs.170121	protein tyrosine phosphatase, receptor t	4.7
	452242	R50956	Hs.159993	glycosyltransferase	4.7
15	401519			C150004767.gij 12737279[ref XP_012163.1	4.6
	414342	AA742181	Hs.75912	KIAA0257 protein	4.6
	426197	AA004410	Hs.100009	acyl-Coenzyme A oxidase 1, palmitoyl	4.6
	429467	NM_004477	Hs.203772	FSHD region gene 1	4.6
	414341	O80004	Hs.75909	KIAA0182 protein	4.6
20	408380	AF123050	Hs.44532	dubiquitin	4.6
	431393	AW971493	Hs.134269	ESTs, Highly similar to cytokine recepto	4.6
	425807	AA365752	Hs.155966	ESTs	4.6
	419111	AA234172	Hs.137418	ESTs	4.6
	425840	AW978731	Hs.301824	hypothetical protein PRO1331	4.6
25	414020	NM_002984	Hs.75703	small inducible cytokine A4 (homologous	4.5
	427078	A1676082	Hs.111902	ESTs	4.5
	419326	W94915	Hs.42419	ESTs	4.5
	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fls, clone L	4.5
30	408705	AA312135	Hs.48967	HSPCO34 protein	4.5
	429250	H56586	Hs.196308	tryptophan rich basic protein	4.5
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	4.5
	449673	AA002064	Hs.18920	ESTs	4.5
	438440	AA807228	Hs.225161	ESTs	4.5
	427210	BE396283	Hs.173987	eukaryotic translation initiation factor	4.5
35	428673	AW601325	Hs.337757	Homo sapiens mRNA; cDNA DKFZp586M063 (fr	4.5
	456874	M12529	Hs.169401	apolipoprotein E	4.4
	416814	AW192307	Hs.80042	dolichyl-P-Glc:Man9GlcNAc2-PP-dolichylgl	4.4
	443123	AA094538	Hs.272808	putative transcription regulation nuclea	4.4
	436420	AA443966	Hs.31595	ESTs	4.4
40	443250	A1041630	Hs.132107	ESTs	4.4
	411952	AA099050		gb:zk85d12.r1 Soares_pregnanLuterus_NbH	4.4
	423645	AP000692	Hs.129781	chromosome 21 open reading frame 5	4.4
	423698	AA328798	Hs.1098	DKFZp434J1813 protein	4.4
	423641	AL137256	Hs.130489	ATPase, aminophospholipid transporter-II	4.4
45	430259	BE560182	Hs.127826	RaLGEF-like protein 3, mouse homolog	4.4
	453787	AB011792	Hs.36094	extracellular matrix protein 2, female o	4.4
	428328	AA426080	Hs.98489	ESTs, Weakly similar to I38022 hypotheti	4.4
	442281	N34742	Hs.170066	Homo sapiens cDNA FLJ13492 fls, clone PL	4.4
	438446	AW016809	Hs.119021	ESTs	4.3
50	450704	H85157	Hs.40696	ESTs	4.3
	438666	AW014403	Hs.128727	ESTs	4.3
	417308	H60720	Hs.81892	KIAA0101 gene product	4.3
	428626	AL046842	Hs.194019	atractin	4.3
	442122	AW503976	Hs.10849	basement membrane-induced gene	4.3
55	447188	H65423	Hs.17631	hypothetical protein DKFZp434E2135	4.3
	447858	AW080339	Hs.80426	ESTs	4.3
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	4.3
	426827	AW087805	Hs.172665	methyltetrahydrofolate dehydrogenase	4.3
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-II	4.3
60	425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ122743 fls, clone H	4.3
	417986	AA481003	Hs.97128	ESTs	4.3
	438828	AL134275	Hs.6434	hypothetical protein DKFZp761F2014	4.3
	408086	AW157022	Hs.343551	hypothetical protein FLJ22584	4.3
	410853	H04588	Hs.30469	ESTs	4.3
65	414002	NM_006732	Hs.75678	FBJ murine osteosarcoma viral oncogene h	4.2
	431318	AA502700	Hs.293147	ESTs, Moderately similar to A46010 X-link	4.2
	406654	AA836381	Hs.315111	nuclear receptor co-repressor/HDAC3 comp	4.2
	416782	L35035	Hs.79886	ribose 5-phosphate isomerase A (ribose 5	4.2
	418701	AA814848	Hs.96343	ESTs, Weakly similar to ALUC_HUMAN IIII	4.2
70	419083	AM79560	Hs.98613	Homo sapiens cDNA FLJ12292 fls, clone MA	4.2
	429900	AA460421	Hs.30875	ESTs	4.2
	437672	AW748265	Hs.5741	flavohemoprotein b57	4.2
	439518	W76326		gb:zd60d04.r1 Soares_fetal_heart_NbHH19W	4.2
	450661	AW952160	Hs.146550	ESTs	4.2
75	443907	AU076484	Hs.9963	TYRO protein tyrosine kinase binding pro	4.2
	409151	AA305105	Hs.50785	SEC22, vesicle trafficking protein (S. c	4.2
	430868	AW972830		gb:EST384925 MAGE resequences, MAGL Homo	4.2
	456804	A1421645	Hs.139851	caveolin 2	4.2
	414291	A1289619	Hs.13040	G protein-coupled receptor 86	4.2
80	420544	AA877577	Hs.98732	Homo sapiens Chromosome 16 BAC clones CIT	4.2
	448430	AJ500642	Hs.289067	Homo sapiens cDNA FLJ11404 fls, clone HE	4.2
	429570	BE242256	Hs.2441	KIAA0022 gene product	4.2
	444100	AA383343	Hs.22116	CDC14 (cell division cycle 14, S. cerevi	4.2
	443622	A1911527	Hs.11805	ESTs	4.1

	436576	AM58213	Hs.77542	ESTs	4.1
	443958	BE241880	Hs.10029	cathepsin C	4.1
	410037	AB020725	Hs.58009	KIAA0918 protein	4.1
5	411968	AI207410	Hs.69280	Homo sapiens, clone IMAGE:3636299, mRNA,	4.1
	421129	BE439899	Hs.89271	ESTs	4.1
	421492	BE176890	Hs.104916	hypothetical protein FLJ21940	4.1
	428966	AF059214	Hs.194687	cholesterol 25-hydroxylase	4.1
	430363	AI851854	Hs.210778	hypothetical protein FLJ10989	4.1
10	431475	AI567669	Hs.40342	putative nuclear protein	4.1
	448468	AI765890	Hs.16341	MAWD binding protein	4.1
	448664	AI879317	Hs.334691	splicing factor 3a, subunit 1, 120kD	4.1
	404390			Target Exon	4.1
	408815	AW957974	Hs.25485	hypothetical protein FLJ22341	4.1
15	417512	X76534	Hs.82226	glycoprotein (transmembrane) nmh	4.1
	414888	AL039185	Hs.77558	thyroid hormone receptor interactor 7	4.1
	418295	AW970043	Hs.236039	hypothetical protein FLJ11090	4.1
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	4.1
	433887	AW204232	Hs.278522	ESTs	4.1
20	436566	AI364997	Hs.7572	ESTs	4.1
	430157	BE348706	Hs.278543	ESTs	4.1
	451259	NM_006052	Hs.25146	Down syndrome critical region gene 3	4.1
	458776	AV654978	Hs.19304	cystathionase (cystathionine gamma-lyase	4.1
	400301	X03635	Hs.1657	estrogen receptor 1	4.1
25	443546	AI085198	Hs.164226	ESTs	4.1
	451491	AI972094	Hs.286221	Homo sapiens cDNA FLJ13741 fis, clone PL	4.1
	452234	AW084176	Hs.223295	ESTs, Weakly similar to I36022 hypotheti	4.1
	430389	AL117429	Hs.240845	DKFZP434D146 protein	4.0
	413275	W94748	Hs.48821	ESTs	4.0
30	418432	M14156	Hs.85112	Insulin-like growth factor 1 (somatomedi	4.0
	432261	R42216	Hs.12342	Homo sapiens clone 24538 mRNA sequence	4.0
	433409	AI278802	Hs.25661	ESTs	4.0
	452185	AA120761	Hs.28307	WW domain binding protein 4 (formin bind	4.0
	417187	AB011151	Hs.334659	hypothetical protein MGC14139	4.0
35	421921	H83363	Hs.6820	translocase of inner mitochondrial membr	4.0
	447247	AW369351	Hs.287955	Homo sapiens cDNA FLJ13090 fis, clone NT	4.0
	415710	J04543	Hs.78637	annexin A7	4.0
	457794	AA688282	Hs.246850	ESTs	4.0
	451124	AI186203	Hs.31432	cardiac ankyrin repeat protein	4.0
40	424401	H87220	Hs.169881	death effector domain-containing	4.0
	435905	AW997484	Hs.5003	KIAA0458 protein	4.0
	442731	AI868167	Hs.131044	ESTs	4.0
	418650	BE386750	Hs.86978	prolyl endopeptidase	3.9
	423749	U09948	Hs.132390	zinc finger protein 36 (KOX 18)	3.9
45	439394	AA149250	Hs.56105	ESTs	3.9
	442287	AW952703	Hs.8182	synaptic nuclei expressed gene 1b	3.9
	436758	AW977167	Hs.155272	ESTs	3.9
	451030	H40587	Hs.181426	ESTs, Moderately similar to YSHUT threon	3.9
	406934			Target Exon	3.9
50	439231	AW581935	Hs.141480	Homo sapiens mRNA; cDNA DKFZp434N079 (fr	3.9
	444765	AA431791	Hs.113823	ClpX (caseinolytic protease X, E. coli)	3.9
	447276	AL049795	Hs.17987	hypothetical protein MGC1203	3.9
	431912	AI660552	Hs.76549	ESTs, Weakly similar to A56154 Abi subst	3.9
	428493	AK001745	Hs.184628	hypothetical protein FLJ10883	3.9
55	412978	AI431708	Hs.820	homeo box C6	3.9
	414962	AF273304	Hs.235376	XPMC2 protein	3.9
	447482	AB033059	Hs.18705	KIAA1233 protein	3.9
	449590	AA694070	Hs.268835	ESTs	3.9
	450203	AF097994	Hs.301528	L-kynurenine:alpha-aminoacidipate aminotra	3.9
60	450699	T77447	Hs.177864	ESTs	3.9
	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	3.8
	452588	AA889120	Hs.110637	homeo box A10	3.8
	422661	NM_014700	Hs.119004	KIAA0885 gene product	3.8
	437231	BE303000	Hs.288929	hypothetical protein FLJ13258 similar to	3.8
65	450505	NM_004460		fibroblast activation protein, alpha	3.8
	407317	AI204033	Hs.271461	ESTs, Weakly similar to I38022 hypotheti	3.8
	410330	AW023630	Hs.159425	ESTs	3.8
	444143	AW747996	Hs.160999	ESTs, Moderately similar to A56194 throm	3.8
	416156	X84908	Hs.78080	phosphorylase kinase, beta	3.8
70	422976	AA347720	Hs.122569	KIAA0264 protein	3.8
	403100			C2001027-g[17296271]gb AAFS1562.1 (AE0	3.8
	422449	AF168418	Hs.116784	thyroid hormone receptor interactor 4	3.8
	424163	NM_007071	Hs.142245	HERV-H LTR-associating 3	3.8
	424808	AA382523	Hs.105689	MSTP031 protein	3.8
75	425878	AW964806	Hs.38085	Homo sapiens, Similar to RIKEN cDNA 0610	3.8
	432363	AA534489		gbcn776g11.s1 NCI_CGAP_Co3 Homo sapiens	3.8
	443441	AW291196	Hs.02195	ESTs	3.8
	432529	AI989507	Hs.162245	ESTs	3.8
	432908	AI861895	Hs.304506	ESTs	3.8
80	424723	BE409813	Hs.152337	protein arginine N-methyltransferase 3(h	3.8
	424855	AW204725	Hs.25560	ESTs	3.8
	414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	3.8
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	3.8
	421828	AW891965	Hs.279789	histone deacetylase 3	3.8

	451524	AK001466	Hs.26516	hypothetical protein FLJ10604	3.8
	418821	AA436002	Hs.183161	ESTs	3.8
	422049	W25760	Hs.77631	glycine cleavage system protein H (amino	3.8
5	453160	AI263307	Hs.239884	H2B histone family, member L	3.8
	416072	AL110370	Hs.79000	growth associated protein 43	3.7
	424906	AI566086	Hs.153716	Homo sapiens mRNA for Hmab33 protein, 3'	3.7
	446554	AA151730	Hs.301769	nucleic acid diphosphate linked moi	3.7
	449523	NM_000579	Hs.54443	chemokine (C-C motif) receptor 5	3.7
10	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	3.7
	417348	AI940507	Hs.318526	hypothetical protein FLJ12661	3.7
	430289	AK001952	Hs.238039	hypothetical protein FLJ11090	3.7
	435401	R44477	Hs.10056	hypothetical protein FLJ14621	3.7
	448807	AI571940	Hs.7549	ESTs	3.7
15	413403	AA129105	Hs.188425	ESTs, Moderately similar to S65657 alpha	3.7
	418323	NM_002118	Hs.1162	major histocompatibility complex, class	3.7
	449125	AI671439	Hs.196029	Homo sapiens mRNA for KIAA1657 protein,	3.7
	408089	H59799	Hs.42644	thioredoxin-like	3.7
	428242	H55709	Hs.2250	leukemia inhibitory factor (cholinergic	3.7
20	439209	AF087593	Hs.91954	ESTs	3.6
	434927	I46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	3.6
	431735	AW977724	Hs.75968	thymosin, beta 4, X chromosome	3.6
	456619	AV647917	Hs.107153	inhibitor of growth family, member 1-like	3.6
	458082	AW978811	Hs.314451	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
25	411213	AA676939	Hs.69285	neuropilin 1	3.6
	414709	AA704703	Hs.77031	Sp2 transcription factor	3.6
	415339	NM_015156	Hs.78398	KIAA0071 protein	3.6
	418203	X54942	Hs.83758	CDC28 protein kinase 2	3.6
	427283	AL119796	Hs.174185	ectonucleotide pyrophosphatase/phosphodi	3.6
30	452260	AA453208		RAB9, member RAS oncogene family	3.6
	439606	AI361238	Hs.41136	ESTs	3.6
	420077	AW512260	Hs.87767	ESTs	3.6
	451009	AA013140	Hs.115707	ESTs	3.6
	436473	AI193122	Hs.132275	ESTs	3.6
35	413198	AW157712	Hs.47534	ESTs, Weakly similar to I38022 hypotheti	3.6
	443067	AI077389	Hs.269818	ESTs, Weakly similar to Z195_HUMAN ZINC	3.6
	452281	T93500	Hs.28792	Homo sapiens cDNA FLJ11041 fis, clone PL	3.6
	452551	AI692181	Hs.49169	KIAA1634 protein	3.6
	433269	AI343543	Hs.126890	ESTs	3.6
40	445817	NM_003642	Hs.13340	histone acetyltransferase 1	3.6
	447033	AI357412	Hs.157601	ESTs	3.6
	414171	AA360328	Hs.885	RAP1A, member of RAS oncogene family	3.6
	427138	N77824	Hs.173717	phosphatidic acid phosphatase type 2B	3.6
	442991	BE281238	Hs.8886	hypothetical protein FLJ20424	3.6
45	434974	AA778711	Hs.4310	eukaryotic translation initiation factor	3.5
	443399	AI452659	Hs.61153	proteasome (prosome, macropain) 26S subu	3.5
	401807			C7001350g1[6578126]b[AAF17706.1]AF0496	3.5
	413979	BE218090	Hs.279453	ESTs	3.5
	414680	AA743331		hemoglobin, alpha 2	3.5
50	417380	T06809	Hs.332086	ESTs	3.5
	425710	AF030880	Hs.159275	solute carrier family, member 4	3.5
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoiet	3.5
	445183	AB007877	Hs.12385	KIAA0417 gene product	3.5
	426831	NM_003416	Hs.2078	zinc finger protein 7 (KIX 4, clone HF.1	3.5
55	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	3.5
	418594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	3.5
	446416	AV658289	Hs.163959	ESTs	3.5
	449008	AW678003	Hs.22826	tropomodulin 3 (ubiquitous)	3.5
	456719	Z43784		ankyrin 3, node of Ranvier (ankyrin G)	3.5
60	432101	AI918950	Hs.123642	EphA3	3.5
	453565	BE298808	Hs.33363	DKFZP434N093 protein	3.5
	449217	AA278536	Hs.23262	ribonuclease, RNase A family, k6	3.5
	412922	M60721	Hs.74870	H2.0 (Drosophila)-like homeo box 1	3.5
	450066	H58499	Hs.252692	ESTs, Weakly similar to I38022 hypotheti	3.5
65	429302	AU076674	Hs.198899	eukaryotic translation initiation factor	3.5
	451246	AW189232	Hs.39140	cutaneous T-cell lymphoma tumor antigen	3.5
	415528	R17236		glycyl12c04.r1 Soares infant brain 1NIB H	3.5
	435513	AW404075	Hs.42785	DC11 protein	3.5
	440843	M78878	Hs.7314	KIAA0614 protein	3.5
70	409065	AW236991	Hs.102495	ESTs, Moderately similar to I38022 hypot	3.5
	439132	H72803	Hs.38363	ESTs	3.5
	451173	AI765082	Hs.48317	ESTs	3.5
	422673	N59027		glycyl59d11.r1 Soares fetal liver spleen	3.4
	401597	AA172106		Rag C protein	3.4
	401744			Target Exon	3.4
75	432723	D29577	Hs.3085	KIAA0054 gene product, Helicase	3.4
	449465	NM_004380	Hs.23598	CREB binding protein (Rubinstein-Taybi s	3.4
	450528	AW382884	Hs.204715	ESTs	3.4
	432125	AW972667		Homo sapiens cDNA FLJ12300 fis, clone MA	3.4
80	435411	AW444619	Hs.138211	ESTs	3.4
	434629	AA789081	Hs.4029	glioma-amplified sequence-41	3.4
	437158	AW090198		KIAA1150 protein	3.4
	416375	H95567	Hs.124700	ESTs	3.4
	419441	AW023731	Hs.274368	MSTP032 protein	3.4

5	432741	AI732358	Hs.185118	ESTs, Moderately similar to A37413 calbl	3.4
	439192	AW970536	Hs.105413	ESTs	3.4
	440474	AI207936	Hs.7195	gamma-aminobutyric acid (GABA) A recepto	3.4
	428456	AF151063	Hs.184456	hypothetical protein	3.4
	447397	BE247676	Hs.18442	E-1 enzyme	3.4
10	426828	NM_000020	Hs.172670	activin A receptor type II-like 1	3.4
	418293	AI224483	Hs.16063	hypothetical protein FLJ21877	3.4
	424779	AI046851	Hs.153053	CD37 antigen	3.4
	415015	NM_002109	Hs.77798	histidyl-tRNA synthetase	3.4
	426900	AK000166	Hs.288809	hypothetical protein FLJ20159	3.4
15	408113	T82427	Hs.194101	Homo sapiens cDNA: FLJ20869 fis, clone A	3.4
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	3.4
	414671	AA832479	Hs.72080	ESTs	3.4
	431689	AA305688	Hs.267695	UDP-Gal:betaGlcNAc beta 1,3-galactosyltr	3.4
	444480	AI150730	Hs.265640	ESTs, Moderately similar to A47582 B-cel	3.4
20	403389			C3001393*gi3327090 dbj BAA31613.1 (AB	3.3
	440749	W22336	Hs.7392	hypothetical protein MGC3198	3.3
	408374	AW025430	Hs.155591	forkhead box F1	3.3
	410494	M36564	Hs.64016	protein S (alpha)	3.3
	426997	BE620738	Hs.173125	peptidyl/prolyl isomerase F (cyclophilin	3.3
25	433505	AW504027	Hs.15301	Homo sapiens cDNA FLJ12596 fis, clone NT	3.3
	400277			Eos Control	3.3
	411031	W37943	Hs.34892	KIAA1323 protein	3.3
	417295	AW893524	Hs.43148	ESTs	3.3
	438459	T49300	Hs.35304	Homo sapiens cDNA FLJ13655 fis, clone PL	3.3
30	432169	Y00971	Hs.2910	phosphoribosyl pyrophosphate synthetase	3.3
	437872	AK002015	Hs.5887	RNA binding motif protein 7	3.3
	443912	R37257	Hs.184780	ESTs	3.3
	445270	AI762154	Hs.54982	Homo sapiens cDNA FLJ14014 fis, clone HE	3.3
	425836	AW855696	Hs.90960	ESTs	3.3
35	414565	AA502972	Hs.183390	hypothetical protein FLJ13590	3.3
	415700	AI963908	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	3.3
	428186	AW504300	Hs.295605	mannosidase, alpha, class 2A, member 2	3.3
	436499	AJ276678	Hs.283102	HEF like Protein	3.3
	448164	R61680	Hs.26904	ESTs, Moderately similar to Z195_HUMAN Z	3.3
40	426848	H72531	Hs.36190	ESTs	3.3
	439653	AW021103	Hs.6831	hypothetical protein FLJ20373	3.3
	450094	AI174947	Hs.295769	Homo sapiens mRNA; cDNA DKFZp564D1164 (f	3.3
	402474			NM_004079:Homo sapiens cathepsin S (CTSS	3.3
	424800	AL035588	Hs.153203	MyoD family inhibitor	3.3
45	430280	AA361258	Hs.237868	interleukin 7 receptor	3.3
	408968	AI852236	Hs.49376	hypothetical protein FLJ20644	3.3
	463648	AL079983	Hs.116774	Integrin, alpha 1	3.3
	451367	AA923729	Hs.26322	cell cycle related kinase	3.2
	444445	AA342329	Hs.115920	Homo sapiens cDNA: FLJ22816 fis, clone K	3.2
50	445472	AB006531	Hs.12784	Homo sapiens mRNA for KIAA0293 gene, par	3.2
	400658			ENSP00000237081*:KIAA1217 PROTEIN (FRAGM	3.2
	408101	AW968504	Hs.123073	CDK2-related protein kinase 7	3.2
	410366	AI267589	Hs.302689	hypothetical protein	3.2
	411048	AK001742	Hs.67991	hypothetical protein DKFZp434G0522	3.2
55	421246	AW582562	Hs.102897	CGI-47 protein	3.2
	422763	AA033699	Hs.83938	ESTs, Moderately similar to MAS2_HUMAN M	3.2
	426227	U67058	Hs.154299	Human proteinase activated receptor-2 mR	3.2
	439047	AW979177		gb:EST391287 MAGE resequences, MAGP Homo	3.2
	444451	AV650179	Hs.282431	ESTs	3.2
60	420568	F09247	Hs.247735	protocadherin alpha 10	3.2
	406973	M34996	Hs.198253	major histocompatibility complex, class	3.2
	402802			NM_001397:Homo sapiens endothelin conver	3.2
	431304	BE157283		gb:RC4-HT0373-130200-011-a03 HT0373 Homo	3.2
	406247			Target Exon	3.2
65	411653	AF070578	Hs.71168	Homo sapiens clone 24674 mRNA sequence	3.2
	412639	AW961284	Hs.296235	ESTs	3.2
	419169	AI336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	3.2
	433561	BE540937	Hs.20104	hypothetical protein FLJ00052	3.2
	436207	AA334774	Hs.12845	hypothetical protein MGC13159	3.2
70	438461	AW075485	Hs.286049	phosphoserine aminotransferase	3.2
	455473	AW984788		gb:RC1-HN0015-120400-021-c07 HN0015 Homo	3.2
	441683	BE564214	Hs.102946	ESTs	3.2
	417386	AL037228	Hs.82043	D123 gene product	3.2
	427288	AW732802	Hs.2132	epidermal growth factor receptor pathway	3.2
75	442355	AA466539	Hs.8262	lysosomal-associated membrane protein 2	3.2
	422473	U94780	Hs.117242	meningioma expressed antigen 6 (coiled-c	3.2
	407816	AW500857	Hs.40137	anaphase-promoting complex 1; meiotic ch	3.2
	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	3.2
	453864	AW021407	Hs.21068	hypothetical protein	3.2
80	449944	AB014805	Hs.22599	atrophin-1 interacting protein 1; activi	3.2
	435129	AI381659	Hs.267086	ESTs	3.2
	424894	HB3520	Hs.153678	reproduction 8	3.2
	416959	D28459	Hs.80512	ubiquitin-conjugating enzyme E2A (RAD6 h	3.2
	410185	BE294068	Hs.737	Immediate early protein	3.2
	451149	AL047586	Hs.10283	RNA binding motif protein 8B	3.2
	410531	AW752953		gb:QVO-CT0224-261099-035-g02 CT0224 Homo	3.2
	411954	AA652523	Hs.269496	ESTs, Weakly similar to I38022 hypotheti	3.2

5	423748	AI149048	Hs.30211	hypothetical protein FLJ22313	3.2
	444489	AI151010	Hs.157774	ESTs	3.2
	453124	AI139058	Hs.125790	leucine-rich repeat-containing 2	3.2
	452413	AW082633	Hs.212715	ESTs	3.1
	409390	AI927212	Hs.3734	ESTs	3.1
10	453078	AF053551	Hs.31584	metaxin 2	3.1
	453024	AW846787		gb:QV3-CT0194-181099-004-e01 CT0194 Homo	3.1
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	3.1
	441124	T97717	Hs.119563	ESTs	3.1
	416128	AA173632		CCG14 (cell division cycle 14, S. cerevi	3.1
15	445101	T75202	Hs.12314	Homo sapiens mRNA; cDNA DKFZp586C1019 (f	3.1
	407949	W21874	Hs.247057	ESTs, Weakly similar to 2109260A B cell	3.1
	413492	D87470	Hs.75400	KIAA0260 protein	3.1
	421044	AF061871	Hs.101302	Human DNA sequence from clone RP1-238D15	3.1
	422603	BE242587	Hs.118651	hematopoietically expressed homeobox	3.1
20	427399	NM_014883	Hs.177664	KIAA0814 gene product	3.1
	434804	AA649530	Hs.348148	gb:ms44R05.s1 NCI_CGAP_Alv1 Homo sapiens	3.1
	442906	AW296888	Hs.170939	ESTs	3.1
	445840	AI277811	Hs.146291	ESTs	3.1
	446084	AL137658	Hs.13768	Homo sapiens mRNA; cDNA DKFZp434I1216 (f	3.1
25	435293	AI040777	Hs.117170	ESTs	3.1
	400750			Target Exon	3.1
	416852	AF283776	Hs.80285	Homo sapiens mRNA; cDNA DKFZp586C1723 (f	3.1
	423666	AW976434	Hs.3623	hypothetical protein FLJ11220	3.1
	409558	BE253407	Hs.72363	Homo sapiens mRNA for FLJ00116 protein,	3.1
30	400194			NM_003763:Homo sapiens syntaxin 16 (STX1	3.1
	400479			Target Exon	3.1
	402895			ENSP00000252117:Myelin transcription fac	3.1
	403423			Target Exon	3.1
	408161	AW952912	Hs.300383	hypothetical protein MGC3032	3.1
35	410886	AW809324		gb:MR4-ST0121-141099-010-G06_1 ST0121 Ho	3.1
	414922	D00723	Hs.77631	glycine cleavage system protein H (amino	3.1
	420121	AW968271	Hs.191534	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
	430519	AF129534	Hs.49210	F-box only protein 4	3.1
	447147	AA910353	Hs.292815	ESTs, Weakly similar to T23482 hypotheti	3.1
40	422481	AL050163	Hs.117339	DNA-X-activation protein 10	3.1
	430467	D87742	Hs.241552	KIAA0268 protein	3.1
	409549	AB029015	Hs.54886	phospholipase C, epsilon 2	3.1
	423554	M90516	Hs.1674	glutamine-fructose-6-phosphate transamin	3.1
	431286	AW263476	Hs.44268	myelin gene expression factor 2	3.1
45	430226	BE245562	Hs.2651	adrenergic, beta-2-, receptor, surface	3.1
	408051	AI623351	Hs.172148	ESTs	3.1
	420090	AA220238	Hs.94986	ribonuclease P (38kD)	3.1
	400295	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	3.1
	414279	AW021691		GCN5 (general control of amino-acid synt	3.1
50	440426	AI159800	Hs.7181	Homo sapiens cDNA FLJ13663 fls, clone PL	3.1
	423872	AB020316	Hs.134015	uronyl 2-sulfotransferase	3.1
	420154	AI093155	Hs.95420	JM27 protein	3.1
	447560	AF065214	Hs.18858	phospholipase A2, group IVC (cytosolic,	3.1
	453293	AA382267	Hs.10653	ESTs	3.1
55	434398	AA121088	Hs.3838	serum-inducible kinase	3.0
	414135	NM_004419	Hs.2128	dual specificity phosphatase 5	3.0
	441527	W19504	Hs.7884	solute carrier family 21 (organic anion	3.0
	423957	AW978309	Hs.136235	Homo sapiens cDNA FLJ13542 fls, clone PL	3.0
	444001	AI095087	Hs.152299	ESTs, Moderately similar to S65657 alpha	3.0
60	411315	AW836547		gb:PM3-LT0032-030100-006-a08 LT0032 Homo	3.0
	414178	AW957372	Hs.46791	ESTs, Weakly similar to I38022 hypotheti	3.0
	441401	AI824338	Hs.126891	ESTs	3.0
	457718	F18572	Hs.22978	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.0
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytotoxicin)	3.0
65	424240	AB023185	Hs.143535	calcium/calmodulin-dependent protein kin	3.0
	447476	BE293486	Hs.20680	ESTs, Weakly similar to I38022 hypotheti	3.0
	419440	AB020689	Hs.90419	KIAA0882 protein	3.0
	421786	AF188653	Hs.21351	ESTs	3.0
	433285	AW975944	Hs.237396	ESTs	3.0
70	409997	AI906055	Hs.57749	synaptic nuclei expressed gene 2; KIAA10	3.0
	417874	BE616160	Hs.82829	protein tyrosine phosphatase, non-recept	3.0
	420956	AA351584	Hs.100543	Homo sapiens clone 24505 mRNA sequence	3.0
	445345	AW003860	Hs.12532	chromosome 1 open reading frame 21	3.0
	450671	AI356967	Hs.43086	ESTs, Weakly similar to A46010 X-linked	3.0
75	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	3.0
	434953	BE049102	Hs.179982	ESTs, Weakly similar to TRHY_HUMAN TRICH	3.0
	436469	AK001455	Hs.5198	Down syndrome critical region gene 2	3.0
	428130	AW444985	Hs.77603	ESTs	3.0
	414839	X83692	Hs.77462	DNA (cytosine-5-)-methyltransferase 1	3.0
80	445784	AI253155	Hs.146065	ESTs	3.0
	446677	AI800311	Hs.156291	ESTs	3.0
	426448	R06054		gb:ye85g07.r1 Soares fetal liver spleen	3.0
	445921	AW016211	Hs.146181	ESTs	3.0
	405673	M34996	Hs.198253	major histocompatibility complex, class	3.0
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	3.0
	427157	U51166	Hs.173824	thymine-DNA glycosylase	3.0
	435907	AW304025	Hs.258397	ESTs	3.0

451102	AA015683	Hs.41185	Homo sapiens mRNA; cDNA DKFZp564O1262 (f	3.0
416882	A1633044		tryptophanyl tRNA synthetase 2 (mitochond	3.0
414052	AW578949	Hs.283552	ESTs, Weakly similar to unnamed protein	3.0
450580	N40087		ESTs	3.0

TABLE 62B

Play: Unique Eos probeset identifier number
 CAT number: Genes cluster number
 Accession: Genbank accession numbers

Play	CAT Number	Accession
410531	1207200_1	AW752953 H88044 BE156092
410886	1225822_1	AW809324 BE144977 BE144956
411315	1238570_1	AW836547 AW836513 AW836587
411962	126744_1	AA099050 AA099526 T47733
414279	143227_1	AW021691 A1537404 R45431 A1333439 A1741845 A1874468 R44190 R52535 R52617 A1220925 A1979148 A1744688 AW242437 AA818148 A1963837 AA399623 A1676204 A1420077 N24944 D51042 AA282766 AA137264 AW236107 AW769 AA743331 AA837388 AW664540 AA775711 AA150965 BE465475 AA968994 AA886905 A1141054 AW194991 AA252147 AA319500 A1184288 AA708749 AA644620 AA652769 AA242975 AA151074 T19880 R17236 R52580 F11642
415528	1539409_1	AA173632 A1174958 AA581361 A1700024 AA173988 BE165417 A1366964
416128	157163_1	A1633044 AW016212 AW241143 AA769058 R43272 AW068958 AA210918 AA293774 A1748815 A1763294 A1333114 A1277384 A1088297 A1468477 A1824624 AW189606 A1631751 Z40749 A184673 A1671316 AA189024 AW235412 BE1784
416882	162718_1	N59027 AA314694 N53937 R08100 R06054 AA376789 AW956453
422673	219674_1	AW072916 A1184913 AA489195 AW466994 AW469044 N59350 A1819642 A1280239 A1220572 AA789302 A1473611 AW841126 D60937
426448	267323_1	AW972830 AA527647 AA489820 AA570362
430935	325772_1	BE167283 BE157287 AA502438
430968	326269_1	A1685464 AW971336 AA513587 AA525142
431304	331286_1	AW972667 AA526539 A1057032 AW167842
431676	336411_1	AA534489 AW970240 AW970323
432125	341776_1	AW090198 AW173544 AW439860 AW007307 A1762577 W86516 AA160485 AA974203 A1589521 AW451857 AW450602 A1702529 AA630766
432363	345469_1	A1801808 AW611634 A1393606 AW235355 AW000736 AW468599 A1582546 AA962057 AA523012 AW51
437158	43392_5	AA156781 AW233839 U52054 AA024963 AA778446 BE073977 AW444904 AW602574 BE164040 BE164012 BE163972 BE163974 BE163992
437866	44433_2	AA837481 AW468444 BE185091 AW468002 AA687333 AA811830 AA581806 A1866686 A1572124 AA04
439047	468139_1	AW979177 AA846994 AA829672
439518	47334_1	W76328 AFD86341 W72300
450508	836_1	NM_004480 U09278 U76833 AW630065 AW471133 C02434 W45237 AW793518 BE070112 A1587478 A1624429 AW190535 A1446661 A1478772
450580	83929_1	AW022667 AA528235 AA599775 AW613820 A1435793 AW594230 A1051768 A1200108 A1680295
452260	9074_1	N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816869 AW816840
453024	944876_28	AW816892 AW816841 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW8
455473	1292917_1	AA453208 NM_004251 U44103 A1571547 N57463 AW007521 A1479232 T82809 R57109 AW796099 A1633027 A1765395 A1763029 A1758228
456719	222707_1	BE326331 A1934576 A1922378 AW276431 A1718465 N36566 AA904753 BE464245 A1338752 A1
		AW846787 AW803370 AW903378 AW752032 AW839052 AW839051 AW839054 AW839058 AW903374 AW839045 AW903373 AW903352
		AW839043 AW839049 AW903372 AW846755 AW846767 AW903368 AW846766 BE146826 AW839056 AW846802 AW
		AW984788 AW984816 AW984811 AW984807 AW984819 AW984790 AW984782 AW984784 AW984780 AW984814 AW984795 AW984793
		AW984789 AW984823 AW984801 AW984802 AW984800 AW984799 AW984825 AW984782 AW984821 AW984820 AW
		Z43784 R13382 AW572911 AA449369 H17037 R19603 A1632555 AW004030 BE502530 Z25032 AA805324 AA449241 A1651825 A1264883
		AW196918 AA948267 A1853735 A1263703 AA319159 AW964436 A1803440 AW594171 A1867447 AW2

TABLE 62C

Play: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Play	Ref	Strand	Nt_position
400479	8439786	Minus	115386-116348
400658	8118459	Minus	73525-73644
400750	8119067	Plus	198991-199188, 199316-199548
401197	9719706	Plus	178341-178452
401519	6649315	Plus	157315-157950
401597	3293210	Plus	65838-68031
401744	2576349	Plus	14595-14751
401807	7331538	Plus	152325-152912
402474	7547175	Minus	53528-53528, 55765-55920, 57530-57757
402802	3287156	Minus	53242-53432
402895	9967547	Plus	85537-85671, 86379-86469
403100	8954402	Minus	13683-13874
403389	9438331	Minus	163415-163634
403423	7105492	Plus	68340-68615
403851	7708872	Plus	22733-23007
404390	8887030	Minus	39524-40072
405141	8980911	Plus	99861-100054
405934	6758795	Plus	159913-160606
406038	8388537	Plus	37764-37877
406247	7417725	Minus	46234-46461

Table 63A lists about 366 genes significantly down-regulated in prostate cancer compared to normal prostate. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" normal prostate to "average" prostate cancer tissues was greater than or equal to 2.5. The "average" normal prostate level was set to the 75th percentile of normal prostate tissues. The "average" prostate cancer level was set to the 75th percentile amongst tumor samples. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst all the tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 63A: ABOUT 366 GENES SIGNIFICANTLY DOWN-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL PROSTATE

Pkey:	Unique Eos probeset identifier number			
ExAccn:	Exemplar Accession number, Genbank accession number			
UnigeneID:	Unigene number			
Unigene Title:	Unigene gene title			
R1:	Ratio of normal prostate tissue to prostate tumor tissue			
Pkey	ExAccn	Unigene ID	Unigene Title	R1
425932	M91650	Hs.1968	semonogelin I	89.4
407245	X90568	Hs.172004	titin	35.4
425545	N98529	Hs.158295	Homo sapiens, clone MGC12401, mRNA, com	32.2
426752	X69490	Hs.172004	titin	29.5
400440	X63957	Hs.83870	nebulin	20.7
412519	AA196241	Hs.73960	troponin T1, skeletal, slow	13.9
413778	AA090235	Hs.75535	myosin, light polypeptide 2, regulatory,	12.0
420813	X51501	Hs.89949	prolactin-induced protein	11.8
416337	Z44881	Hs.9012	ESTs, Weakly similar to S26650 DNA-bind	10.2
407013	U35637		gb:Human nebulin mRNA, partial cds	9.1
433331	AI738815	Hs.117323	ESTs	8.9
432117	AL036195	Hs.2909	protamine 1	8.3
453863	X02544	Hs.572	orosomucoid 1	8.2
431847	AI791314		gb:aa46g12.y5 Stratagene lung carcinoma	7.4
408855	T83061	Hs.319946	Homo sapiens mRNA for KIAA1727 protein,	7.1
448059	AI459021	Hs.170425	ESTs	6.8
403612			Target Exon	6.4
409001	U58195		Interleukin enhancer binding factor 1	6.2
441490	N46901	Hs.266720	ESTs	6.2
435805	AW470260	Hs.48496	ESTs	6.0
401917	AL050149		RAN binding protein 3	5.9
455549	BE065051		gb:RC1-BT0313-110500-017-c04 BT0313 Homo	5.7
450218	R02018	Hs.168640	apoptosis, progressive (mouse) homolog	5.6
404806			Target Exon	5.6
432326	AI280308	Hs.274361	amiloride-sensitive cation channel 2, ne	5.5
459708	AA776881	Hs.168812	Homo sapiens cDNA FLJ14132 fis, clone MA	5.5
440808	AK001339	Hs.7432	hypothetical protein FLJ10477	5.5
458339	AW976853	Hs.172843	ESTs	5.2
454278	AF217525	Hs.49002	Down syndrome cell adhesion molecule	5.2
417032	AA192469	Hs.271838	ESTs	5.2
434352	AF129505	Hs.86492	small muscle protein, X-linked	5.1
439175	AF086021	Hs.271113	ESTs	5.0
439749	AL389942	Hs.157752	Homo sapiens mRNA full length insert cDN	4.9
417364	N73749	Hs.222475	ESTs	4.9
400831			C1100935g 3746443 gb AAC63969.1 (AFO	4.8
416935	AA190712		gb:zp87f09.r1 Stratagene HeLa cell s3 B3	4.8
442082	RA1823	Hs.7413	ESTs	4.8
452625	AA724771	Hs.61425	ESTs	4.7
440955	AI523846	Hs.169859	ESTs	4.7
456815	NM_013348	Hs.144011	potassium inwardly-rectifying channel, su	4.7
430611	AA837120	Hs.156481	ESTs	4.6
415981	R35694		gb:yg67b04.r1 Soares infant brain 1N18 H	4.6
441040	AW449782	Hs.178903	ESTs	4.6
442764	AI762254	Hs.131122	ESTs	4.6
411426	BE141714		gb:QV0-HT0101-061099-032-c04 HT0101 Homo	4.6
433081	Z85986	Hs.188757	Homo sapiens, clone MGC:5564, mRNA, comp	4.6
401896			Target Exon	4.5
445323	AW207282	Hs.213049	ESTs	4.5
456895	AI535663	Hs.39379	ESTs	4.5
417729	Z43798	Hs.6777	ESTs	4.5
431627	AW609720	Hs.265540	HSPC042 protein	4.5
420721	AA927802	Hs.159471	ZAP3 protein	4.4
449519	W04244	Hs.49829	ESTs	4.4
442089	AI801500	Hs.128457	ESTs	4.4
436781	AI914535	Hs.221377	ESTs	4.4
402797			Target Exon	4.4
404267			NM_004346: Homo sapiens runt-related tra	4.3
442931	AI024376	Hs.150473	ESTs	4.3
418626	AW299508	Hs.135230	ESTs	4.3
423772	AA306637		EAP30 subunit of ELL complex	4.3
457136	AA428240	Hs.126083	ESTs	4.3
436404	AW968556	Hs.137240	Homo sapiens mRNA for partial 3'UTR, seq	4.3
456840	AI590296	Hs.174782	ESTs, Weakly similar to KIAA1437 protein	4.3
403649			Target Exon	4.2
435865	AA704538	Hs.119740	ESTs	4.2
423871	AA331806		gb:EST35805 Embryo, 8 week I Homo sapien	4.2

	436190	AK001059		gb:Homo sapiens cDNA FLJ10197 fis, clone	4.2
	400164			Eos Control	4.1
	435519	AJ216950	Hs.125461	hypothetical protein FLJ11539	4.1
5	425094	AJ955956	Hs.21417	ESTs	4.1
	415928	R46799	Hs.23966	ESTs	4.1
	415746	AA167670	Hs.21413	solute carrier family 12, (potassium-chl	4.1
	426663	AK028767	Hs.262603	ESTs	4.1
	453752	AL120800		gb:DKFZp762E152_r1 762 (synonym: hmel2)	4.1
10	404260			Target Exon	4.0
	453412	AJ003290		gb:AJ003290 Selected chromosome 21 cDNA	4.0
	401411			ENSP00000247172*HYPOTHETICAL 126.2 kDa	4.0
	415925	H09474	Hs.202341	Homo sapiens cDNA: FLJ23573 fis, clone L	4.0
	402817	H24186		hypothetical protein	4.0
15	449233	BE048401	Hs.196511	ESTs	3.9
	435457	AA662421	Hs.59125	ESTs	3.9
	444105	AW189097	Hs.166597	ESTs	3.9
	430610	A1821465	Hs.188810	ESTs, Weakly similar to ALU6_HUMAN ALU S	3.9
	411320	AW836646		gb:PM3-LT0032-090100-006-e05 LT0032 Homo	3.8
20	409679	BE250521		ras homolog gene family, member A	3.8
	415386	Z43087		gb:HSC13A121 normalized infant brain cDN	3.8
	446175	AL035568	Hs.291	glutamyl aminopeptidase (aminopeptidase	3.8
	459707	AA631362	Hs.120866	gb:np86b01.s1 NCL_CGAP_Thy1 Homo sapiens	3.8
	406917	X65964		gb:H.sapiens nestin gene.	3.8
25	455887	BE154173		gb:PM1-HT0340-201259-004-f12 HT0340 Homo	3.8
	443313	AF796730	Hs.55513	ESTs	3.8
	452351	AA025647		gb:z85d01.r1 Soares_fetal_heart_NbH189W	3.8
	400489			C10001858:gil[6679124]ref[NP_032759.1] ne	3.7
	411829	AW865749		gb:QV3-SN0021-100500-185-c03 SN0021 Homo	3.7
30	408229	AW176091		gb:QV0-BT0107-250899-007-b08 BT0107 Homo	3.7
	427318	AF186081	Hs.175783	zinc transporter	3.7
	417820	R02530	Hs.191198	ESTs	3.7
	404660			C800841*:gil[12654691]gb[AAH01185.1]AA:10	3.7
	409144	AW341187	Hs.279714	ESTs	3.7
35	438524	AA922236	Hs.221037	ESTs	3.7
	459200	Y09306	Hs.30148	homeodomain-interacting protein kinase 3	3.7
	418833	AW974899	Hs.292776	ESTs	3.7
	424887	AA348112	Hs.259461	ESTs	3.7
	404984			Target Exon	3.7
40	454549	AW806910		gb:QV4-ST0023-160400-172-f04 ST0023 Homo	3.7
	426736	AA431615	Hs.130722	ESTs	3.7
	434562	AA639618	Hs.325116	Homo sapiens, clone MGC:2962, mRNA, comp	3.6
	438040	A122422	Hs.121846	ESTs	3.6
	443618	T82009	Hs.300700	hypothetical protein FLJ20727	3.6
45	442097	AW015789	Hs.128474	ESTs	3.6
	435186	AL119470	Hs.145631	ESTs	3.6
	429853	AB020625	Hs.225949	butyrophilin-like 3	3.6
	456521	AW373450	Hs.286212	hypothetical protein FLJ11729	3.6
	453282	AK000043	Hs.32922	hypothetical protein FLJ20036	3.6
50	400749			NM_003105*:Homo sapiens sortilin-related	3.6
	450295	A1766732	Hs.210628	ESTs	3.5
	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	3.5
	434378	AA631739	Hs.335440	EST	3.5
	421342	AA504749		gb:z853f08.r1 NCL_CGAP_GCB1 Homo sapiens	3.5
55	406704	M21665	Hs.929	myosin, heavy polypeptide 7, cardiac mus	3.5
	428043	A1824977	Hs.145319	ESTs	3.5
	438211	T08401	Hs.290856	ESTs, Moderately similar to ALU4_HUMAN A	3.5
	405258			Target Exon	3.4
	440207	A1371978	Hs.128326	ESTs	3.4
60	445045	A1652676	Hs.147256	ESTs	3.4
	408177			Target Exon	3.4
	438535	L09078		gb:Homo sapiens mRNA fragment	3.4
	405735			ENSP00000252164*:K1AA1578 protein (Fragm	3.4
	445797	A1253414		gb:aq14f04.x1 Stanley Frontal NS pool 2	3.4
65	444286	A1625304	Hs.190312	ESTs	3.4
	442027	A1652928	Hs.126395	ESTs	3.4
	447889	AW469180	Hs.346398	ESTs	3.4
	405152			Target Exon	3.4
	402460			C1001261*:gil[2696979]emb[CAA70854.1] (Y0	3.4
70	448516	AW898585		gb:RC1-NN0073-260400-011-g09 NN0073 Homo	3.4
	450588	AA010319	Hs.60389	ESTs	3.4
	447600	A1420990		ESTs	3.4
	406085			Target Exon	3.3
	417959	AW977642	Hs.291742	ESTs	3.3
75	418672	L44284	Hs.12915	ESTs	3.3
	446593	W79572	Hs.13277	hypothetical protein FLJ22064	3.3
	446516	AW996692	Hs.257557	ESTs, Weakly similar to I38022 hypotheti	3.3
	415896	H08311	Hs.14822	ESTs, Weakly similar to I78885 serine/th	3.3
	410140	AL134435	Hs.247837	neurexin 3	3.3
80	458539	A1733837	Hs.145661	ESTs	3.3
	422399	AW410380	Hs.116056	mesenchymal stem cell protein DSC43	3.3
	413381	BE090690		gb:RC1-BT0720-280300-011-g02 BT0720 Homo	3.3
	429422	AK001494	Hs.202596	Homo sapiens cDNA FLJ10632 fis, clone NT	3.3
	428561	AW973652	Hs.283105	ESTs	3.2

5	445608	AI830851	Hs.200014	ESTs, Weakly similar to ACIDIC PROLINE-R	3.2
	449017	AW002425	Hs.224142	ESTs	3.2
	415908	H08623	Hs.22833	ESTs	3.2
	457733	AW974812	Hs.291971	ESTs	3.2
	449340	AW235786	Hs.195359	hypothetical protein MGC10964	3.2
10	428134	AA421773	Hs.161008	ESTs	3.2
	434407	AW815333		gb:QV0-ST0215-060100-083-g01 ST0215 Homo	3.2
	429973	AM23317	Hs.164680	ESTs	3.2
	418092	R46154	Hs.338439	ESTs	3.2
	411356	H45377		gb:yn99h03.r1 Soares adult brain N2b5HB5	3.1
15	443366	AI053501	Hs.278869	ESTs, Moderately similar to 2109260A B c	3.1
	422069	AJ010063	Hs.343603	ttn-cap (telitronin)	3.1
	420778	AW970512		gb:EST382593 MAGE resequences, MAGK Homo	3.1
	403451			Target Exon	3.1
	451686	AA059246	Hs.110293	ESTs	3.1
20	423837	AW937053	Hs.276150	gb:PM3-DY0037-231299-001-g11 DT0037 Homo	3.1
	422731	AL138411		gb:DKFZp434A1229_r1 434 (synonym: htes3)	3.1
	450049	AI681234	Hs.258509	EST	3.1
	428656	AB037798	Hs.188790	KIAA1377 protein	3.1
	401278			Target Exon	3.1
25	418087	AA961813	Hs.127838	ESTs	3.1
	421813	BE048255		gb:z49b05.y1 NCL_CGAP_Brn52 Homo sapien	3.1
	402490			Target Exon	3.1
	448001	AW283237	Hs.202037	ESTs	3.1
	445316	AI219833	Hs.186767	ESTs	3.1
30	405150			Target Exon	3.1
	413784	BE165819	Hs.207684	ESTs	3.1
	425198	AA352090	Hs.128003	hypothetical protein FLJ21213	3.1
	433224	ABD40919	Hs.210958	KIAA1486 protein	3.1
	421894	AJ418464	Hs.190836	ESTs	3.1
35	419386	AA236867		ESTs, Weakly similar to I38022 hypotheti	3.1
	402422			Target Exon	3.1
	435849	BE305242	Hs.16098	claudin 2	3.1
	405422			ENSP00000216658:HYPOTHETICAL 133.5 kDa	3.0
	420543	AA278221	Hs.173344	ESTs	3.0
40	410627	AA181339	Hs.929	myosin, heavy polypeptide 7, cardiac mus	3.0
	409079	W87707	Hs.82065	Interleukin 6 signal transducer (gp130,	3.0
	406600			Target Exon	3.0
	408025	AI692784	Hs.41767	PTD02 protein	3.0
	426349	AI308855	Hs.301497	arginyltransferase 1	3.0
45	444576	AI400974	Hs.182045	ESTs	3.0
	430561	AC005551	Hs.130714	Homo sapiens HSPC323 mRNA, partial cds	3.0
	441335	BE222470	Hs.150825	ESTs, Weakly similar to antigen NY-CO-33	3.0
	459547	R34107	Hs.321450	pregnancy specific beta-1-glycoprotein 1	3.0
	435713	AA699313	Hs.114071	ESTs	3.0
50	407275	AI364186		gb:qw34h07.x1 NCL_CGAP_UI4 Homo sapiens	3.0
	456103	Z38430	Hs.72350	ESTs	3.0
	435200	AA670310	Hs.145903	ESTs	3.0
	449245	AI638539	Hs.224296	ESTs	3.0
	428132	AA421765		gb:zu24g02.s1 Soares_NaHMPu_S1 Homo sapi	3.0
55	443454	AI057494	Hs.133421	ESTs	2.9
	423732	AF058056	Hs.132183	solute carrier family 16 (monocarboxylic	2.9
	411944	AW877139		gb:QV2-PT0010-180400-133-g01 PT0010 Homo	2.9
	432718	AA563943	Hs.244371	ESTs	2.9
	435534	AA830927	Hs.117306	ESTs	2.9
60	430348	AA476915	Hs.189225	ESTs, Weakly similar to I38022 hypotheti	2.9
	410289	AW901618	Hs.61935	Homo sapiens mRNA; cDNA DKFZp761071 (fr	2.9
	453126	AA032155	Hs.61822	ESTs	2.9
	458421	AA233154	Hs.12532	chromosome 1 open reading frame 21	2.9
	441543	AI733014	Hs.269715	ESTs	2.9
65	442252	AI733395	Hs.129124	ESTs	2.9
	418254	AI459453	Hs.222760	ESTs	2.9
	443727	Z25389	Hs.18459	ESTs	2.9
	419896	Z99362		gb:HSZ98362 DKFZpharmy1 Homo sapiens cDNA	2.9
	453898	AW003512	Hs.232770	arachidonate lipoxygenase 3	2.9
70	415098	D59687		gb:HUM056E10B Clontech human fetal brain	2.9
	415131	D61119		gb:HUM158C11B Clontech human fetal brain	2.9
	406398			Target Exon	2.9
	433942	AW272166	Hs.123465	ESTs	2.9
	400461			Target Exon	2.9
75	442640	AI205646	Hs.147220	ESTs	2.9
	438814	AA826278	Hs.249596	ESTs	2.9
	438361	AA805666	Hs.146217	Homo sapiens cDNA: FLJ23077 fls, clone L	2.9
	422482	AI439905	Hs.344476	gb:dl57g08.x1 NCL_CGAP_Lym12 Homo sapien	2.8
	407142	AA412535		gb:z199b10.s1 Soares_testis_NHT Homo sap	2.8
80	454319	AW247736	Hs.101617	ESTs, Weakly similar to T32527 hypotheti	2.8
	442907	AJ023763	Hs.79707	ESTs	2.8
	456075	N73442		gb:yz31h09.r1 Soares_multiple_sclerosis_	2.8
	438690	AA815031	Hs.123598	ESTs	2.8
	452570	AW861293	Hs.336940	Homo sapiens cDNA: FLJ20861 fls, clone A	2.8
	408493	BE206854	Hs.45039	phosphoglycerate mutase 2 (muscle)	2.8
	447556	AI885187	Hs.210710	ESTs, Moderately similar to ALLJ6_HUMAN A	2.8
	461632	BE005934	Hs.310625	EST	2.8

	426481	AW963941		gb:EST376014 MAGE resequences, MAGH Homo	2.8
	401656			Target Exon	2.8
	407269	AJ245210		gb:Homo sapiens mRNA for immunoglobulin	2.8
5	435754	AA700752	Hs.117341	ESTs	2.8
	433685	AA599763	Hs.112520	ESTs	2.8
	451004	AA044967		gb:z53d09.r1 Soares retina N2b4HR Homo	2.8
	425223	AA352825	Hs.146065	gb:EST60880 Activated T-cells XX Homo sa	2.8
	405770			NM_002362:Homo sapiens melanoma antigen,	2.8
10	456227	T84239	Hs.189788	ESTs	2.8
	454445	AW749432		gb:RC3-BT0386-301299-011-a09 BT0386 Homo	2.8
	419494	W01060	Hs.34382	ESTs	2.8
	427639	AW444530	Hs.105362	Homo sapiens, clone MGC:18257, mRNA, com	2.8
	428079	AA421020	Hs.208919	ESTs	2.7
15	406337			C14000021:gil7242973[abj]BAA92547.1 (AB	2.7
	401884			Target Exon	2.7
	406881	D16154		gb:Human gene for cytochrome P-450c11, e	2.7
	428986	AA442884	Hs.201201	ESTs	2.7
	450044	R68444	Hs.51891	ESTs	2.7
20	403630			C3001708*:gil4758028[ref]NP_004360.1 co	2.7
	445514	A1241280	Hs.148906	ESTs	2.7
	446362	AW812481	Hs.104105	ESTs	2.7
	432492	AW275110	Hs.271106	ESTs	2.7
	430889	U22491	Hs.248117	G protein-coupled receptor 7	2.7
25	434316	AW411330	Hs.118796	annexin A6	2.7
	413155	BE067852		gb:CM0-BT0365-061299-122-g09 BT0365 Homo	2.7
	433329	AF015041	Hs.199291	nimb (Drosophila) homolog-like	2.7
	446523	NM_003063	Hs.334629	sarcoplasmic	2.7
	449923	BE258051		gb:601111034F1 NIH_MGC_16 Homo sapiens c	2.7
30	453826	AL138129		gb:DKFZp547F152_r1 547 (synonym: hbr1)	2.7
	405678			CX001454:gil8393794[ref]NP_058681.1 myo	2.7
	432769	D26361	Hs.3104	KIAA0042 gene product	2.7
	455791	BE090689		gb:RC1-BT0720-280300-011-f08 BT0720 Homo	2.7
	449109	AW270992	Hs.120949	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.7
35	436255	F01143	Hs.284284	zinc finger 1111	2.7
	415984	R19046	Hs.5010	gb:yg21111.r1 Soares infant brain 1N1B H	2.7
	402844			C1000118*:gil3951913[ref]NP_052832.1 pr	2.7
	458666	AA452512	Hs.76719	U6 snRNA-associated Sm-like protein	2.7
	414620	AA150120	Hs.244621	ribosomal protein S14	2.7
40	404979			Target Exon	2.7
	412318	AW936911	Hs.326729	hypothetical protein MGC11082	2.7
	424361	AK001551	Hs.145944	Homo sapiens cDNA FLJ10689 fis, clone NT	2.7
	412542	AW961516	Hs.95097	ESTs	2.7
	414975	AW173248	Hs.344285	EST	2.7
45	457021	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	2.7
	457851	AW450205	Hs.305890	BCL2-like 1	2.7
	439204	AF087987	Hs.42695	EST	2.7
	415642	U19878	Hs.336224	transmembrane protein with EGF-like and	2.7
	446847	T51454	Hs.82845	Homo sapiens cDNA: FLJ21930 fis, clone H	2.7
50	443359	AI792583	Hs.135354	ESTs	2.7
	447336	AW139383	Hs.245437	ESTs	2.7
	449045	BE072483	Hs.278337	Homo sapiens cDNA FLJ11537 fis, clone HE	2.7
	422185	AL117530	Hs.112822	DKFZP434B172 protein	2.7
	436030	R02287	Hs.121052	ESTs	2.7
55	449589	AW752437	Hs.135258	ESTs, Weakly similar to ALU7_HUMAN ALU S	2.6
	438092	A1345905	Hs.127383	ESTs	2.6
	415054	AI733907		gb:zo86h09.y5 Stratagene ovarian cancer	2.6
	412908	AA121913	Hs.293886	pregnancy-associated plasma protein-E	2.6
	409583	AW440117	Hs.256879	ESTs	2.6
60	410483	BE163557		gb:QV3-HT0460-230200-101-b08 HT0460 Homo	2.6
	435383	R61083		wee1 (S. pombe) homolog	2.6
	426629	AI203933	Hs.97142	ESTs	2.6
	415831	H15145	Hs.30609	ESTs	2.6
	412281	AI810054	Hs.14119	ESTs	2.6
65	434898	AW500458	Hs.28956	KIAA0460 protein	2.6
	422229	AF134414	Hs.113271	ABO blood group (transferase A, alpha 1-	2.6
	447518	T80061		gb:yd22f08.s1 Soares fetal liver spleen	2.6
	458546	AI215687	Hs.175044	ESTs	2.6
	438648	AA813125	Hs.146335	ESTs	2.6
70	450399	AW511049	Hs.202007	ESTs	2.6
	420833	R47948	Hs.188732	ESTs	2.6
	453903	AW298606	Hs.232777	ESTs	2.6
	443650	AI698330	Hs.151444	ESTs	2.6
	427419	NM_000200	Hs.177888	histatin 3	2.6
75	423741	AA330362		gb:EST34074 Embryo, 12 week II Homo sapi	2.6
	451577	N69101	Hs.40730	ESTs	2.6
	441358	AW173212	Hs.129041	ESTs	2.6
	402706			Target Exon	2.6
	436054	AI076282	Hs.119813	ESTs	2.6
80	402749			Target Exon	2.6
	442472	AW806859		gb:MRO-ST0020-081199-004-c03 ST0020 Homo	2.6
	445762	AI734002	Hs.264590	ESTs, Moderately similar to ALU5_HUMAN A	2.6
	441420	AA932872		gb:oo57d07.s1 NCL_CGAP_Lu5 Homo sapiens	2.6
	405564			Target Exon	2.6

	408003		Target Exon	2.6	
	459584	A1910884	Hs.346429	ESTs	2.6
	441597	AW135032	Hs.203625	ESTs	2.6
5	411280	N50617	Hs.80506	small nuclear ribonucleoprotein polypept	2.6
	420509	M83554	Hs.1314	tumor necrosis factor receptor superfam	2.6
	445060	AAB30811	Hs.282908	ESTs	2.6
	436260	BE172762	Hs.292710	ESTs, Weakly similar to ALU5_HUMAN ALU S	2.6
	428717	T78001	Hs.133546	hypothetical protein FLJ21120	2.6
10	401716			C16000902:gn 403440 gb AAA73168.1 (MB17	2.6
	416628	W03955		gb z862d04.r1 Soares fetal liver spleen	2.6
	443864	N37059	Hs.36250	ESTs, Weakly similar to I38022 hypothe	2.6
	440702	AA904178	Hs.148233	ESTs	2.6
	456310	AA226522		gb nc25c06.r1 NCL_CGAP_Prl Homo sapiens	2.6
15	451255	AA020857	Hs.90744	ESTs	2.6
	456737	BE072246		gb QV4-BT0536-271299-059-b12 BT0536 Homo	2.6
	445326	A1220072	Hs.344672	ESTs	2.6
	408432	AW195262		gb ccn67b05.x1 NCL_CGAP_CML1 Homo sapiens	2.6
	446874	BE326671	Hs.170058	ESTs	2.6
20	441053	AA913819	Hs.188025	ESTs	2.6
	455505	AW970640	Hs.309071	ESTs	2.6
	453491	AL040177		gb DKFZp434F0213_r1 434 (synonym: htes3)	2.6
	455048	AW852749		gb PM1-CT0247-080100-008-h09 CT0247 Homo	2.6
	456890	NM_004504	Hs.171545	HIV-1 Rev binding protein	2.6
25	444130	A125263	Hs.170410	ESTs	2.5
	422210	BE269319	Hs.171937	steroid dehydrogenase-like	2.5
	424241	AW995948	Hs.182339	Homo sapiens pyruvate dehydrogenase klna	2.5
	451606	AA018791	Hs.7945	AIE-75 binding protein protein	2.5
	400427	AB044934	Hs.287388	histamine H4 receptor	2.5
30	410443	BE062906	Hs.28338	KIAA1546 protein	2.5
	455210	AW865599		gb QV4-SN0024-210400-181-b10 SN0024 Homo	2.5
	429909	AW977090	Hs.184860	CGI-203 protein	2.5
	441191	AW693930	Hs.146816	ESTs	2.5
35	413489	BE144228		gb MR0-HT0165-140200-009-d04 HT0165 Homo	2.5
	448215	N34740	Hs.6658	ESTs	2.5
	419354	M52839	Hs.1252	apolipoprotein H (beta-2-glycoprotein I)	2.5
	447610	AW296286	Hs.255534	ESTs	2.5
	450724	R55428		gb y79b05.r1 Soares breast 2NbHBst Homo	2.5
	414523	AU076633	Hs.76353	serine (or cysteine) proteinase inhibito	2.5
40	414776	AA155598	Hs.212839	hypothetical protein FLJ14195; KIAA1714	2.5
	447730	AI421251	Hs.114085	Homo sapiens mRNA for KIAA1755 protein,	2.5
	434152	AI792665	Hs.291190	ESTs	2.5
	412671	AW977734	Hs.37931	gb EST389953 IMAGE resequences, MAGO Homo	2.5
	456401	W28146		gb 43111 Human retina cDNA randomly prim	2.5
45	404878			Target Exon	2.5
	408520	AA225063	Hs.161614	ESTs	2.5
	411332	AW837212		gb QV2-LT0038-140300-081-c01 LT0038 Homo	2.5
	448920	AW408009	Hs.22580	alkylglycerone phosphata synthase	2.5
	429908	AL080137	Hs.193743	ESTs	2.5
50	433712	AF090887	Hs.306562	Homo sapiens clone HQ0085	2.5
	438353	BE538951	Hs.306995	Homo sapiens, clone IMAGE:3447073, mRNA,	2.5
	446224	AW450551	Hs.13308	ESTs	2.5

TABLE 63B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

60	Pkey	CAT Number	Accession
	408229	1048482_1	AW176091 H24234
	408432	1056567_1	AW195262 R27868 AW811252
	409579	114787_1	BE250521 AA076837 BE249870 AA984291 AW502442 AW501551 A1221491 AA194239 D63046 AA193426 AA773243 AA193293
65	410483	1204995_1	BE163567 BE073688 BE073747 BE073780 BE073739 BE073748 BE163495 AW760178 BE163491 BE073763 BE073671
	411320	1238624_1	AW836646 AW836580 AW836610 AW836636 AW836603 AW836632
	411332	1239102_1	AW837212 AW837408 AW837265 AW837380 AW837213 AW837411 AW837418
	411356	1240273_1	H45377 H21137 AW838640
	411426	1245515_1	BE141714 AW845993 AW845989
70	411829	1260309_1	AW865749 BE179419 BE179492
	411944	1266482_1	AW877139 AW877135 AW877018 AW991835 AW877128 AW877108 AW877017 AW877107
	413155	1351148_1	BE067952 BE067945 BE067942 BE067943 BE067949 BE067954 BE067953 BE067956 BE067946
	413391	1365950_1	BE090690 BE090688 BE090681 BE090693 BE090675
	413489	1373392_1	BE144228 BE144291
75	415054	151827_1	A1733907 AA159708 A1732614
	415098	1522174_1	D59657 D59694 D59656 D59589
	415131	1523680_1	D81119 D81508 D81734
	415386	1535560_1	Z43087 F07410 H15506 H54108 R95033 H98000
	415981	1564242_1	R35694 H12035 R53312
80	416628	1604848_1	W03955 H82332 H69247 H72486
	416935	163179_1	AA190712 AA190665 AA252564
	419386	184356_1	AA236867 AA237066 AA354236 AW957759 H08961
	419896	1888662_1	Z99362 Z99363
	420778	195399_1	AW970512 AA280251 A1652287 BE466438 A1650725 AA551854 AA281574 AW571481

5	421342	201427_1	AA504749 AA287498
	421813	207654_1	BE048255 AA313083 AA298419
	422731	220507_1	AL138411 AL138412 AA315860
	423741	231582_1	AA330362 AW962525 HB7796
	423772	23188_1	AA306637 NM_007241 AF156102 BE388339 BE814027 AW935016 AA315261 AW376418 AW304951 AI859820 AA367436 AW516957 BE614519
			AI453152 AI453149 AI453139 AW168378 AI139491 AI538368 AW458227 AI680027 AW090513 AA662830 F30395 AI351985 AI424349 AW009699
			C02215 AI6625
10	423871	232749_1	AA331906 AA332484
	426481	267878_1	AW963941 AW963944 AA379825 AA379564
	428132	287430_1	AA421766 AA458078 AI290275 AA455679
	431847	338402_1	AI791314 AI791434 AA516511
	434407	385744_1	AW815333 AW815409 AA632563
	436383	405360_1	R61083 R13743 AA679174 AA679193 Z42903
15	436190	41555_1	AK001069 AA633055
	436535	45946_1	L09078 L03145 L09094 L09098 L03165 L09102
	441420	516748_1	AA932872 W28068 W28643 T96110
	442472	543371_1	AW806859 AW806852 AF049582
	445797	650943_1	AI253414 AI366014 R34822
20	447518	724787_1	T80061 AI382804
	447600	728288_1	AI420990 AI399725 AI401757
	448516	756241_1	AW898595 AW898588 AW898590 AW898663 AW898592 AI526093
	449923	81926_1	BE258051 R45768 AA004732 BE255126
	450724	844585_1	R55428 AI820704 AI732283 R54983
25	451004	85453_1	AA044967 H86327 AA013079 AA058776 BE242713 AA019987
	452351	91233_1	AA025647 R45716 AW753786
	453412	966264_1	AJ003290 AJ003288 AW276947
	453491	969172_1	AL040177
	453752	979899_1	AL120800 BE378580
30	453826	982669_1	AL138129 AL138179 BE064231
	454445	1204468_1	AW749432 AW749434 R47332
	454549	1223789_1	AW806910 AW866461 AW866396 AW866373 AW866811 AW866616
	455048	1250599_1	AW852749 AW852755 AW852620
	455210	1260650_1	AW866599 AW866294 AW866468 AW866467
35	455643	1348708_1	BE065051 BE156165 BE064764 BE155231 BE064648 BE064671 BE064636
	455737	1353892_1	BE072246 BE072229 BE072225 BE072210 BE072221 BE072258 BE072211 BE072242
	455791	1385954_1	BE090689 BE090685 BE090697 BE090680 BE090691 BE090696 BE090698 BE090686
	455887	1380835_1	BE154173 BE154098 BE154096
	456075	1476756_1	N73442 R98100 BE410380
40	456310	177089_1	AA225522 AA225465 AI820979 AW973985 AI791935 AA558735
	456401	1844549_2	W28146 W28187

TABLE 63C

45	Key:	Unique number corresponding to an Eos probeset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
	NL_position:	Indicates nucleotide positions of predicted exons.		
50	Key	Ref	Strand	NL_position
	400461	9929654	Plus	32727-32846,32929-33051
	400489	9798071	Minus	148495-148806
55	400749	7331445	Minus	9162-9293
	400831	8576271	Minus	56502-57407
	401278	9799936	Plus	98428-98573
	401411	7793787	Minus	144144-144329
	401656	9100664	Minus	1-382
60	401716	6715703	Plus	174722-174911
	401884	8140731	Minus	69182-90053
	401898	8568194	Plus	115129-115294
	401917	9502466	Plus	25064-25229
	402422	9796344	Minus	32843-33008
65	402480	9796884	Minus	108901-109254,110246-110581,113613-113960
	402490	9797848	Plus	149982-150929
	402706	8894426	Minus	148540-148805
	402749	9212740	Minus	68787-68882,76602-76768
	402797	3421043	Minus	15758-16930
70	402817	6822166	Minus	48611-49012
	402844	9369286	Plus	54958-55313
	403451	9838240	Plus	77382-78300
	403612	8489060	Minus	94723-94859
	403630	8568999	Minus	13909-14486,16251-15760,16898-17431,41742-42440
75	403649	8705159	Minus	27141-27247
	404250	9366879	Plus	51396-51513
	404267	9581792	Minus	12209-12313,18241-18397
	404606	8212935	Minus	22310-23269
	404650	9797068	Plus	168215-168916
80	404678	9797204	Plus	115196-115448
	404979	4160139	Minus	87762-88217
	404984	6939882	Plus	87221-87505
	405001	6015406	Minus	104646-104819
	405150	9829758	Plus	128475-128773

5	405152	9965561	Minus	137662-137969
	405258	7329310	Plus	129930-130076
	405422	7243869	Minus	101938-102079, 102261-102443, 102896-103202
	405564	2114222	Minus	16766-17344
	405678	4079670	Plus	151821-152027
	405735	9931101	Minus	29854-29976
	405770	2735037	Plus	61057-62075
	406003	8247800	Plus	42079-42516
10	406085	9123888	Plus	18665-18843
	406177	7279760	Minus	18930-19148
	406337	9213455	Plus	90117-90337
	406398	9256276	Minus	118691-118959
	406600	8248616	Minus	36296-36610

15

Table 64A lists about 703 genes up-regulated in BPH compared to normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" BPH to "average" normal adult tissues was greater than or equal to 3.0. The "average" BPH level was set to the 75th percentile amongst BPH tissues. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

20

TABLE 64A: ABOUT 703 GENES UP-REGULATED IN BENIGN PROSTATIC HYPERPLASIA COMPARED TO NORMAL ADULT TISSUES

25	Pkey:	Unique Eos probeset identifier number		
	ExAccn:	Exemplar Accession number, Genbank accession number		
	UnigeneID:	Unigene number		
	Unigene Title:	Unigene gene title		
	R1:	Ratio of BPH tissue to normal adult body tissue		
30	Pkey	ExAccn	Unigene ID	Unigene Title
	420154	AI093155	Hs.95420	JM27 protein
	425747	AA535210	Hs.171995	kalikrein 3, (prostate specific antigen
	419526	AI821895	Hs.193481	ESTs
	432441	AW292426	Hs.163484	ESTs
35	431616	AA508552	Hs.195839	ESTs, Weakly similar to I38022 hypotheti
	407202	N58172	Hs.109370	ESTs
	432101	AI918950	Hs.123642	EphA3
	400289	X07730	Hs.171995	kalikrein 3, (prostate specific antigen
	425075	AA506324	Hs.1852	acid phosphatase, prostate
40	414569	AF109298	Hs.118258	prostate cancer associated protein 1
	410929	H47233	Hs.30643	ESTs
	400287	S39329	Hs.181350	kalikrein 2, prostatic
	445057	AI420227	Hs.149358	ESTs, Weakly similar to A46010 X-linked
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, D
	415889	AI267700		ESTs
45	428336	AA503115	Hs.183752	microseminoprotein, beta-
	450693	AW450461	Hs.203965	ESTs
	400286	AA032279	Hs.61635	six transmembrane epithelial antigen of
	407168	R45175	Hs.117183	ESTs
50	408369	R38438	Hs.182575	solute carrier family 15 (H7??) transport
	454119	BE549773	Hs.40610	uncoupling protein 4
	428819	AL136623	Hs.193914	KIAA0575 gene product
	400302	N48056	Hs.1915	folate hydrolase (prostate-specific memb
	400297	AI127076	Hs.306201	hypothetical protein DKFZp564O1278
55	416432	M14156	Hs.85112	Insulin-like growth factor 1 (somatomedi
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypotheti
	433444	AW975324	Hs.128816	ESTs
	432240	AI694767	Hs.129179	Homo sapiens cDNA FLJ13591 fis, clone PL
	428342	AI739188		Homo sapiens cDNA FLJ13458 fis, clone PL
60	401424			NM_001172:Homo sapiens arginase, type II
	432435	BE218686	Hs.282070	ESTs
	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and
	446100	AW967109	Hs.13804	hypothetical protein dJ462023.2
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1
65	407275	AI364186		gbxw34h07.x1 NCLCGAP_U4 Homo sapiens
	452340	NM_002202	Hs.506	ISL1 transcription factor, LIM/homeodoma
	432473	AI202703	Hs.152414	ESTs
	410330	AW023630	Hs.159425	ESTs
	431579	AW971082	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH
70	452782	AB037785	Hs.30652	KIAA1344 protein
	418548	AI820861	Hs.193465	ESTs
	400292	AA250737	Hs.72472	BMP-R1B
	433647	AA003367	Hs.222294	ESTs
	453160	AI263307	Hs.239884	H2B histone family, member L
75	409262	AK000631	Hs.52256	hypothetical protein FLJ20624
	431474	AL133890	Hs.190642	CEGP1 protein
	429220	AW207208		ESTs
	428134	AA421773	Hs.161008	ESTs
	408622	AA056060	Hs.202577	Homo sapiens cDNA FLJ12166 fis, clone MA
80	456497	AW987956	Hs.123648	ESTs, Weakly similar to AF108460 1 ubinu
	434792	AA648263	Hs.132458	ESTs
	433466	AA508353	Hs.105314	relaxin 1 (H1)
	439176	AI445444	Hs.190394	ESTs, Weakly similar to B28098 line-1 pr
	428398	AI249368	Hs.98558	ESTs

	429290	AF203032	Hs.198760	neurofilament, heavy polypeptide (200kD)	9.3
	407709	AA456135	Hs.23023	ESTs	9.3
	415293	R49462	Hs.106541	ESTs	9.1
5	429918	AW873986	Hs.119383	ESTs	9.1
	440260	AI972867	Hs.7130	copine IV	9.1
	453095	AW294531	Hs.11325	ESTs	9.1
	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	8.9
	456516	BE172704	Hs.222746	KIAA1610 protein	8.8
10	430722	AW968543	Hs.203270	ESTs, Weakly similar to ALU1_HUMAN ALU S	8.8
	458072	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fls, clone K	8.8
	453006	AI362575	Hs.303171	ESTs	8.7
	418339	AA639902	Hs.104215	ESTs, Moderately similar to SPCN_HUMAN S	8.7
	420424	AB033036	Hs.97594	KIAA1210 protein	8.7
15	450542	R39773	Hs.7130	copine IV	8.7
	434036	AI659131	Hs.197733	hypothetical protein MGC2849	8.7
	428927	AA441837	Hs.90250	ESTs	8.6
	418829	AA516531	Hs.56989	NK homeobox (Drosophila), family 3, A	8.5
	420345	AW295230	Hs.25231	ESTs	8.5
20	446336	AW815036	Hs.151251	ESTs	8.4
	419743	AW408782	Hs.5957	Homo sapiens clone 24416 mRNA sequence	8.4
	428728	NM_016625	Hs.191381	hypothetical protein	8.3
	417169	R13550	Hs.246773	ESTs	8.2
	453387	AI990741	Hs.252809	ESTs	8.2
25	434666	AF151103	Hs.112259	T cell receptor gamma locus	8.1
	417958	AA787382	Hs.193417	ESTs	8.0
	433433	AI692623	Hs.121513	Homo sapiens clone Z3-1 placenta expres	7.9
	444609	AW571659	Hs.278081	ESTs	7.8
	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	7.8
30	433923	AI823453	Hs.146825	ESTs	7.7
	437587	AI591222	Hs.72325	Human DNA sequence from clone RP1-187J11	7.7
	441890	R81733	Hs.33106	ESTs	7.6
	453370	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	7.6
	441247	AW118681	Hs.128051	Homo sapiens thymic stromal lymphopoietin	7.5
35	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	7.5
	431446	AL137517	Hs.306204	hypothetical protein DKFZp564O1278	7.4
	413597	AW302885	Hs.117183	ESTs	7.4
	404592			NM_022739: Homo sapiens E3 ubiquitin lig	7.3
	408557	BE182896	Hs.211193	ESTs	7.3
40	420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	7.3
	438231	AW594539	Hs.165689	ESTs	7.3
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fls, clone C	7.1
	449300	AI668959	Hs.346514	ESTs	7.1
	417332	AW972717	Hs.289482	hypothetical protein FLJ21511	7.1
45	453930	AA419466	Hs.36727	hypothetical protein FLJ10903	7.1
	449249	TS2285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	7.0
	430187	AI799809	Hs.158989	ESTs	7.0
	434217	AW014795	Hs.23349	ESTs	7.0
	431217	NM_013427	Hs.250830	Rho GTPase activating protein 8	6.9
50	430188	AL049242	Hs.234794	Homo sapiens mRNA; cDNA DKFZp564B083 (fr	6.9
	415786	AW419196	Hs.257924	hypothetical protein FLJ13782	6.9
	421059	AI654133	Hs.30212	thyroid receptor interacting protein 15	6.8
	426384	AI472078	Hs.303662	ESTs	6.8
	458509	AA654650	Hs.282906	ESTs	6.8
55	449821	AI671141	Hs.211122	ESTs	6.8
	407118	AA158790	Hs.262036	ESTs, Weakly similar to Z223_HUMAN ZINC	6.8
	443250	AI041530	Hs.132107	ESTs	6.7
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matrilysin,	6.7
	408197	AA282282	Hs.107410	ESTs, Weakly similar to A46010 X-linked	6.6
60	454457	AW753456		gb:QV2-CT0261-261099-011-411 CT0261 Homo	6.6
	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fls, clone PL	6.5
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	6.5
	431467	N71831	Hs.256398	Homo sapiens mRNA; cDNA DKFZp434E0528 (f	6.5
	424433	H04607	Hs.9218	ESTs	6.5
65	450164	AI239923	Hs.63931	ESTs	6.5
	423566	AW976434	Hs.3623	hypothetical protein FLJ11220	6.5
	450497	H64159	Hs.15328	ESTs	6.5
	425312	AA364940	Hs.145958	ESTs	6.4
	426140	AF131798	Hs.343768	Homo sapiens clone 25119 mRNA sequence	6.4
70	440911	AA909536	Hs.143562	ESTs	6.4
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	6.3
	432600	AI821085		gb:ns95a12.y5 NCL_GGAP_Pr3 Homo sapiens	6.3
	436375	AI733610	Hs.187832	ESTs	6.3
	416370	N90470	Hs.203697	ESTs, Weakly similar to I38022 hypotheti	6.3
75	431359	AW993522	Hs.292934	ESTs	6.2
	424736	AF230877	Hs.152701	microtubule-interacting protein that ass	6.1
	403657			Target Exon	6.1
	424846	AI077324	Hs.1832	neuropeptide Y	6.1
	439589	AW602166	Hs.222399	CEGP1 protein	6.1
80	436396	AI683487	Hs.152213	wingless-type MMTV integration site fami	6.1
	448004	AW451477	Hs.257456	ESTs	6.1
	431770	BE221880	Hs.268555	5'-3' exonuclease 2	6.0
	453861	AI026838	Hs.30120	ESTs, Weakly similar to NUCLE_HUMAN NUCLE	6.0
	415621	AI048602	Hs.55468	ESTs	6.0

	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	6.0
	442481	N98928		gb:za32:c04.r1 Soares fetal liver spleen	6.0
	432527	AW975028	Hs.102754	ESTs	5.9
	447156	AW274731	Hs.157920	ESTs	5.9
5	404003			Target Exon	5.9
	424853	BE549737	Hs.132967	Human EST clone 122887 mariner transposo	5.9
	427726	AJ359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	5.9
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	5.9
10	438138	R98299	Hs.177502	ESTs	5.9
	440129	AA865818	Hs.174836	ESTs, Weakly similar to S71886 Ste20-lik	5.8
	434973	AW449285	Hs.313636	EST	5.8
	406627	AL135018	Hs.33074	Homo sapiens, clone IMAGE:3606518, mRNA,	5.8
	459241	AA032276	Hs.99010	ESTs, Moderately similar to T14342 NSD1	5.8
	434465	AJ623511	Hs.118567	ESTs	5.8
15	429716	R25885	Hs.211933	collagen, type XIII, alpha 1	5.7
	443960	AI093577	Hs.255416	hypothetical protein FLJ21986	5.7
	453200	AA033832	Hs.212433	ESTs	5.7
	428002	AA418703		gb:zv98:c03.s1 Soares_NhHMPu_S1 Homo sapi	5.7
20	432966	AA650114	Hs.325198	ESTs	5.7
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	5.7
	420848	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukemia	5.7
	425810	AI923627	Hs.31903	ESTs	5.6
	414312	AA155584	Hs.191060	ESTs	5.6
25	404571			NM_015802*:Homo sapiens progesteron induce	5.6
	424850	AA151057	Hs.153498	chromosome 18 open reading frame 1	5.6
	435092	AA830149		gb:acc4408.s1 NCL_CGAP_GCB1 Homo sapiens	5.6
	427078	AI676062	Hs.111902	ESTs	5.6
	422805	AA436989	Hs.121017	H2A histone family, member A	5.6
30	417511	AI049176	Hs.82223	chordin-like	5.6
	449625	NM_014253		cdx (odd Oz/ten-m, Drosophila) homolog 1	5.6
	433927	AI557019	Hs.116467	small nuclear protein PRAC	5.5
	441676	BE564206	Hs.49889	ESTs	5.5
	421513	X00949	Hs.105314	relaxin 1 (H1)	5.5
35	432682	AI376400	Hs.159588	ESTs	5.5
	435021	AA922192	Hs.54709	ESTs	5.5
	454171	AW854832		gb:QV2-CT0261-201099-011-005 CT0261 Homo	5.5
	426681	AB040956	Hs.135890	KIAA1523 protein	5.5
	439079	AF085937	Hs.38348	ESTs	5.5
40	443635	AI080230	Hs.134214	ESTs	5.5
	400080			Eos Control	5.5
	410196	AI936442	Hs.59838	hypothetical protein FLJ10808	5.5
	436578	AI091435	Hs.134859	ESTs	5.5
	424051	AL110203	Hs.138411	Homo sapiens mRNA; cDNA DKFZp566J1922 (f	5.4
45	450325	AI935962	Hs.26289	ESTs	5.4
	421863	AI952677	Hs.108972	Homo sapiens mRNA; cDNA DKFZp434P228 (fr	5.4
	432161	AK000400	Hs.341181	ESTs, Weakly similar to envelope [H.sapi	5.4
	435072	AW592176	Hs.116932	ESTs	5.4
	428647	AA830050	Hs.124344	ESTs	5.4
50	441111	AI806867	Hs.126594	ESTs	5.4
	433087	AI720686	Hs.152520	ESTs	5.3
	450244	AA007534	Hs.125052	ESTs	5.3
	400294	N95798	Hs.278695	Homo sapiens protein mRNA, complete cds	5.3
	415539	AI733881	Hs.72472	BMP-R1B	5.3
55	437267	AW511443	Hs.258110	ESTs	5.3
	441916	AA893571	Hs.129075	ESTs	5.3
	452784	BE463857	Hs.151258	hypothetical protein FLJ21062	5.3
	448715	AI337735	Hs.173919	ESTs, Moderately similar to ZN91_HUMAN Z	5.3
	452531	AA429462	Hs.293946	ESTs, Weakly similar to I35022 hypothet	5.3
60	426503	AA380153		gb:EST93093 Skin tumor I Homo sapiens cD	5.3
	423101	M83941	Hs.123642	EphA3	5.3
	445704	AI493742	Hs.167700	ESTs, Moderately similar to I38022 hypot	5.3
	450813	AI739625	Hs.203376	ESTs	5.3
	409079	W87707	Hs.82085	Interleukin 6 signal transducer (gp130,	5.2
65	415890	H08225	Hs.268712	ESTs	5.2
	454968	AW849046		gb:IL3-CT0214-150300-085-H06 CT0214 Homo	5.2
	441054	AA913591	Hs.126480	ESTs	5.2
	408386	AF055634	Hs.44553	unc5 (C.elegans homolog) c	5.2
	437762	AA767376	Hs.291631	ESTs, Moderately similar to S65657 alpha	5.2
70	448072	AI458306	Hs.24908	ESTs	5.2
	419536	AA603305		gb:np12d11.s1 NCL_CGAP_Py3 Homo sapiens	5.2
	421040	AA715026	Hs.135280	ESTs	5.2
	446495	D60923	Hs.153460	ESTs	5.2
	415263	AA948033	Hs.130853	ESTs	5.2
	426748	AL048409	Hs.97177	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
75	438338	W92147	Hs.118394	ESTs	5.2
	445238	AA863971	Hs.187506	ESTs	5.1
	450362	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	5.1
80	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	5.1
	450582	AI339732		G-rich RNA sequence binding factor 1	5.1
	438447	AI082883	Hs.30732	hypothetical protein FLJ13409; KIAA1711	5.1
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	5.0
	440995	T57773	Hs.10263	ESTs	5.0
	412775	AA709046	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	5.0

5	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	5.0
	418334	AA319233	Hs.5521	ESTs	5.0
	435401	R44477	Hs.10056	hypothetical protein FLJ14621	5.0
	418564	AA631143	Hs.278595	Homo sapiens prostein mRNA, complete cds	5.0
	407198	H91679		gb:Y04907.s1 Soares fetal liver spleen	5.0
10	403696			C4001100*cg5852342(gb)AAD54015.1) (AF0	5.0
	452891	N75582	Hs.212875	ESTs, Weakly similar to DYH9_HUMAN CLIA	5.0
	457374	AA493662		gb:nh05d12.s1 NCI_CGAP_Try1 Homo sapiens	5.0
	430261	AA305127	Hs.237225	hypothetical protein HT023	5.0
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	5.0
15	448041	AW292769	Hs.206228	ESTs	5.0
	451244	AW008798	Hs.343877	hypothetical protein FLJ20039	5.0
	443180	R15875	Hs.258576	claudin 12	4.9
	414422	AA147224	Hs.249195	Homeo box A13	4.9
	418866	T65754		gb:yc11c07.s1 Stratagene lung (937210) H	4.9
20	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	4.9
	428715	AW293716	Hs.53126	ESTs	4.9
	436937	AA830893	Hs.119769	ESTs	4.8
	435136	R27299	Hs.10172	ESTs	4.8
	438132	AA907076	Hs.122060	ESTs	4.8
25	447058	AI939456	Hs.160870	ESTs	4.8
	419187	AA234852	Hs.44693	ESTs	4.8
	433523	H29682		ESTs	4.8
	420871	AA702972	Hs.65300	ESTs	4.8
	450317	AI692689		gb:wd86g05.x1 NCI_CGAP_Lu24 Homo sapiens	4.8
30	453843	D25215	Hs.35804	hect domain and RLD 3	4.8
	430172	AA488591	Hs.161889	ESTs	4.8
	431657	AI345227	Hs.106448	ESTs, Weakly similar to B34087 hypotheti	4.7
	452843	AI798769	Hs.208320	ESTs	4.7
	458229	AI929602	Hs.177	phosphatidylinositol glycan, class H	4.7
35	420954	AA282074	Hs.237323	N-acetylglucosamine-phosphate mutase	4.7
	452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	4.7
	440354	AA889386	Hs.125468	ESTs	4.7
	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU S	4.7
	443361	AI792628	Hs.133273	ESTs	4.6
40	409731	AA125085	Hs.56145	thymosin, beta, identified in neuroblast	4.6
	420026	AI831190	Hs.166676	ESTs	4.6
	450330	AW500775	Hs.24817	hypothetical protein FLJ20136	4.6
	415788	AW628686	Hs.78851	KIAA0217 protein	4.6
	417173	U61397	Hs.81424	ubiquitin-like 1 (senitin)	4.6
45	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.6
	434408	AI031771	Hs.132586	ESTs	4.6
	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	4.6
	447805	AW627832	Hs.302421	gemin4	4.6
	438875	AA827640	Hs.189059	ESTs	4.6
50	419511	AA429750	Hs.75113	general transcription factor IIIA	4.6
	445242	BE156478	Hs.21108	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.6
	428218	AA424286	Hs.123642	EphA3	4.6
	452277	AL049013	Hs.28783	KIAA1223 protein	4.6
	418836	AI655499	Hs.161712	ESTs	4.5
55	417601	NM_014735	Hs.82292	KIAA0215 gene product	4.5
	430697	AA484207	Hs.211867	ESTs	4.5
	430701	AI760833	Hs.293971	ESTs	4.5
	437252	AI433833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.5
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	4.5
60	420133	AA426117	Hs.165543	ESTs	4.5
	431740	N75450	Hs.183412	ESTs, Moderately similar to AF116721 87	4.5
	439752	T78968	Hs.14411	ESTs	4.5
	447816	NM_007233	Hs.274329	TP53 target gene 1	4.5
	431060	AF039307	Hs.249171	homeo box A11	4.5
65	445372	N36417	Hs.144928	ESTs	4.5
	452056	AI377431	Hs.141693	hypothetical protein MGC10858	4.5
	416602	NM_006159	Hs.79389	nel (chicken)-like 2	4.4
	418019	R69911	Hs.176275	ESTs	4.4
	423352	AA324808	Hs.193576	ESTs	4.4
70	438042	AW296971	Hs.180610	ESTs	4.4
	452978	AA029994	Hs.61523	ESTs	4.4
	412843	AW971239	Hs.138433	ESTs	4.4
	417412	X16886	Hs.82112	interleukin 1 receptor, type I	4.4
	445210	H09323	Hs.27133	ESTs	4.4
75	416706	AA314676	Hs.288945	hypothetical protein FLJ13448	4.4
	420808	BE548277	Hs.103104	ESTs	4.4
	428249	AA130914	Hs.183291	zinc finger protein 268	4.4
	442242	AV847808	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	4.4
	444030	AW021254	Hs.135055	ESTs	4.4
80	435655	AW105653	Hs.6947	HSPC069 protein	4.4
	400533			ENSP00000209376*-PRED65 protein (Fragmen	4.4
	435285	AW272603	Hs.266134	ESTs	4.4
	450216	AA873345	Hs.60226	Homo sapiens, clone IMAGE:3621638, mRNA,	4.3
	432950	AW150945	Hs.144758	ESTs	4.3
	459527	AW977556	Hs.291735	ESTs, Weakly similar to I78885 serine/th	4.3
	426413	AA377823		gb:EST80805 Synovial sarcoma Homo sapien	4.3
	430535	AW968485		gb:EST390561 MAGE resequences, MAGE Homo	4.3

5	416312	W02640	Hs.16247	ESTs, Weakly similar to 2004399A chromos	4.3
	454159	AW968065	Hs.44143	polybromo 1	4.3
	435176	AA744875	Hs.189413	ESTs	4.3
	451061	AW291487	Hs.213659	ESTs, Weakly similar to KIAA1357 protein	4.3
	407910	AA650274	Hs.41295	fibronectin leucine rich transmembrane p	4.3
10	420111	AA255652		gb:zs21h11.r1 NC1_CGAP_GCB1 Homo sapiens	4.3
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	4.3
	459045	N69101	Hs.40730	ESTs	4.3
	405348			C7001654:gl 12608061 kb BAB21849.1 (AB	4.3
	422906	U80773	Hs.121580	Human EST clone 42944 mariner transposon	4.3
15	449603	AI655662	Hs.197698	ESTs	4.3
	409705	M37762	Hs.56023	brain-derived neurotrophic factor	4.3
	423782	AI472209	Hs.323117	ESTs	4.3
	432887	AI926047	Hs.162859	ESTs	4.3
	420905	AA521307	Hs.186651	ESTs	4.2
20	416814	AW192307	Hs.80042	dolichyl-P-Glc:Man9GlcNAc2-PP-dolichylgl	4.2
	427908	AA417272	Hs.24122	ESTs	4.2
	432765	AJ003429		gb:AJ003429 Selected chromosome 21 cDNA	4.2
	444246	H93281	Hs.10710	hypothetical protein FLJ20417	4.2
	450597	AI701835	Hs.207077	ESTs	4.2
25	434022	R18374	Hs.117956	ESTs	4.2
	427761	AA412205	Hs.140996	ESTs	4.2
	433209	ABD40907	Hs.278436	KIAA1474 protein	4.2
	413525	BE145899		gb:MR0-HT0208-221299-204-b10 HT0208 Homo	4.2
	436679	AI127483	Hs.120451	ESTs, Weakly similar to unnamed protein	4.2
30	449655	AI021987	Hs.59970	ESTs	4.2
	440774	AI420611	Hs.153934	ESTs	4.2
	427521	AW973352	Hs.290585	ESTs	4.2
	440594	AW445167	Hs.126036	ESTs	4.2
	458912	AI911066		ESTs	4.2
35	410790	AW803357		gb:IL2-UM0079-090300-050-A08 UM0079 Homo	4.1
	415245	N59650	Hs.27252	ESTs	4.1
	435743	T66861	Hs.12962	ESTs	4.1
	442786	H50733	Hs.256261	ESTs, Moderately similar to ALU8_HUMAN A	4.1
	436714	AA728964	Hs.293399	ESTs	4.1
40	423789	AK002084	Hs.132851	hypothetical protein FLJ11222	4.1
	408177	AI241733	Hs.43871	ESTs	4.1
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	4.1
	430523	AW451385	Hs.161954	ESTs	4.1
	445206	AI350199	Hs.268890	ESTs	4.1
45	452335	AW188944	Hs.61272	ESTs	4.1
	438431	AW207860	Hs.299116	ESTs	4.1
	448907	AA004825	Hs.103281	ESTs	4.1
	430487	D87742	Hs.241552	KIAA0268 protein	4.1
	448152	AI741053	Hs.170770	ESTs	4.1
50	448515	H68441	Hs.13528	hypothetical protein FLJ14054	4.1
	423242	AL038402	Hs.125783	DEME-6 protein	4.1
	412715	NM_000947	Hs.74519	primase, polypeptide 2A (58KD)	4.1
	400748			Target Exon	4.1
	413081	BE064415		gb:RC4-BT0311-241199-012-b03 BT0311 Homo	4.1
55	446416	AV658299	Hs.163959	ESTs	4.1
	451840	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	4.1
	427203	AW629517	Hs.244855	ESTs	4.0
	440840	AW629666		ESTs, Weakly similar to S64054 hypotheti	4.0
	442338	AI781976	Hs.158080	ESTs	4.0
60	446307	T50083	Hs.22247	ESTs	4.0
	455276	BE176479		gb:RC3-HT0585-160300-022-b09 HT0585 Homo	4.0
	415881	Z43123	Hs.144513	ESTs	4.0
	418259	AA215404		ESTs	4.0
	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.0
65	432229	AW290976	Hs.143687	ESTs	4.0
	418310	AA814100	Hs.86693	ESTs	4.0
	416760	H85182	Hs.191327	ESTs, Highly similar to KIAA1102 protein	4.0
	419063	AI479560	Hs.98613	Homo sapiens cDNA FLJ12292 fls, clone MA	4.0
	421312	AA824627	Hs.291670	ESTs	4.0
70	448131	AI575054	Hs.200481	ESTs	4.0
	439731	AI953135	Hs.45140	hypothetical protein FLJ14084	4.0
	418243	W51873	Hs.171857	Homo sapiens testis protein mRNA, partial	4.0
	434072	H70854	Hs.283059	Homo sapiens PRO1082 mRNA, complete cds	4.0
	434844	AF167116	Hs.22350	hypothetical protein LOC56757	4.0
75	452221	C21322	Hs.288057	hypothetical protein FLJ22242	4.0
	432697	AW975050	Hs.293892	ESTs, Weakly similar to ALU4_HUMAN ALU S	4.0
	446354	AW449650	Hs.346336	ESTs	4.0
	447072	D61594	Hs.17279	lysylprotein sulfotransferase 1	4.0
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	4.0
80	441568	AI733322	Hs.127176	ESTs	4.0
	441736	AW292779	Hs.8182	ESTs	4.0
	457498	AI732230	Hs.191737	ESTs	3.9
	433234	AB040928	Hs.65366	KIAA1495 protein	3.9
	434222	AF119886	Hs.283941	Homo sapiens PRO2591 mRNA, complete cds	3.9
	448568	AA149121	Hs.71947	ESTs	3.9
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	3.9
	424940	AA985308	Hs.283902	ESTs	3.9

	416288	Hs1299	gbyp07c06.s1 Soares breast 3N6H8st Homo	3.9
	420301	AA767525	paired box gene 5 (B-cell lineage specif	3.9
	429066	AA868555	ESTs	3.9
5	435878	R08330	ESTs	3.9
	446862	AV660697	ESTs	3.9
	447530	AW192063	ESTs, Moderately similar to JC5238 galac	3.9
	452619	AW298597	Homo sapiens, clone IMAGE:4298025, mRNA,	3.9
	401403		Target Exon	3.9
10	448779	BE042877	ESTs	3.9
	420533	AF089510	ESTs	3.9
	411084	T18987	ESTs, Moderately similar to KIAA0877 pro	3.9
	419629	AB020595	KIAA0888 protein	3.9
	423453	AW450737	CGI-09 protein	3.9
15	434833	AF156548	ESTs, Weakly similar to AT1A_HUMAN POTEN	3.9
	455646	BE064420	gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.9
	411479	AW848047	gb:IL3-CT0214-291299-052-A12 CT0214 Homo	3.9
	419038	AW134924	ESTs	3.9
	421129	BE438899	ESTs	3.9
20	424332	AA338919	ESTs	3.9
	441766	R53790	hypothetical protein FLJ14393	3.9
	447033	AI357412	ESTs	3.9
	439306	BE220199	WD40 protein Clao1	3.8
	410352	AW969725	KIAA0373 gene product	3.8
25	407861	AW672939	origin recognition complex, subunit 2 (y	3.8
	410262	AW821182	microfibrillar-associated protein 1	3.8
	439560	BE565647	hypothetical protein FLJ12820	3.8
	440450	AI333129	ESTs	3.8
	458611	AI268407	DC-specific transmembrane protein	3.8
30	419589	AW973708	Homo sapiens cDNA FLJ13446 fls, clone PL	3.8
	431576	M75665	hydroxysteroid (11-beta) dehydrogenase 1	3.8
	447280	BE517907	ESTs	3.8
	438379	N23018	C-terminal binding protein 2	3.8
	416009	Z43062	gb:HSC12E041 normalized infant brain cDN	3.8
35	416534	H69043	Homo sapiens cDNA FLJ14366 fls, clone HE	3.8
	423044	AA320829	protocadherin 18	3.8
	424701	NM_005923	mitogen-activated protein kinase kinase	3.8
	433507	AI817338	ESTs	3.8
	437718	AI927288	ESTs	3.8
40	418831	AW448930	ESTs	3.8
	424830	AW270580	ESTs, Weakly similar to putative p150 [H	3.8
	426981	AL044675	KIAA0530 protein	3.8
	431447	AA505138	ESTs	3.8
	435932	W03928	ESTs	3.8
45	442447	AA999723	ESTs	3.8
	403242		Target Exon	3.8
	433908	AW298141	ESTs	3.8
	452323	W44356	ESTs, Weakly similar to T33468 hypotheti	3.7
	412095	AI624707	Homo sapiens cDNA: FLJ21592 fls, clone C	3.7
50	418759	AA227879	ESTs	3.7
	422299	AK000181	hypothetical protein FLJ20174	3.7
	452452	BE173515	gb:RC2-HT0560-210200-012-03 HT0560 Homo	3.7
	423096	AA732684	progesterone induced protein	3.7
	454037	AW998716	gb:PM4-BN0057-250300-002-f11 BN0067 Homo	3.7
55	428055	AA420584	ESTs	3.7
	447785	AL041765	ESTs	3.7
	451746	M06178	ESTs	3.7
	453293	AA382267	ESTs	3.7
	436671	AW137159	ESTs	3.7
60	407437	AF220264	gb:Homo sapiens MOST-1 mRNA, complete cd	3.7
	408418	AW963697	KIAA1435 protein	3.7
	420092	AA814043	ESTs	3.7
	446947	AF148747	polycythemia rubra vera 1; cell surface	3.7
	441865	AA384728	hypothetical protein FLJ23316	3.7
65	419875	AA853410	proenkephalin	3.7
	431231	AA853552	ESTs	3.7
	418348	AI537187	hypothetical protein FLJ23560	3.7
	419261	X07876	wingless-type MMTV integration site fami	3.7
	422899	D16471	Human mRNA, 3' terminal portion	3.7
70	429163	AA884766	gb:am20a10.s1 Soares_NFL_T_GBC_S1 Homo s	3.7
	439075	AF085933	ESTs	3.7
	440947	AA910403	ESTs	3.7
	404581		trichorhinopharyngeal syndrome 1 gene (T	3.6
	430096	U91935	Retina-derived POU-domain factor-1	3.6
75	430320	BE245290	uncharacterized hypothalamus protein HCD	3.6
	444794	AI419991	ESTs	3.6
	426991	AK001535	Homo sapiens cDNA FLJ10674 fls, clone NT	3.6
	431316	AA502663	ESTs	3.6
	414178	AW957372	ESTs, Weakly similar to I38022 hypotheti	3.6
80	450630	AA010429	ESTs	3.6
	411057	AI881006	ESTs	3.6
	436326	BE085236	aldo-keto reductase family 1, member B1	3.6
	410268	AA316181	six transmembrane epithelial antigen of	3.6
	423590	AW952412	ESTs, Weakly similar to A40348 Elav/Sex-	3.6

	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	3.6
	451193	N29860	Hs.44098	ESTs	3.6
	416239	AL038450	Hs.48948	ESTs	3.6
5	444190	AI878918	Hs.10526	cysteine and glycine-rich protein 2	3.6
	407902	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	3.6
	423349	AF010258	Hs.127428	homeo box A9	3.6
	426917	AA913814	Hs.172854	DKFZP586B0923 protein	3.6
	429430	AI381837	Hs.165335	ESTs	3.6
	433563	AI732637	Hs.277901	ESTs	3.6
10	425465	L18964	Hs.1904	protein kinase C, α iso	3.5
	452498	AK000101	Hs.29700	hypothetical protein FLJ20094	3.5
	401132			C12000517*gi4758712refNP_004659.1[a	3.5
	421105	AA766501	Hs.125113	ESTs	3.5
	435177	AI018174	Hs.42936	ESTs	3.5
15	449343	AI151418		protein phosphatase 3 (formerly 2B), cat	3.5
	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	3.5
	419563	AA526235	Hs.193162	Homo sapiens cDNA FLJ11983 fis, clone HE	3.5
	419994	AA282881	Hs.190057	ESTs	3.5
	427304	AA761526	Hs.163853	ESTs	3.5
20	434763	AA648618		gbms07a11.1 NCLCGAP_Ew1 Homo sapiens	3.5
	447497	AW167254	Hs.205722	ESTs	3.5
	449988	AW372068	Hs.201420	ESTs, Moderately similar to ALU7_HUMAN A	3.5
	422321	AA906427	Hs.181035	hypothetical protein MGC11296	3.5
	418723	AA504428	Hs.10487	Homo sapiens, clone IMAGE:3954132, mRNA,	3.5
25	438680	AA906121	Hs.173421	ESTs	3.5
	452903	AI953425	Hs.345291	ESTs, Weakly similar to I38022 hypotheti	3.5
	443273	AI042063	Hs.132156	ESTs	3.5
	403510			Target Exon	3.5
30	435681	AA684192	Hs.148979	ESTs	3.5
	451722	H86374	Hs.40861	ESTs	3.5
	435981	H74319	Hs.188620	ESTs	3.5
	449845	AW971183	Hs.9883	DnaJ (Hsp40) homolog, subfamily C, membe	3.5
	436024	AI800041	Hs.180555	ESTs	3.5
35	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	3.5
	443324	R44013	Hs.164225	ESTs	3.5
	458332	AI000341	Hs.220491	ESTs	3.5
	435688	H72286	Hs.128387	ESTs	3.4
	435047	AA454985	Hs.54973	cadherin-like protein VR20	3.4
40	432806	NM_002104	Hs.3066	granzyme K (serine protease, granzyme 3;	3.4
	409047	AW961434	Hs.31539	ESTs	3.4
	404848			ENSP00000240769*BG15303.1 (similar to C	3.4
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	3.4
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	3.4
45	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfamily	3.4
	436340	R42246	Hs.21606	ESTs	3.4
	441596	AA939300	Hs.205768	ESTs	3.4
	442231	W02434	Hs.222413	ESTs	3.4
	447124	AW976438	Hs.17428	RBP1-like protein	3.4
50	449517	AW500106	Hs.23543	serine/threonine protein kinase MASK	3.4
	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
	453682	T79703		gb:yd71e08.r1 Soares fetal liver spleen	3.4
	456995	T89832	Hs.170278	ESTs	3.4
	444324	AI301330	Hs.143838	ESTs	3.4
55	400379	NM_018432		Homo sapiens ovarian cancer related prot	3.4
	418964	AA811857	Hs.220913	ESTs	3.4
	424026	AI798295	Hs.137576	ribosomal protein L34 pseudogene 1	3.4
	427033	AI457449	Hs.192817	ESTs	3.4
	453942	AW190920	Hs.19528	hypothetical protein SP329	3.4
60	431421	AW969118	Hs.108144	ESTs, Weakly similar to unnamed protein	3.4
	408784	AW971350	Hs.63386	ESTs	3.4
	420184	AA188408	Hs.95665	hypothetical protein	3.4
	420721	AA827802	Hs.159471	ZAP3 protein	3.4
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	3.4
65	436703	AW860814	Hs.146381	RNA binding motif protein, X chromosome	3.4
	429165	AW009896	Hs.118258	prostate cancer associated protein 1	3.4
	427674	NM_003528	Hs.2178	H2B histone family, member Q	3.4
	412505	AA974491	Hs.21734	ESTs	3.4
	431408	AA504757	Hs.105738	ESTs	3.4
70	438801	AA825971	Hs.124284	ESTs	3.4
	445432	AV853771		gb:AV653771 GLC Homo sapiens cDNA clone	3.4
	418575	AA225313	Hs.222886	ESTs, Weakly similar to TRHY_HUMAN TRICH	3.3
	436345	AA873008	Hs.121572	ESTs	3.3
	423023	N50128	Hs.173400	ESTs	3.3
75	427615	BE410107	Hs.179817	CGI-82 protein	3.3
	429588	AI080271	Hs.134533	ESTs	3.3
	400362	AF068294	Hs.272414	Homo sapiens HDCMB45P mRNA, partial cds	3.3
	425523	AB007948	Hs.158244	KIAA0479 protein	3.3
	426237	AK001104	Hs.168241	hypothetical protein FLJ10242	3.3
	427473	AW274439	Hs.252709	ESTs	3.3
80	434520	AA206273	Hs.177011	hypothetical protein	3.3
	447282	AI989963	Hs.197505	ESTs	3.3
	433554	AW957666	Hs.8108	disabled (Drosophila) homolog 1	3.3
	414818	BE541217	Hs.23606	ESTs	3.3

	418985	AI042330	Hs.87128	hypothetical protein FLJ23309	3.3
	436854	AA749167	Hs.173911	ESTs	3.3
	430865	AI073424	Hs.5232	HSPC125 protein	3.3
5	447182	BE241868	Hs.17585	KIAA0801 gene product	3.3
	423645	AI215632	Hs.147487	ESTs	3.3
	429227	AI951456	Hs.21275	hypothetical protein FLJ11011	3.3
	411928	AA888524	Hs.197289	rab3 GTPase-activating protein, non-cata	3.3
	418051	AW192535	Hs.19479	ESTs	3.3
10	418719	AW975580	Hs.161707	ESTs	3.3
	437714	AA766346	Hs.293242	ESTs	3.3
	455710	BE072049		gb:PM4-BT0532-170100-004-f05 BT0532 Homo	3.3
	421590	AF004715	Hs.105940	jerky (mouse) homolog-like	3.3
	445707	AI248720	Hs.114390	ESTs	3.3
	411436	AW846433		gb:QV0-CT0179-070300-143-b02 CT0179 Homo	3.3
15	426657	NM_015965	Hs.171731	solute carrier family 14 (urea transport	3.3
	423412	AF109300		prostate cancer associated protein 5	3.3
	438962	AW377314	Hs.5364	DKFZP584I052 protein	3.3
	415319	AA659823	Hs.34955	Homo sapiens cDNA FLJ13485 fs, clone PL	3.3
20	429318	AW861930	Hs.102500	hypothetical protein dJ511E16.2	3.3
	433213	AW655130	Hs.137190	ESTs	3.3
	453973	AI291895	Hs.61993	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	3.2
	428043	T92248	Hs.2240	uteroglobin	3.2
25	407385	AA610160	Hs.272072	ESTs, Weakly similar to t38022 hypotheti	3.2
	423595	R82825	Hs.220702	ESTs	3.2
	407021	U62077		gb:Human mariner1 transposase gene, comp	3.2
	418986	AI123555	Hs.81796	ESTs	3.2
	438118	AW753311	Hs.346690	ESTs	3.2
30	447516	W05355	Hs.102971	hypothetical protein FLJ14751	3.2
	449570	AA001793		gb:zh86c06.r1 Soares_fetal_liver_spleen_	3.2
	450687	AA495800		gb:zw05b07.s1 Soares_NhlHMPu_S1 Homo sapi	3.2
	425657	T89839	Hs.119471	ESTs	3.2
	459646	AW883968	Hs.321190	gb:QV3-OT0063-290300-135-c04 OT0063 Homo	3.2
35	408480	AI360337	Hs.164568	fibroblast growth factor 7 (keratinocyte	3.2
	451025	AW028689	Hs.301985	ESTs	3.2
	401416			C14000338:gt[7459502]pir[574665] outer	3.2
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	3.2
	454860	AW835767		gb:QV4-LT0016-240200-110-b08 LT0016 Homo	3.2
40	436995	AI160015	Hs.118112	ESTs	3.2
	428736	AK001331	Hs.192662	hypothetical protein FLJ10469	3.2
	420120	AL049810	Hs.95243	transcription elongation factor A (SII)-	3.2
	422352	AA766296	Hs.99200	ESTs	3.2
	429037	X01895	Hs.194765	H.sapiens GENX-5624 mRNA, 3' UTR	3.2
45	432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	3.2
	445218	T79971	Hs.12432	Homo sapiens clone 24407 mRNA sequence	3.2
	447597	AI886036	Hs.213675	ESTs	3.2
	437886	AA156781		metallothionein 1E (functional)	3.2
	416882	AI633044		tryptophanyl tRNA synthetase 2 (mitochon	3.2
50	410870	U81599	Hs.66731	homeo box B13	3.2
	436899	AF085833	Hs.135624	ESTs	3.2
	415862	RS1034	Hs.144513	ESTs	3.2
	420969	AI636310	Hs.28310	ESTs	3.2
	415467	R60891	Hs.260274	ESTs	3.2
55	412666	AL080116	Hs.74420	origin recognition complex, subunit 3 (y	3.2
	417380	T06809	Hs.332086	ESTs	3.2
	418319	AW611703	Hs.190173	ESTs, Weakly similar to A45010 X-linked	3.2
	410089	AI538323	Hs.52620	Integrin, beta 8	3.2
	422165	AL041199	Hs.1481	histidine decarboxylase	3.2
60	448044	AI458682		gb:tk13e01.x1 NCI_CGAP_Lu24 Homo sapiens	3.2
	452862	AW378065	Hs.8687	ESTs	3.2
	405546			Target Exon	3.1
	439584	AA838114	Hs.221812	ESTs	3.1
	419839	U24577	Hs.93304	phospholipase A2, group VII (platelet-ac	3.1
65	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fs, clone L	3.1
	429568	AA454993	Hs.138343	ESTs, Weakly similar to I78885 vertae/th	3.1
	434512	AW139932	Hs.188941	ESTs	3.1
	452102	U04343	Hs.27954	CD85 antigen (CD28 antigen ligand 2, B7-	3.1
	425856	AA364908	Hs.98927	hypothetical protein FLJ13993	3.1
70	416836	DS4745	Hs.80247	cholecystokinin	3.1
	432589	AL135725	Hs.131708	ESTs	3.1
	420512	AA262886	Hs.143817	ESTs	3.1
	417208	AA291183	Hs.81648	hypothetical protein FLJ11021 similar to	3.1
	410821	AI114811	Hs.92526	ESTs, Weakly similar to T00365 hypotheti	3.1
75	423855	AA331761	Hs.254859	ESTs	3.1
	425905	AB032959	Hs.318584	novel C3HC4 type Zinc finger (ring finger	3.1
	427773	AA412230	Hs.98124	ESTs	3.1
	441817	AW969706	Hs.293332	ESTs	3.1
	456860	AA909249	Hs.112282	solute carrier family 30 (zinc transport	3.1
80	421823	N40850	Hs.28625	ESTs	3.1
	416812	H91010	Hs.44940	ESTs	3.1
	445784	AI253155	Hs.146065	ESTs	3.1
	434384	AA631910	Hs.162849	ESTs	3.1
	416140	AI918035	Hs.301198	roundabout (axon guidance receptor, Dros	3.1

5	407426	AF129533		gb:Homo sapiens F-box protein Fbl3b (FBL	3.1
	416423	H54376	Hs.268921	ESTs	3.1
	418037	A1990212	Hs.86447	ESTs	3.1
	419197	N48921	Hs.27441	KIAA1615 protein	3.1
	420179	N74530	Hs.21168	ESTs	3.1
10	433610	AA806822	Hs.112547	ESTs	3.1
	436295	N73895		gb:aa62d06.s1 Soares fetal liver spleen	3.1
	444800	AW119071	Hs.153287	ESTs	3.1
	418858	AW961605	Hs.21145	hypothetical protein RG083M05.2	3.1
	446469	BE094848	Hs.15113	homogenisate 1,2-dioxygenase (homogenit	3.1
15	431992	NM_002742	Hs.2891	protein kinase C, mu	3.1
	405510			ENSP00000233779: hypothetical 68.0 kDa p	3.1
	407349	AA825449	Hs.83332	Homo sapiens cDNA: FLJ22437 fs, clone H	3.1
	410869	AW808361		gb:MR1-ST0111-111099-003-f04 ST0111 Homo	3.1
	425354	U62027	Hs.155935	complement component 3a receptor 1	3.1
20	425480	AB023198	Hs.158135	KIAA0381 protein	3.1
	441492	AI148998	Hs.146346	ESTs	3.1
	447078	AW885727	Hs.9914	ESTs	3.1
	459324	AW080953		gb:xc28c12.x1 NCL_CGAP_Co18 Homo sapiens	3.1
	433852	A1376329	Hs.126829	ESTs	3.0
25	448658	H71739	Hs.200227	ESTs, Moderately similar to A53959 throm	3.0
	452242	R50956	Hs.158993	glycosyltransferase	3.0
	424690	BE538366	Hs.151777	eukaryotic translation initiation factor	3.0
	405264			NM_030813*: Homo sapiens suppressor of po	3.0
	407253	AA411175	Hs.141939	ESTs, Moderately similar to S65657 alpha	3.0
30	452234	AW084176	Hs.223296	ESTs, Weakly similar to I38022 hypothesi	3.0
	434497	AI821803	Hs.136680	ESTs	3.0
	420955	AW988283	Hs.123126	ESTs	3.0
	403481			Target Exon	3.0
	412988	BE046680		gb:hmr42h03.x1 NCL_CGAP_RDF2 Homo sapiens	3.0
35	452679	Z42387	Hs.83883	transmembrane, prostate androgen induced	3.0
	416542	T96118	Hs.226313	ESTs	3.0
	418948	AI217097		gb:xd43h07.x1 Soares_fetal_heart_NbHH19W	3.0
	426174	AA547959	Hs.115838	ESTs	3.0
	430459	BE178639	Hs.278634	ESTs	3.0
40	439182	AF086030	Hs.21621	hypothetical protein DKFZp762O076	3.0
	446258	AI283476	Hs.263478	ESTs	3.0
	448888	AA158659	Hs.334712	hypothetical protein FLJ14744	3.0
	453455	AA063553	Hs.221931	ESTs, Weakly similar to JC1087 RNA helic	3.0
	414441	AA234759	Hs.132850	ESTs	3.0
45	427302	AA400540	Hs.135282	Homo sapiens cDNA FLJ11564 fs, clone HE	3.0
	437048	AA743240	Hs.91582	ESTs	3.0
	450963	AI864668	Hs.48832	ESTs	3.0
	432336	NM_002759	Hs.274382	protein kinase, Interferon-inducible dou	3.0
	459535	AV654907		gb:AV654907 GLC Homo sapiens cDNA clone	3.0
50	448734	BE614070	Hs.326416	Homo sapiens mRNA; cDNA DKFZp554H1916 f	3.0
	451458	AW503398	Hs.293863	ESTs, Moderately similar to I38022 hypot	3.0
	407829	AA045084	Hs.29725	hypothetical protein FLJ13197	3.0
	420407	AA814732	Hs.145010	lipopolysaccharide-specific response 5-II	3.0
	426743	AA383833	Hs.245022	ESTs	3.0
55	442326	H92862	Hs.124813	hypothetical protein MGC14817	3.0
	449913	AA004896	Hs.333016	ESTs	3.0
	454096	AW062757		gb:CM0-CT0103-120889-037-g07 CT0103 Homo	3.0
	437323	AA371145	Hs.194397	leptin receptor	3.0
	407137	T97307		gb:ya53h05.s1 Soares fetal liver spleen	3.0
60	450580	N40087		ESTs	3.0
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	3.0
	418365	AW014345	Hs.161690	ESTs	3.0
	423784	AK000039	Hs.132828	Homo sapiens cDNA FLJ14913 fs, clone PL	3.0
	435877	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	3.0
65	414951	AW794931	Hs.100861	hypothetical protein FLJ14600	3.0
	418819	AA228776	Hs.191721	ESTs	3.0
	426634	AA811845	Hs.106290	Kelch motif containing protein	3.0
	431869	AA521136	Hs.190176	ESTs	3.0
	435008	AF150262	Hs.182898	ESTs	3.0
70	448880	AW205507	Hs.32360	ESTs, Highly similar to I38587 retroviri	3.0
	451391	AA017410	Hs.40568	ESTs	3.0
	452959	AI933416	Hs.189674	ESTs	3.0

TABLE 64B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

75	Pkey	CAT Number	Accession
	410790	1221131_1	AW803357 AW803423 AW812233 R06814
80	410869	1225123_1	AW808361 AW808404 AW808385 AW808594 AW808654 AW808613 AW808551 AW808676 AW808350 AW808406 AW808694 AW808934 AW808829 AW808385 AW808422 AW808401 AW808409 AW808760 AW808863 AW808521 AW808539 AW808609 AW808472 AW808739 AW808704 AW808558 AW808714 AW808420 AW8 411436 1245860_1 AW846433 AW846159 AW846377 AW846528

411479	1247077_1	AW848047 AW848202 AW848531 AW8486142 AW848702 AW848121 AW848632 AW848140 AW848571 AW848009 AW848067 AW848069
412988	1342150_1	AW848905 AW848214
413081	1348563_1	BE046680 BE046738 BE044958
413525	1374635_1	BE064415 BE064430 BE064448
415989	156454_1	BE145899 BE145848 BE145849 BE145853 BE145927 BE145925
416009	1566379_1	AI267700 AI720344 AA191424 AI023543 AI469633 AA172056 AW958465 AA172236 AW953397 AA355086
416288	1585983_1	Z43062 R13213 H14422
416882	162718_1	H51299 H44619 H46391 R86024 H51892 T72744
418259	173388_1	AI633044 AW016212 AW241143 AA769058 R43272 AW068958 AA210918 AA293774 AI748815 AI763294 AI333114 AI277384 AI088297 AI468477
418866	179788_1	AI824624 AW189606 AI631751 Z40749 AI984673 AI871316 AA189024 AW235412 BE178426 R24677 R40635 H05100 R40597
418948	180808_1	AA215404 AI980908 BE464132 AW271459 N74332 AI262061
419536	185688_1	T65754 AA229857 AA229658
420111	190755_1	AI217097 AW886090 W38035 W38792 AA232835 AW935043
420352	192979_1	AA603305 AA244095 AA244183
423412	228001_1	AA255652 AA280911 AW967920 AA262684
424200	236595_1	BE258835 AW986316 AA258918 AW843305 R14744 AI580388 BE071923 R36280
426413	266650_1	AF109300 AI299378 AI202654
426503	268283_1	AA337221 AA336755 AW966196
426991	27415_1	AA377823 AW954494 AI022688
428002	285602_1	AA380153 AA380233 AW963529
428342	290035_2	AK001536 AA191092 AW510354 AI554256 AL353968 AA134266
429163	300543_1	AA418703 AA418711 BE071915 BE071920 BE071912
429220	301384_1	AI739188 AA428249 AI199636 AW505198 AW977291 AA824583 AA863419 AA724079 AI015524 AI377728 AW293582 AI928140 AA731438
430535	319643_1	AI092404 AI085630 AA731340
432600	350959_1	AA884768 AW974271 AA592975 AA447312
432765	353907_1	AW207206 AW341473 AA448195 AI951341
433523	368873_1	AW958485 AW968670 AA480922 BE350425
434763	392847_1	AI821085 AW973484 AA554802 AI821831 AA557438 AA640756 AA650339
436296	41733_1	AJ003429 AJ003367 AA564825
436326	41795_2	H28882 AW655533 AW149901 AI572917 AA598500 AI686466 AI336390 AW864390 AW864320
437866	44433_2	AA648818 AW974389 H51771
439092	468554_1	N73895 AJ001872
439306	47088_1	BE085236 BE085317 X04236 AA577934 AA578392 AA502836 AA595852 AA578258 AW270791 AA507151 AA559152 T57040 BE503281
440640	50357_2	AW593405 AI825755 AI350499 AI655710 AI972281 AI854949 BE073961 BE073982 BE041399 AW750214 AA228488 BE074016 AI908706
440947	505904_1	AW270601 AW873282
442481	543588_1	AA155781 AW293839 U52054 AA024963 AA778446 BE073977 AW444904 AW602574 BE164040 BE164012 BE163972 BE163974 BE163992
445432	63943_1	AA837481 AW68444 BE185091 AW468002 AA687333 AA811830 AA581806 AI866686 AI572124 AA043777 AA040926 D20160 AI536733
448044	747196_1	AA812489 AW874142 AI47188
449343	80517_2	AA830149 AW978407 M85983 AW503637
449570	81018_1	BE220199 W01813 AF086118 N70760 BE221405
449525	8113_1	AW629666 AW959831 AW205739 BE620243 AA412367 AW300025 AW061920 AI288591 AW238114 AI302862 AI038548 AA534496 AI797207
450317	831856_1	AA921877
450580	83929_1	AA910403 AI815593 W58361 AW162520 AI816550
450582	83933_1	N99828 BE079873 AI110738 AF074645
450687	84327_1	AV653771 BE089370
452462	918580_1	AI458682 H24240 R14537 R18426 AW867082
453682	977454_1	AI151418 W60401 AW631238 AI346936 AA862855 W60310 N72501 H90060 BE150445 AW380821 AI540906 C04881 W03542 AA641764 H97053
454037	998287_1	AW889353 AA521308 AA001203 W92828 AI207798 AA746655 R78710 W24617 AA024805 C01747 AW173095 W61229 W92685 AA742467
454096	1007449_1	H00789 R76925 AW1828
454171	1049240_1	AA001793 AA001871
454457	1207274_1	NH_014253 AF100772 BE088769 AL022718 BE161779 AW863569 BE161640 AI039060 BE168542 AW236554 AA323193 AA235370 AW779760
454860	1237732_1	IA48574 AI375997 R45432 D59344 AI203107 F07491 R35360 R25094 AI913631 AI498402 T61382 AI016320 N45526 T61415 AA331486
454968	1247029_1	AI82689 R14223 R18395
455276	1272541_1	N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816888 AW816889 AW816940
455546	1348557_1	AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150683 AW687764 AW023806 AW022095
455710	1352388_1	AA164518 AA730973 W00417 W65303
457374	328758_1	AI339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878
458912	823104_1	AA495800 AA495737 AA010736 AA654716 AA840726
		BE173615 BE173560 AI902860
		T79703 T96307 AI079725
		AW998716 AW022148 N68020
		AW062757 AW176890 AW062758 AW176895 AW176899 AW176900 AW176897 AW176928 AW176865 AW176892
		AW854832 AW854798 AW854857 AW854816 AW854834 AW854817
		AW753456 AW753036 AW854868 AW854862
		AW835767 AW835537 BE160187
		AW849046 AW847956 AW849039 AW847957 AW848279 AW848598 AW849034 AW849033
		BE176479 BE176678 BE176357 BE176550 AW866079 BE176676 BE176615 BE176555 BE176489 BE176610 BE176362
		BE064420 BE064435 BE064429 BE064414 BE084400 BE064517
		BE072049 BE069471 BE069489 BE069478 BE069479 BE069492 BE069485 BE072122 BE072124 BE069491 BE069486 BE069464
		AA493682 AW897396 BE154814
		AI911066 AI933734 AI680858 AJ003599

TABLE 64C

Pkey: Unlque number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
------	-----	--------	-------------

5	400533	6881826	Minus	277132-277595
	400746	7329328	Minus	147703-147896
	401132	8705350	Minus	85679-85795
	401403	7710986	Plus	146180-146294
	401416	7452889	Minus	121456-121626
	401424	8176894	Plus	24223-24428
	403242	7637817	Minus	11297-12511
	403481	9965004	Plus	93496-93633
10	403510	7652047	Plus	61866-62027
	403667	6850483	Minus	1344-1442,1545-1697
	403696	3135242	Minus	143467-143634
	404003	8655948	Plus	198349-199096
	404561	9795980	Minus	69039-70100
15	404571	7249169	Minus	112450-112648
	404592	9943985	Minus	39087-39225
	404648	8248647	Minus	23955-24034,25143-25264
	405264	7329374	Plus	28556-28684
	405348	2914717	Minus	43310-43462
20	405510	7630909	Minus	101028-101174
	405548	1532168	Plus	11552-11686

25 Table 65A lists about 347 genes up-regulated in BPH compared to prostate cancer tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" BPH to "average" prostate cancer tissues was greater than or equal to 3.0. The "average" BPH level was set to the 75th percentile amongst BPH tissues. The "average" prostate cancer tissue level was set to the 85th percentile amongst malignant prostate tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

30 TABLE 65A: ABOUT 347 GENES UP-REGULATED IN BENIGN PROSTATIC HYPERPLASIA COMPARED TO PROSTATE CANCER TISSUES

35	Pkey:	Unique Eos probeset Identifier number			
	ExAccn:	Exemplar Accession number, Genbank accession number			
	UnigeneID:	Unigene number			
	Unigene Title:	Unigene gene title			
35	R1:	Ratio of BPH tissue to prostate tumor tissue			
	Pkey	ExAccn	Unigene ID	Unigene Title	R1
	428134	AA421773	Hs.161008	ESTs	9.4
	446336	AW815036	Hs.151251	ESTs	9.3
40	456373	BE247706	Hs.89751	membrane-spanning 4-domains, subfamily A	8.9
	458072	AI890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fls, clone K	8.8
	400533			ENSP00000208376*-PRED65 protein (Fragmen	8.7
	418310	AA814100	Hs.86693	ESTs	8.7
45	404592			NM_022739*Homo sapiens E3 ubiquitin lig	8.1
	464457	AW753456		gb:QV2-CT0261-261099-011-d11 CT0261 Homo	7.7
	400080			Eos Control	7.4
	459646	AW883968	Hs.321190	gb:QV3-OT0063-290300-135-c04 OT0063 Homo	7.4
	420362	BE258635		gb:601117374F1 NIH_MGC_16 Homo sapiens c	7.3
50	438231	AW594539	Hs.156689	ESTs	7.3
	418387	R18085		gb:yg16b12.r1 Soares infant brain 1N18 H	7.2
	442481	N99828		gb:za32c04.r1 Soares fetal liver spleen	7.1
	449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	7.0
	457653	AI820719	Hs.154662	DnaJ (Hsp40) homolog, subfamily A, membe	6.9
55	404967			Target Exon	6.9
	430535	AW969486		gb:EST380561 MAGE resequences, MAGJ Homo	6.9
	454860	AW835767		gb:QV4-LT0016-240200-110-b08 LT0016 Homo	6.9
	423789	AK002084	Hs.132851	hypothetical protein FLJ11222	6.8
	412988	BE046680		gb:hn42h03.x1 NCL_CGAP_RDF2 Homo sapiens	6.8
60	400440	X83957	Hs.83870	nebulin	6.6
	454171	AW854832		gb:QV2-CT0261-201099-011-005 CT0261 Homo	6.6
	400086			Eos Control	6.4
	440911	AA909536	Hs.143562	ESTs	6.4
	425312	AA364940	Hs.145958	ESTs	6.4
65	426140	AF131788	Hs.343768	Homo sapiens clone 25119 mRNA sequence	6.4
	419015	T79262	Hs.14463	ESTs	6.3
	453789	AA628517	Hs.118502	ESTs	6.2
	424940	AA965308	Hs.283902	ESTs	6.1
	403667			Target Exon	6.1
70	428014	AI800518	Hs.118156	ESTs	6.0
	417758	U27699	Hs.82535	solute carrier family 6 (neurotransmitte	6.0
	419999	AI760942	Hs.191754	ESTs	6.0
	405348			C7801664.g[1]12698061[db]BAB21849.1] (AB	6.0
	404003			Target Exon	5.9
75	453200	AA033832	Hs.212433	ESTs	5.7
	428002	AA418703		gb:zy98c03.s1 Soares_NhHMPu_S1 Homo sapi	5.7
	432319	AW510770	Hs.126386	ESTs	5.7
	445444	AA380876	Hs.270	pleckstrin homology, Sec7 and coiled-coi	5.6
	443361	AI792628	Hs.133273	ESTs	5.6
80	411518	AW850246		gb:IL3-CT0219-291099-021-E07 CT0219 Homo	5.6
	439079	AF085937	Hs.38348	ESTs	5.5
	422081	AW136820	Hs.196011	ESTs	5.5
	408197	AA282262	Hs.107410	ESTs, Weakly similar to A46010 X-linked	5.5
	423529	T87318	Hs.120411	ESTs	5.5

	436578	AI091435	Hs.134869	ESTs	5.5
	450920	AA011626	Hs.133324	ESTs	5.5
	435072	AW592176	Hs.116932	ESTs	5.4
5	414403	AW969551	Hs.76064	ribosomal protein L27a	5.4
	443744	AI084326	Hs.271548	ESTs, Weakly similar to I78985 serine/th	5.4
	433087	AI720686	Hs.152520	ESTs	5.3
	441916	AA993571	Hs.129075	ESTs	5.3
	414818	BE541217	Hs.23606	ESTs	5.3
10	452531	AA429462	Hs.293946	ESTs, Weakly similar to I38022 hypotheti	5.3
	454968	AW849048		gb:TL3-CT0214-150300-085-H06 CT0214 Homo	5.2
	415890	H08225	Hs.268712	ESTs	5.2
	408385	AF055634	Hs.44553	unc5 (C.elegans homolog) c	5.2
	437752	AA767376	Hs.291831	ESTs, Moderately similar to S65657 alpha	5.2
15	446495	D60923	Hs.153460	ESTs	5.2
	435375	AI733610	Hs.187832	ESTs	5.2
	426748	AL048409	Hs.97177	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	424994	AW954525		gb:EST366595 MAGE resequences, MAGC Homo	5.2
	405321			Target Exon	5.1
20	416706	AA314676	Hs.288946	hypothetical protein FLJ13448	5.1
	438206	AA780385	Hs.187885	ESTs	5.1
	445238	AA883971	Hs.187506	ESTs	5.1
	455747	BE074910		gb:RC5-BT0580-170300-021-F12 BT0580 Homo	5.1
	420633	AI809510	Hs.118971	ESTs	5.1
25	457374	AA493662		gicnh05d12.s1 NCL_OGAP_Thy1 Homo sapiens	5.0
	440354	AA889386	Hs.125468	ESTs	5.0
	440388	AI693520	Hs.223000	ESTs	4.9
	421168	AA284658	Hs.281493	ESTs	4.9
	403481			Target Exon	4.8
30	438132	AA907076	Hs.122060	ESTs	4.8
	403333			NM_002518*.Homo sapiens neuronal PAS dom	4.8
	450317	AI692689		gb:wd86g05.x1 NCL_OGAP_Lu24 Homo sapiens	4.8
	433597	AA708205	Hs.100343	ESTs	4.8
	430172	AA468591	Hs.161889	ESTs	4.8
35	452843	AI796769	Hs.208320	ESTs	4.7
	452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	4.7
	427302	AA400540	Hs.135282	Homo sapiens cDNA FLJ11554 fis, clone HE	4.7
	442123	AI697790	Hs.159961	EST	4.7
	438727	AW978756	Hs.205679	ESTs	4.7
40	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.6
	442160	AI337127	Hs.156325	ESTs	4.6
	442255	AI827248	Hs.224398	Homo sapiens cDNA FLJ11469 fis, clone HE	4.6
	434589	AF147363		gb:Homo sapiens full length insert cDNA	4.6
	404995			ENSP00000251890*.Monocyte leukemia zinc	4.6
45	422906	U80773	Hs.121580	Human EST clone 42944 mariner transposon	4.5
	405549			C7001976*.gij4758712[ref]NP_004659.1[al	4.5
	430697	AA484207	Hs.211867	ESTs	4.5
	443998	AI620661	Hs.296276	ESTs	4.5
	455801	BE140643		gb:RC0-HT0015-310599-016 HT0015 Homo sap	4.5
50	444800	AW119071	Hs.163287	ESTs	4.5
	403371			Target Exon	4.5
	438431	AW207860	Hs.293116	ESTs	4.5
	421926	AA300591		gb:EST13437 Testis tumor Homo sapiens cD	4.5
	439752	T78968	Hs.14411	ESTs	4.5
55	414441	AA234759	Hs.132950	ESTs	4.5
	454665	AW812866		gb:RC3-ST0186-300100-017-b03 ST0186 Homo	4.5
	454585	BE069128		gb:QV3-BT0379-310100-071-g06 BT0379 Homo	4.4
	452978	AA029994	Hs.61523	ESTs	4.4
	438042	AW296971	Hs.180610	ESTs	4.4
60	418059	AA211586		gb:zn66d05.s1 Stragelene muscle 937209 H	4.4
	451469	NM_014809	Hs.26441	KIAA0319 gene product	4.4
	433072	AI928037	Hs.158832	ESTs	4.4
	443318	AI051603	Hs.133141	ESTs	4.4
	424686	AA345604		gb:EST51529 Gall bladder II Homo sapiens	4.3
65	416312	W02640	Hs.16247	ESTs, Weakly similar to 2004399A chromos	4.3
	415467	R60891	Hs.260274	ESTs	4.3
	459045	N69101	Hs.40730	ESTs	4.3
	415417	F12038	Hs.140970	ESTs, Weakly similar to ALU6_HUMAN ALU S	4.3
	409111	AL043362	Hs.7984	pleckstrin homology, Sec7 and collectri	4.3
70	441620	R69595	Hs.26676	ESTs	4.2
	427808	AA417272	Hs.24122	ESTs	4.2
	432765	AJ003429		gb:AJ003429 Selected chromosome 21 cDNA	4.2
	448108	AW300021	Hs.170685	ESTs	4.2
	436345	AA873008	Hs.121572	ESTs	4.2
75	409500	U08098	Hs.54576	sulfotransferase, estrogen-preferring	4.2
	413525	BE145859		gb:MRO-HT0208-221299-204-b10 HT0208 Homo	4.2
	403305	NM_006825		transmembrane protein (63kD), endoplasmic	4.2
	436338	W92147	Hs.118394	ESTs	4.2
	427521	AW973352	Hs.290585	ESTs	4.2
80	430124	AW204994	Hs.253450	ESTs	4.2
	410790	AW803357		gb:IL2-UM0079-090300-050-A08 UM0079 Homo	4.1
	434360	AW015415	Hs.127780	ESTs	4.1
	416385	HS4253	Hs.205241	ESTs, Weakly similar to S65057 alpha-1C-	4.1
	442786	H50733	Hs.256261	ESTs, Moderately similar to ALU8_HUMAN A	4.1

	445206	AI350199	Hs.269990	ESTs	4.1
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	4.1
	448152	AI741053	Hs.170770	ESTs	4.1
5	453713	R20640	Hs.79133	cadherin 8, type 2	4.1
	400746			Target Exon	4.1
	413081	BE064415		gb:RC4-BT0311-241199-012-b03 BT0311 Homo	4.1
	442338	AI761976	Hs.156080	ESTs	4.0
	455388	AW936234		gb:QV0-DT0020-090200-105-g05 DT0020 Homo	4.0
10	455276	BE176479		gb:RC3-HT0585-160300-022-b09 HT0585 Homo	4.0
	421312	AA824627	Hs.291670	ESTs	4.0
	431421	AW969118	Hs.108144	ESTs, Weakly similar to unnamed protein	4.0
	448882	AJ001531	Hs.22404	protease, serine, 12 (neurotrypsin, molo	4.0
	441568	AJ733322	Hs.127176	ESTs	4.0
15	455646	BE064420		gb:RC4-BT0311-241199-012-c06 BT0311 Homo	3.9
	424765	AA428211	Hs.284256	hypothetical protein FLJ14033 similar to	3.9
	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	3.9
	453367	AI990741	Hs.252809	ESTs	3.9
	434222	AF119868	Hs.263941	Homo sapiens PRO2591 mRNA, complete cds	3.9
20	454806	AW872430	Hs.273743	ESTs	3.9
	429066	AA868555	Hs.178222	ESTs	3.9
	435878	R08330	Hs.20152	ESTs	3.9
	453055	AW291436	Hs.31917	Homo sapiens, clone MGC:9558, mRNA, comp	3.9
	447530	AW192063	Hs.248865	ESTs, Moderately similar to JCS238 galac	3.9
25	407834	AW084991	Hs.26100	ESTs	3.9
	400398	AF137395	Hs.283879	ubiquitin 3	3.9
	421353	AW292857	Hs.255130	ESTs	3.9
	401459			C14000482*.g 9790241 ref NP_062626.1 S	3.9
	403433			NM_001622:Homo sapiens alpha-2-HS-glycop	3.9
30	444911	U06117	Hs.250	xanthine dehydrogenase	3.9
	436350	AA713861	Hs.121091	ESTs	3.9
	447930	R44574	Hs.107510	ESTs	3.9
	410559	AW754192		gb:RC2-CT0321-131299-012-a04 CT0321 Homo	3.8
	452320	AA042873	Hs.180412	ESTs	3.8
35	402145			Target Exon	3.8
	458438	AI141520	Hs.151464	ESTs, Weakly similar to ALUC_HUMAN !!!	3.8
	440450	AI333129	Hs.156147	ESTs	3.8
	437587	AI591222	Hs.72325	Human DNA sequence from clone RP1-187J11	3.8
	416009	Z43062		gb:HSC12E041 normalized Infant brain cDN	3.8
40	434381	AA631834		gb:np77h05.s1 NCL CGAP_Py2 Homo sapiens	3.8
	416534	H69043	Hs.224961	Homo sapiens cDNA FLJ14366 fis, clone HE	3.8
	433523	H29982		ESTs	3.8
	411436	AW846433		gb:QV0-CT0179-070300-143-b02 CT0179 Homo	3.8
	424830	AW270580	Hs.189311	ESTs, Weakly similar to putative p150 [H	3.8
45	431447	AA505138	Hs.291341	ESTs	3.8
	435932	W03928	Hs.114524	ESTs	3.8
	442447	AA999723	Hs.129607	ESTs	3.8
	419831	AW448930	Hs.5415	ESTs	3.8
	403242			Target Exon	3.8
50	455490	AW953477		gb:EST365547 MAGE resequences, MAGB Homo	3.8
	449264	AK37649	Hs.196105	ESTs	3.8
	443635	AI080230	Hs.134214	ESTs	3.7
	428200	AI039624	Hs.98388	ESTs	3.7
	452462	BE173615		gb:RC2-HT0580-210200-012-003 HT0580 Homo	3.7
55	418759	AA227879	Hs.187621	ESTs	3.7
	450497	H64159	Hs.15328	ESTs	3.7
	447785	AL041785	Hs.340375	ESTs	3.7
	451746	M86178	Hs.311258	ESTs	3.7
	416321	H94331	Hs.34024	ESTs	3.7
60	448135	AJ470974	Hs.343799	ESTs	3.7
	405510			EN6P00000233779*:Hypothetical 68.0 kDa p	3.7
	407437	AF220264		gb:Homo sapiens MOST-1 mRNA, complete cd	3.7
	451859	H44491	Hs.252938	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	455135	AW857989		gb:PM2-CT0328-281299-003-a04 CT0328 Homo	3.7
65	409189	AA125984		gb:zn27h05.r1 Stratagene neuroepithelium	3.7
	420300	AA258245	Hs.127573	Homo sapiens FKSG41 (FKSG41) mRNA, compl	3.7
	427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	3.7
	434306	AIW081757	Hs.44241	Homo sapiens cDNA: FLJ21447 fis, clone C	3.7
	456354	X56411	Hs.1219	alcohol dehydrogenase 4 (class II), pl p	3.7
70	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	3.7
	422899	D16471	Hs.121571	Human mRNA, Xq terminal portion	3.7
	447458	AI741082	Hs.158961	ESTs	3.7
	411421	BE272110	Hs.21177	ESTs	3.7
	439075	AF085933	Hs.292620	ESTs	3.7
75	440947	AA910403		ESTs	3.7
	417565	AD034005	Hs.47831	ESTs	3.6
	430096	U91935	Hs.233321	Retina-derived POU-domain factor-1	3.6
	448658	H71739	Hs.200227	ESTs, Moderately similar to A53959 throm	3.6
	404561			trichorhinophalangeal syndrome I gene (T	3.6
80	429073	AAA46167	Hs.47385	ESTs	3.6
	419002	T78625	Hs.268594	ESTs	3.6
	450530	AA010429	Hs.191939	ESTs	3.6
	455067	AW854538		gb:RC3-CT0255-200100-024-b02 CT0255 Homo	3.6
	412768	AW996044	Hs.26239	Human DNA sequence from clone RP11-438B2	3.6

	439481	AF086294	Hs.125844	ESTs	3.6
	419622	AA452054	Hs.119338	ESTs	3.6
	449821	AI571141	Hs.211122	ESTs	3.6
5	451193	N28850	Hs.44098	ESTs	3.6
	412701	AW984757		gb:RC1-HN0015-040400-011-g10 HN0015 Homo	3.6
	419611	AB031479	Hs.91600	SEEK1 protein	3.6
	433563	AI732837	Hs.277901	ESTs	3.6
	427235	AI126288	Hs.192232	ESTs	3.6
10	449045	BE072483	Hs.278337	Homo sapiens cDNA FLJ11537 fis, clone HE	3.5
	401132			C12000517:gij4758712[ref NP_004659.1] a	3.5
	421105	AA766501	Hs.125113	ESTs	3.5
	405264			NM_030813:Homo sapiens suppressor of po	3.5
	417675	AI808607	Hs.3781	similar to murine leucine-rich repeat pr	3.5
15	449988	AW372068	Hs.201420	ESTs, Moderately similar to ALU7_HUMAN A	3.5
	434763	AA648618		gb:as07a11.1 r1 NCI_CGAP_Ew1 Homo sapiens	3.5
	416379	N38857	Hs.203933	ESTs	3.5
	407557	Z83803		gb:H.sapiens mRNA for axonemal dynein he	3.5
	437956	AA773283	Hs.203559	hypothetical protein FLJ12701	3.5
20	403510			Target Exon	3.5
	451722	H86374	Hs.40861	ESTs	3.5
	435681	AA694192	Hs.148979	ESTs	3.5
	427125	AA683362	Hs.97612	ESTs	3.5
	424287	AL133105	Hs.144633	hypothetical protein DKFZp434F2322	3.4
25	434497	AI821803	Hs.136580	ESTs	3.4
	453682	T79703		gb:yd71e08.r1 Soares fetal liver spleen	3.4
	404848			ENSP00000240769:BG15303.1 (similar to C	3.4
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	3.4
	442231	W02434	Hs.222413	ESTs	3.4
30	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
	436340	R42246	Hs.21606	ESTs	3.4
	441596	AA538300	Hs.206768	ESTs	3.4
	456995	T89832	Hs.170278	ESTs	3.4
	456304	AI820973		gb:nc21c02.y5 NCI_CGAP_Pr1 Homo sapiens	3.4
35	427033	AI457449	Hs.192817	ESTs	3.4
	400379	NM_018432		Homo sapiens ovarian cancer related prol	3.4
	410551	R38730	Hs.21816	ESTs	3.4
	423357	AI285124	Hs.157505	ESTs	3.4
	450582	AI339732		G-rich RNA sequence binding factor 1	3.4
40	437662	AA765387	Hs.145095	ESTs	3.4
	442388	AW863442	Hs.129485	ESTs	3.4
	445004	AI204616	Hs.148701	ESTs	3.4
	450597	AI701635	Hs.207077	ESTs	3.4
	438801	AA825971	Hs.124284	ESTs	3.4
45	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	3.4
	450003	AA777809	Hs.191895	ESTs	3.4
	431408	AA504757	Hs.105738	ESTs	3.4
	428923	BE047698	Hs.188785	ESTs	3.4
	407344	AI038025	Hs.271418	gb:ox29f07.x1 Soares_tetal_tetus_Nb2HFB_	3.3
50	425523	AB007948	Hs.158244	KIAA0479 protein	3.3
	427473	AW274439	Hs.252709	ESTs	3.3
	437115	AA744703	Hs.129030	ESTs	3.3
	434520	AA205273	Hs.177011	hypothetical protein	3.3
	447282	AI989963	Hs.197505	ESTs	3.3
55	453328	AW282636	Hs.348145	ESTs	3.3
	418985	AI042339	Hs.87128	hypothetical protein FLJ23309	3.3
	449268	AA059050	Hs.59847	ESTs	3.3
	432550	AW287206	Hs.164018	ESTs	3.3
	423101	M83941	Hs.123642	EphA3	3.3
60	424853	BE549737	Hs.132967	Human EST clone 122887 mariner transpos	3.3
	410700	AA352335	Hs.55641	hypothetical protein FLJ20073	3.3
	418719	AW975590	Hs.161707	ESTs	3.3
	402703			Target Exon	3.3
	455710	BE072049		gb:PM4-BT0532-170100-004-f06 BT0532 Homo	3.3
65	452011	AW628911	Hs.211429	ESTs	3.3
	453973	AI291895	Hs.81993	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	420355	AW958263	Hs.123126	ESTs	3.2
	418898	T66847	Hs.194040	ESTs, Weakly similar to I98022 hypotheti	3.2
	418986	AI123555	Hs.81796	ESTs	3.2
70	449570	AA001793		gb:zh88c06.r1 Soares_fetal_liver_spleen_	3.2
	447516	W05356	Hs.102971	hypothetical protein FLJ14751	3.2
	408304	AW810279		gb:MR4-ST0125-151299-029-a09 ST0125 Homo	3.2
	402454			C1002501:gij129082[sp P23270 OLF7_RAT O	3.2
	411552	AW051255		gb:IL3-CT0220-160200-086-H02 CT0220 Homo	3.2
75	407896	D76435	Hs.41154	Zic family member 1 (odd-paired Drosophi	3.2
	435786	H09175	Hs.25085	ESTs	3.2
	447597	AI886036	Hs.213575	ESTs	3.2
	432625	AI243598	Hs.94830	ESTs, Moderately similar to T03094 A-kin	3.2
	459535	AV654907		gb:AV654907 GLC Homo sapiens cDNA clone	3.2
80	447183	AI554733	Hs.173182	ESTs	3.2
	426529	AI203933	Hs.97142	ESTs	3.2
	447892	AI435848	Hs.172978	ESTs	3.2
	457138	AA428240	Hs.126083	ESTs	3.2
	443565	AW466983	Hs.283949	enamelin	3.1

5	451399	AL042110	Hs.326728	ESTs	3.1
	450687	AA495800		gb:zw05b07.s1 Soares_NhHMPu_S1 Homo sapi	3.1
	416812	H91010	Hs.44940	ESTs	3.1
	452102	U04343	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-	3.1
	434512	AW139832	Hs.188941	ESTs	3.1
	458251	AL040927	Hs.210422	ESTs	3.1
	439950	AW937417	Hs.293561	ESTs	3.1
	429669	AA454993	Hs.138343	ESTs, Weakly similar to I78885 serine/th	3.1
10	403805			Target Exon	3.1
	422666	AA677981	Hs.119023	SMC2 (structural maintenance of chromoso	3.1
	408799	AA059412	Hs.47986	hypothetical protein MGC10940	3.1
	429350	AJ754634	Hs.131987	ESTs	3.1
	430454	AW469011	Hs.105635	ESTs	3.1
15	441817	AW969706	Hs.293332	ESTs	3.1
	427773	AA412290	Hs.98124	ESTs	3.1
	415901	H08396	Hs.76118	ubiquitin carboxyl-terminal esterase L1	3.1
	445753	R60715	Hs.25804	ESTs	3.1
	403291			Target Exon	3.1
20	436295	N73895		gb:za62d06.s1 Soares fetal liver spleen	3.1
	455772	W28799		gb:52g11 Human retina cDNA randomly prim	3.1
	418037	AJ990212	Hs.86447	ESTs	3.1
	438142	T90308	Hs.269661	ESTs	3.1
	418423	H54375	Hs.268921	ESTs	3.1
25	448766	R16337	Hs.21958	Homo sapiens mRNA; cDNA DKFZp547D086 (fr	3.1
	457021	AW968934	Hs.173108	Homo sapiens cDNA: FLJ21897 fis, clone H	3.1
	420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	3.1
	420721	AA927802	Hs.159471	ZAP3 protein	3.1
	436013	AA703419	Hs.287749	Homo sapiens cDNA: FLJ23593 fis, clone L	3.1
30	441492	AJ149998	Hs.146346	ESTs	3.1
	410869	AW808361		gb:MR1-ST0111-111099-003-004 ST0111 Homo	3.1
	419386	AA236867		ESTs, Weakly similar to I38022 hypotheti	3.1
	436628	W88732	Hs.36107	ESTs	3.0
	444326	AJ939357	Hs.270710	ESTs	3.0
35	413774	AA131782	Hs.182314	ESTs	3.0
	434352	AF129505	Hs.86492	small muscle protein, X-linked	3.0
	434269	AK001991	Hs.3781	similar to murine leucine-rich repeat pr	3.0
	416422	H80467		ESTs, Moderately similar to ZN91_HUMAN Z	3.0
	416642	T96118	Hs.226313	ESTs	3.0
40	439182	AF086030	Hs.21621	hypothetical protein DKFZp762C078	3.0
	418948	AJ217097		gb:qd43h07.x1 Soares_fetal_heart_NbHH19W	3.0
	433796	AA810867	Hs.186997	ESTs	3.0
	427813	D29833	Hs.2207	salivary proline-rich protein	3.0
	405733			NM_021140: Homo sapiens ubiquitously tra	3.0
45	426743	AA383833	Hs.245022	ESTs	3.0
	449913	AA004696	Hs.333016	ESTs	3.0
	454096	AW062757		gb:CMD-CT0103-120899-037-g07 CT0103 Homo	3.0
	440128	AA865818	Hs.174938	ESTs, Weakly similar to S71885 Sio20-Ik	3.0
	410929	H47233	Hs.30643	ESTs	3.0
50	458167	D56919	Hs.265848	myomegalin	3.0
	429430	AJ381837	Hs.155335	ESTs	3.0
	451391	AA017410	Hs.40568	ESTs	3.0
	414951	AW794831	Hs.100861	hypothetical protein FLJ14600	3.0

55 TABLE 65B

Pkey:	Unique Eos probeset identifier number	
	CAT number: Gene cluster number	
Accession:	Genbank accession numbers	
Pkey	CAT Number	Accession
408304	1050848_1	AW810279 BE146684 BE146693 BE146694 BE146679 AW810472 AW810208 AW810356 AW810193 AW178838 AW178837 AW178857 AW810515 AW810330 AW810514 AW810441 AW810358 AW178852 AW810359 AW810322 AW810327 AW810211 AW178835 AW810535 AW810288 AW810263 AW810325 AW810443 AW8
65	409189	110687_1
		AA125984 AA127189 AA066075 AA070377 AA100017 AA079891 AA113255 AA075168 AA082764 AA083380 N84829 AA084762 AA076512 AA085119 AA085208 AA085045
	410559	1208283_1
	410790	1221131_1
	410869	1225123_1
70		AW754192 W00554 AW857797 AW754203 AW754197 AW754193 AW803357 AW803423 AW812233 R06814 AW808361 AW808404 AW808386 AW808594 AW808654 AW808813 AW808861 AW808676 AW808350 AW808406 AW808694 AW808934 AW808829 AW808385 AW808422 AW808401 AW808409 AW808760 AW808863 AW808521 AW808539 AW808609 AW808472 AW808739 AW808704 AW808558 AW808714 AW808420 AW8
	411436	1245660_1
	411518	1248692_1
	411552	1249255_1
75	412701	1322288_1
	412988	1342150_1
	413081	1348563_1
	413525	1374635_1
80	416009	1566379_1
	416422	1593811_1
	418059	171879_1
	418387	174731_1
	418948	180808_1
		AW754192 W00554 AW857797 AW754203 AW754197 AW754193 AW803357 AW803423 AW812233 R06814 AW808361 AW808404 AW808386 AW808594 AW808654 AW808813 AW808861 AW808676 AW808350 AW808406 AW808694 AW808934 AW808829 AW808385 AW808422 AW808401 AW808409 AW808760 AW808863 AW808521 AW808539 AW808609 AW808472 AW808739 AW808704 AW808558 AW808714 AW808420 AW8
		AW848433 AW846159 AW846377 AW848528 AW850246 AW860251 AW850302 AW851255 AW851432 AW860855 AW984757 AW984797 AW984734 AW984745 BE046680 BE046738 BE044958 BE064415 BE064430 BE064448 BE145899 BE145848 BE145849 BE145853 BE145927 BE145925 Z43062 R13213 H14422 H60457 H68709 H73528 H54335 R87154 AA211586 F35799 AA211641 F29720 AW937387 AW937408 R18085 AA219028 R17712 Z44345 AJ217097 AW886090 W36035 W38792 AA232835 AW936043

5	149386	184356_1	AA236867 AA237066 AA354236 AW957759 H08961
	420352	192979_1	BE258835 AW968316 AA258918 AW843305 R14744 AI580388 BE071923 R36280
	421926	209246_1	AA300691 AW953893 AA300493
	424200	236595_1	AA337221 AA336756 AW966195
	424686	242486_1	AA345504 AA345251 AW953243
	424994	245786_1	AW954525 AI372685 AA349501 AI372687 H10564
	428002	285602_1	AA418703 AA418711 BE071915 BE071920 BE071912
	430535	319643_1	AW968485 AW968670 AA480922 BE350425
10	432765	353907_1	AJ003429 AJ003357 AA564825
	433523	368873_1	H29882 AW665533 AW149901 AI572917 AA598500 AI686466 AI336390 AW864390 AW864320
	434381	385155_1	AA631834 AA633425 AA632455 AI792312 AI792311
	434589	38929_1	AF147363 T47219 T47218
	434763	392847_1	AA648618 AW974389 H51771
15	436295	41733_1	N73895 AJ001872
	440947	505904_1	AA910403 AI815593 W58361 AW162520 AI816550
	442481	543588_1	N99828 BE079873 AI110738 AF074645
	445432	63943_1	AV653771 BE069370
	449570	81018_1	AA001793 AA001871
20	450317	831956_1	AI692689 R14223 R18395
	450582	83933_1	AI339732 AAD10300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878
	450687	84327_1	AA495800 AA495737 AA010736 AA654716 AA640726
	452462	918580_1	BE173515 BE173550 AI902860
	453682	977454_1	T79703 T96307 AL079725
25	454086	1007449_1	AW062757 AW176880 AW062758 AW176895 AW176869 AW176900 AW176897 AW176928 AW176868 AW176892
	454171	1049240_1	AW854832 AW854796 AW854857 AW854816 AW854834 AW854817
	454457	1207274_1	AW753456 AW753036 AW854868 AW854862
	454585	1225852_1	BE069128 BE069023 AW809375
	454665	1228599_1	AW812866 AW812748 AW812747 AW812864 AW812763 AW812722
30	454860	1237732_1	AW835767 AW835537 BE160187
	454968	1247029_1	AW849046 AW847956 AW849039 AW847957 AW848279 AW848698 AW849034 AW849033
	455067	1252050_1	AW854538 AW854418 AW854412
	455135	1254729_1	AW857989 AW858016 AW851677 AW861689 AW861691 AW858056
	455276	1272541_1	BE176479 BE176578 BE176357 BE176550 AW886079 BE176876 BE176615 BE176555 BE176489 BE176610 BE176362
35	455388	1287904_1	AW936234 AW936074 AW936181 AW936179 AW936217 AW936077 AW936227 AW936191
	455490	1297826_1	AW963477 Z41970 F12435 T73989 T09387
	455646	1348657_1	BE064420 BE064435 BE064429 BE064414 BE064400 BE064517
	455710	1352368_1	BE072049 BE069471 BE069489 BE069478 BE069479 BE069492 BE069485 BE072122 BE072124 BE068491 BE069486 BE068464
	455747	1355877_1	BE074910 BE074913 BE074911 BE074903 BE074892 BE074895
40	455772	1363114_1	W28799 BE086078
	455801	1370508_1	BE140643 BE140645 BE140644 BE140657 BE140660 BE140659 BE140661
	456304	176820_1	AI820973 AI734077 AI820984 AA225796 AA225080 AA225101
	457374	328758_1	AA493662 AW897398 BE154814

TABLE 65C

50	Pkey:	Unique number corresponding to an Eos probaset		
	Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.		
	Strand:	Indicates DNA strand from which exons were predicted.		
	Nt_position:	Indicates nucleotide positions of predicted exons.		
55	Pkey	Ref	Strand	Nt_position
	400533	6981826	Minus	277132-277596
	400746	7329328	Minus	147703-147896
	401132	8705350	Minus	85679-85795
	401459	9212270	Minus	182001-183323
60	402145	8018280	Plus	113086-114800
	402454	7534025	Minus	14826-15803
	402703	8705069	Minus	15335-15500
	403242	7637817	Minus	11297-12511
	403291	7230870	Plus	95177-95435
65	403305	8099945	Plus	114632-114805
	403333	8568833	Minus	124794-124941
	403371	9087278	Plus	105655-106050
	403433	9719611	Minus	72225-72437
	403481	9965004	Plus	93498-93633
	403510	7652047	Plus	61888-62027
70	403667	8850483	Minus	1344-1442,1545-1697
	403805	8140491	Minus	51483-51742,53429-53511
	404003	8655948	Plus	198349-199096
	404561	9795980	Minus	69039-70100
75	404592	9943955	Minus	39067-39225
	404848	8248647	Minus	23955-24034,25143-25264
	404957	7523744	Minus	89944-90729
	404995	6008247	Minus	154015-154123
	405264	7329374	Plus	28556-28684
80	405321	3419846	Minus	44654-45210
	405348	2914717	Minus	43310-43462
	405510	7630909	Minus	101028-101174
	405549	1552494	Plus	10878-11048
	405733	9884689	Plus	124832-125051

Table 66A lists about 370 genes up-regulated in BPH compared to prostate cancer and normal adult tissues. These were selected from 59680 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" BPH to "average" prostate cancer and normal adult tissues was greater than or equal to 3.0. The "average" BPH level was set to the 75th percentile amongst BPH tissues. The "average" prostate cancer and normal adult tissue level was set to the 85th percentile amongst malignant prostate tissues and normal adult tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant body tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

TABLE 66A: ABOUT 370 GENES UP-REGULATED IN BENIGN PROSTATIC HYPERPLASIA COMPARED TO PROSTATE CANCER AND NORMAL ADULT TISSUES

Pkey:	Unique Eos probeset identifier number			
ExAccn:	Exemplar Accession number, Genbank accession number			
UnigeneID:	Unigene number			
Unigene Title:	Unigene gene title			
R1:	Ratio of BPH tissue to prostate tumor and normal body tissue			
Pkey	ExAccn	Unigene ID	Unigene Title	R1
410929	H47233	Hs.30643	ESTs	21.1
450693	AW450461	Hs.203965	ESTs	16.7
418432	M14156	Hs.85112	insulin-like growth factor 1 (somatomedi	14.2
432473	AJ202703	Hs.152414	ESTs	11.3
446336	AW815036	Hs.151251	ESTs	10.9
407275	AJ364188		gb:qv34h07.x1 NCL_CGAP_Ut4 Homo sapiens	10.7
428134	AA421773	Hs.161008	ESTs	10.2
400297	AJ127076	Hs.306201	hypothetical protein DKFZp564O1278	9.8
433466	AA508363	Hs.105314	relaxin 1 (H1)	9.5
415293	R49462	Hs.106541	ESTs	9.1
458072	AJ890347	Hs.271923	Homo sapiens cDNA: FLJ22785 fls, clone K	8.8
428927	AA441837	Hs.90250	ESTs	8.6
420345	AW295230	Hs.25231	ESTs	8.5
453367	AJ90741	Hs.252809	ESTs	8.2
454457	AW753456		gb:QV2-CT0261-261099-011-d11 CT0261 Homo	7.7
441247	AW118581	Hs.128051	Homo sapiens thymic stromal lymphopole	7.5
431576	M76665	Hs.275215	hydroxysteroid (11-beta) dehydrogenase 1	7.4
400080			Eos Control	7.4
431448	AL137517	Hs.308201	hypothetical protein DKFZp564O1278	7.4
404592			NM_022739*:Homo sapiens E3 ubiquitin lig	7.3
420352	BE258835		gb:601117374F1 NIH_MGC_16 Homo sapiens c	7.3
438231	AW594539	Hs.155689	ESTs	7.3
410330	AW023530	Hs.159425	ESTs	7.2
449300	AJ656959	Hs.346514	ESTs	7.1
449249	T52285	Hs.193115	Homo sapiens mRNA for KIAA1764 protein,	7.0
426384	AJ472078	Hs.303682	hypothetical protein FLJ13189 (FLJ13189)	6.8
454171	AW854832		gb:QV2-CT0261-201099-011-805 CT0261 Homo	6.6
408197	AA282262	Hs.107410	ESTs, Weakly similar to A46010 X-linked	6.6
429732	U20158	Hs.2488	lymphocyte cytosolic protein 2 (SH2 doma	6.6
421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fls, clone PL	6.5
431467	N71831	Hs.256398	Homo sapiens mRNA: cDNA DKFZp434E0528 (f	6.5
424433	H04607	Hs.9218	ESTs	6.5
442481	N99928		gb:zs32c04.r1 Soares fetal liver spleen	6.4
425312	AA354940	Hs.145958	ESTs	6.4
426140	AF131798	Hs.343768	Homo sapiens clone 25119 mRNA sequence	6.4
440911	AA909536	Hs.143562	ESTs	6.4
400533			ENSP00000209376*:PRED65 protein (Fragmen	6.2
418310	AA814100	Hs.86693	ESTs	6.2
403667			Target Exon	6.1
436395	AJ683487	Hs.152213	wingless-type MMTV integration site fami	6.1
404003			Target Exon	5.9
424853	BE549737	Hs.132967	Human EST clone 122887 mariner transpos	5.9
438138	R98299	Hs.177502	ESTs	5.9
424940	AA985308	Hs.283902	ESTs	5.8
434485	AJ623511	Hs.118567	ESTs	5.8
453200	AA033832	Hs.212433	ESTs	5.7
428002	AA418703		gb:zv98c03.s1 Soares_NhHMPu_S1 Homo sapi	5.7
424860	AA151057	Hs.153498	chromosome 18 open reading frame 1	5.6
445444	AA380876	Hs.270	pleckstrin homology, Sec7 and coiled/coi	5.6
443351	AJ792628	Hs.133273	ESTs	5.6
421513	X00949	Hs.105314	relaxin 1 (H1)	5.5
439079	AF083937	Hs.38348	ESTs	5.5
430535	AW958485		gb:EST380561 MAGE resequences, MAGJ Homo	5.5
436578	AJ091435	Hs.134859	ESTs	5.5
424051	AL110208	Hs.138411	Homo sapiens mRNA: cDNA DKFZp586J1922 (f	5.4
421853	AJ852677	Hs.108972	Homo sapiens mRNA: cDNA DKFZp434P228 (fr	5.4
435072	AW592176	Hs.116932	ESTs	5.4
435375	AJ733610	Hs.187832	ESTs	5.4
444609	AW571659	Hs.278061	ESTs	5.4
416602	NM_006159	Hs.79389	nei (chicken)-like 2	5.4
433087	AJ720686	Hs.152520	ESTs	5.3
439062	AA630149		gb:oc44R08.s1 NCL_CGAP_GCB1 Homo sapiens	5.3
437267	AW511443	Hs.258110	ESTs	5.3
441916	AA993571	Hs.129075	ESTs	5.3
452784	BE463857	Hs.151258	hypothetical protein FLJ21062	5.3
452531	AA429462	Hs.293946	ESTs, Weakly similar to 138022 hypotheti	5.3

	423101	M83941	Hs.123642	EphA3	5.3
	437587	AI591222	Hs.72325	Human DNA sequence from clone RP1-187J11	5.2
	415890	H08225	Hs.268712	ESTs	5.2
5	454968	AW849046		gb:IL3-CT0214-150300-085-H06 CT0214 Homo	5.2
	408385	AF055634	Hs.44553	unc5 (C.elegans homolog) c	5.2
	437752	AA767376	Hs.291631	ESTs, Moderately similar to S65657 alpha	5.2
	446495	D60923	Hs.153460	ESTs	5.2
	422906	U80773	Hs.121580	Human EST clone 42944 mariner transposon	5.2
10	427726	AI359144	Hs.143688	Homo sapiens cDNA: FLJ23031 fis, clone L	5.2
	426748	AL048409	Hs.97177	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.2
	436338	W92147	Hs.118394	ESTs	5.2
	416706	AA314676	Hs.288945	hypothetical protein FLJ13448	5.1
	440129	AA855818	Hs.174936	ESTs, Weakly similar to S71886 Ste20-Hk	5.1
	445238	AA863971	Hs.187506	ESTs	5.1
15	450582	AI339732		G-rich RNA sequence binding factor 1	5.1
	420533	AI809510	Hs.118971	ESTs	5.1
	438447	AI082883	Hs.30732	hypothetical protein FLJ13409; KIAA1711	5.1
	440354	AA889386	Hs.125468	ESTs	5.0
	452891	N75582	Hs.212875	ESTs, Weakly similar to DYH9_HUMAN CILIA	5.0
20	457374	AA433662		gb:nh05d12.a1 NCL_CGAP_Thy1 Homo sapiens	5.0
	408829	NM_005042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfot	5.0
	448041	AW292769	Hs.206228	ESTs	5.0
	457653	AB207119	Hs.154662	DnaI (Hsp40) homolog, subfamily A, membe	4.9
	450497	H64159	Hs.15328	ESTs	4.8
25	438132	AA907076	Hs.122060	ESTs	4.8
	414818	BE541217	Hs.23606	ESTs	4.8
	429433	AA452899	Hs.213586	ESTs, Weakly similar to KIAA1353 protein	4.8
	433523	H29882		ESTs	4.8
	450317	AI892689		gb:wd86g05.x1 NCL_CGAP_Lu24 Homo sapiens	4.8
30	443635	AI080230	Hs.134214	ESTs	4.8
	430172	AA468591	Hs.161889	ESTs	4.8
	452843	AI796769	Hs.208320	ESTs	4.7
	427302	AA400540	Hs.135282	Homo sapiens cDNA FLJ11554 fis, clone HE	4.7
	452031	AA741314	Hs.865	RAP1A, member of RAS oncogene family	4.7
35	423789	AK002084	Hs.132851	hypothetical protein FLJ11222	4.7
	417173	U61397	Hs.81424	ubiquitin-like 1 (sentrin)	4.6
	420931	AF044197	Hs.100431	small inducible cytokine B subfamily (Cy	4.6
	454024	AA993527	Hs.293907	hypothetical protein FLJ23403	4.6
	405348			C7001654.g[12698061]dbj[BAB21849.1] (AB	4.6
40	419511	AA429750	Hs.75113	general transcription factor IIIA	4.6
	447058	AI939458	Hs.180870	ESTs	4.6
	428218	AA424268	Hs.123642	EphA3	4.6
	430697	AA484207	Hs.211857	ESTs	4.5
45	433280	AA581404	Hs.289037	Homo sapiens cDNA FLJ14135 fis, clone MA	4.5
	449821	AI871141	Hs.211122	ESTs	4.5
	420905	AA521307	Hs.186651	ESTs	4.5
	439752	T78968	Hs.14411	ESTs	4.5
	452055	AI377431	Hs.141693	hypothetical protein MGC10858	4.5
50	430188	AL048242	Hs.234794	Homo sapiens mRNA; cDNA DKFZp554B083 (fr	4.4
	423352	AA324808	Hs.193576	ESTs	4.4
	438042	AW296971	Hs.180610	ESTs	4.4
	452978	AA029994	Hs.61523	ESTs	4.4
	420154	AI083155	Hs.95420	JM27 protein	4.4
55	428249	AA130914	Hs.183291	zinc finger protein 268	4.4
	442242	AV647808	Hs.90424	Homo sapiens cDNA: FLJ23285 fis, clone H	4.4
	452498	AK000101	Hs.29700	hypothetical protein FLJ20094	4.4
	459527	AW977556	Hs.291735	ESTs, Weakly similar to I78885 serine/th	4.3
	433597	AA708205	Hs.100343	ESTs	4.3
60	416312	W02640	Hs.16247	ESTs, Weakly similar to 2004399A chromos	4.3
	420111	AA255652		gb:cs21h11.r1 NCL_CGAP_GCB1 Homo sapiens	4.3
	459045	N69101	Hs.40730	ESTs	4.3
	409705	M37762	Hs.56023	brain-derived neurotrophic factor	4.3
	433433	AI692623	Hs.121513	Homo sapiens clone Z'3-1 placenta expres	4.2
65	427808	AA417272	Hs.24122	ESTs	4.2
	432765	AJ003429		gb:AJ003429 Selected chromosome 21 cDNA	4.2
	413525	BE145899		gb:MR0-HT0208-221299-204-b10 HT0208 Homo	4.2
	420355	AW968263	Hs.123126	ESTs	4.2
	427521	AW973352	Hs.290585	ESTs	4.2
70	458912	AI911066		ESTs	4.2
	410790	AW803357		gb:IL2-UM0079-090300-050-A08 UM0079 Homo	4.1
	415245	N59650	Hs.27252	ESTs	4.1
	434360	AW015415	Hs.127780	ESTs	4.1
	442786	H50733	Hs.256261	ESTs, Moderately similar to ALU8_HUMAN A	4.1
75	450597	AI701635	Hs.207077	ESTs	4.1
	424200	AA337221		gb:EST41944 Endometrial tumor Homo sapie	4.1
	445206	AI350199	Hs.269990	ESTs	4.1
	438431	AW207860	Hs.293116	ESTs	4.1
	448152	AI741053	Hs.170770	ESTs	4.1
80	438675	AA827640	Hs.189059	ESTs	4.1
	400746			Target Exon	4.1
	413081	BE064415		gb:RC4-BT0311-241188-012-b03 BT0311 Homo	4.1
	404967			Target Exon	4.0
	427203	AW629517	Hs.244855	ESTs	4.0

	442338	AI761976	Hs.156080	ESTs	4.0
	455276	BE178479		gb:RC3-HT0585-160300-022-b09 HT0585 Homo	4.0
	452903	AI953425	Hs.345291	ESTs, Weakly similar to I38022 hypothe	4.0
5	436136	R27299	Hs.10172	ESTs	4.0
	416780	H85182	Hs.191327	ESTs, Highly similar to KIAA1102 protein	4.0
	421312	AA824627	Hs.291670	ESTs	4.0
	441568	AI733322	Hs.127176	ESTs	4.0
	441736	AW292779	Hs.8182	ESTs	4.0
10	448882	AJ001531	Hs.22404	protease, serine, 12 (neurotrypsin, moto	4.0
	434222	AF119886	Hs.283941	Homo sapiens PRO2591 mRNA, complete cds	3.9
	420301	AA767526	Hs.22030	paired box gene 5 (B-cell lineage specif	3.9
	429066	AA868555	Hs.178222	ESTs	3.9
	435878	R08330	Hs.20152	ESTs	3.9
15	447530	AW192063	Hs.248865	ESTs, Moderately similar to JC5238 galac	3.9
	412988	BE046680		gb:hn42h03.x1 NCL CGAP_RDF2 Homo sapiens	3.9
	410196	AI936442	Hs.59838	hypothetical protein FLJ10608	3.9
	411084	T18987	Hs.125472	ESTs, Moderately similar to KIAA0877 pro	3.9
	419529	AB020695	Hs.91652	KIAA0888 protein	3.9
20	455646	BE064420		gb:RC4-BT0311-241199-012-c08 BT0311 Homo	3.9
	414441	AA234759	Hs.132950	ESTs	3.9
	425810	AI923627	Hs.31903	ESTs	3.9
	409111	AL043362	Hs.7984	pleckstrin homology, Sec7 and coiled/coi	3.9
	411479	AW846047		gb:IL3-CT0214-291299-052-A12 CT0214 Homo	3.9
25	440450	AI333129	Hs.156147	ESTs	3.8
	428342	AI739168		Homo sapiens cDNA FLJ13458 fis, clone PL	3.8
	431421	AW989118	Hs.108144	ESTs, Weakly similar to unnamed protein	3.8
	416009	Z43062		gb:HSC12E041 normalized infant brain cDN	3.8
	416534	H69043	Hs.224961	Homo sapiens cDNA FLJ14366 fis, clone HE	3.8
30	407198	H91679		gb:yv04a07.s1 Soares fetal liver spleen	3.8
	419831	AW448930	Hs.5415	ESTs	3.8
	424830	AW270580	Hs.189311	ESTs, Weakly similar to putative p150 [H	3.8
	431447	AA505138	Hs.291341	ESTs	3.8
	435932	W03928	Hs.114524	ESTs	3.8
35	442447	AA999723	Hs.129607	ESTs	3.8
	403242			Target Exon	3.8
	433808	AW298141	Hs.157975	ESTs	3.8
	454037	AW998716		gb:PM4-BN0087-250300-002-f11 BN0067 Homo	3.7
40	432101	AI918950	Hs.123642	EphA3	3.7
	418759	AA227879	Hs.187621	ESTs	3.7
	452482	BE173615		gb:RC2-HT0560-210200-012-f03 HT0560 Homo	3.7
	448568	AA149121	Hs.71847	ESTs	3.7
	447785	AL041765	Hs.340375	ESTs	3.7
	451746	M86178	Hs.311258	ESTs	3.7
45	438345	AA873008	Hs.121572	ESTs	3.7
	446862	AV660687	Hs.282700	ESTs	3.7
	419875	AA853410	Hs.93557	proenkephalin	3.7
	421040	AA715026	Hs.135280	ESTs	3.7
	454860	AW835757		gb:QV4-LT0016-240200-110-b08 LT0016 Homo	3.7
50	450687	AA495800		gb:zw05b07.s1 Soares NtHMPu_S1 Homo sapi	3.7
	407437	AF220264		gb:Homo sapiens MOST-1 mRNA, complete cd	3.7
	431474	AL133990	Hs.190642	CEGP1 protein	3.7
	448004	AW451477	Hs.257456	ESTs	3.7
	419261	X07876	Hs.89791	wingless-type MMTV integration site fami	3.7
55	422899	O16471	Hs.121571	Human mRNA, 3' terminal portion	3.7
	439075	AF085933	Hs.292620	ESTs	3.7
	440947	AA910403		ESTs	3.7
	447458	AI741082	Hs.158961	ESTs	3.7
	403481			Target Exon	3.6
60	404561			trichorhinophthalangeal syndrome 1 gene (T	3.6
	417665	AI203405	Hs.47831	ESTs	3.6
	430096	U91935	Hs.233321	Retina-derived POU-domain factor-1	3.6
	448658	H71739	Hs.200227	ESTs, Moderately similar to A53959 throm	3.6
	449655	AI021887	Hs.59970	ESTs	3.6
65	450630	AA010429	Hs.191939	ESTs	3.6
	455067	AW854538		gb:RC3-CY0255-200100-024-b02 CT0255 Homo	3.6
	423666	AW976434	Hs.3623	hypothetical protein FLJ11220	3.6
	451193	N29850	Hs.44098	ESTs	3.6
	420026	AI831190	Hs.166676	ESTs	3.6
70	426917	AA913814	Hs.172654	DKFZP566B0923 protein	3.6
	429430	AI381837	Hs.155335	ESTs	3.6
	433563	AI732637	Hs.277901	ESTs	3.6
	443744	AI084326	Hs.271548	ESTs, Weakly similar to I78885 serine/th	3.5
	456373	BE247708	Hs.89751	membrane-spanning 4-domains, subfamily A	3.5
75	419589	AW973708	Hs.201925	Homo sapiens cDNA FLJ13446 fis, clone PL	3.5
	401132			C120005177:gil4758712[re]NP_004659.1] a	3.5
	421105	AA766501	Hs.125113	ESTs	3.5
	435177	AI018174	Hs.42936	ESTs	3.5
	434763	AA648618		gb:ne07a11.r1 NCL CGAP_Ew1 Homo sapiens	3.5
80	449988	AW372068	Hs.201420	ESTs, Moderately similar to ALU77_HUMAN A	3.5
	450216	AA573345	Hs.50226	Homo sapiens, clone IMAGE:3621638, mRNA,	3.5
	403510			Target Exon	3.5
	435681	AA694192	Hs.148979	ESTs	3.5
	451722	H86374	Hs.40861	ESTs	3.5

	430865	AI073424	Hs.5232	HSPC125 protein	3.5
	444800	AW119071	Hs.153287	ESTs	3.5
	428647	AA830050	Hs.124344	ESTs	3.5
5	412775	AA709046	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	3.5
	429643	AA455889	Hs.167279	FYVE-finger-containing Rab5 effector pro	3.5
	443324	R44013	Hs.164225	ESTs	3.5
	430124	AW204994	Hs.253450	ESTs	3.4
	430701	AI760833	Hs.293971	ESTs	3.4
	436714	AA728964	Hs.293399	ESTs	3.4
10	404848			ENSP00000240769*:BG15303.1 (similar to C	3.4
	408480	AI350337	Hs.164568	fibroblast growth factor 7 (keratinocyte	3.4
	412494	AL133900	Hs.792	ADP-ribosylation factor domain protein 1	3.4
	417435	NM_005181	Hs.82129	carbonic anhydrase III, muscle specific	3.4
15	430403	AF039390	Hs.241382	tumor necrosis factor (ligand) superfamily	3.4
	436340	R42246	Hs.21606	ESTs	3.4
	441596	AA939300	Hs.206768	ESTs	3.4
	442231	W02434	Hs.222413	ESTs	3.4
	447124	AW976438	Hs.17428	RBP1-like protein	3.4
20	450297	AW901347	Hs.38592	hypothetical protein FLJ23342	3.4
	453682	T79703		gb:yd71e08.r1 Soares fetal liver spleen	3.4
	456955	T89832	Hs.170278	ESTs	3.4
	405510			ENSP00000233779*:Hypothetical 68.0 kDa p	3.4
	400379	NM_018432		Homo sapiens ovarian cancer related prot	3.4
25	419964	AA811657	Hs.220913	ESTs	3.4
	427033	AI457449	Hs.192817	ESTs	3.4
	422321	AA906427	Hs.181035	hypothetical protein MGC11295	3.4
	430829	AW451999	Hs.194024	ESTs	3.4
	420721	AA927802	Hs.159471	ZAP9 protein	3.4
30	433628	AI821784	Hs.188578	ESTs	3.4
	436703	AW880814	Hs.146381	RNA binding motif protein, X chromosome	3.4
	429716	R25685	Hs.211933	collagen, type XIII, alpha 1	3.4
	427235	AI126289	Hs.192232	ESTs	3.4
	459646	AW883958	Hs.321190	gb:QV3-OT0063-290300-135-c04 OT0063 Homo	3.4
35	428923	BE047698	Hs.188785	ESTs	3.4
	431408	AA504757	Hs.105738	ESTs	3.4
	438801	AA825971	Hs.124284	ESTs	3.4
	445432	AV653771		gb:AV653771 GLC Homo sapiens cDNA clone	3.4
	450003	AA777809	Hs.191995	ESTs	3.4
40	448108	AW300021	Hs.170885	ESTs	3.3
	425523	AB007948	Hs.158244	KIAA0479 protein	3.3
	427473	AW274439	Hs.252709	ESTs	3.3
	434520	AA205273	Hs.177011	hypothetical protein	3.3
	447282	AI999063	Hs.197505	ESTs	3.3
45	447182	BE241868	Hs.17585	KIAA0601 gene product	3.3
	432229	AW290976	Hs.143587	ESTs	3.3
	418985	AI042330	Hs.67128	hypothetical protein FLJ23309	3.3
	418719	AW975590	Hs.161707	ESTs	3.3
	465710	BE072049		gb:PM4-BT0532-170100-004-r06 BT0532 Homo	3.3
50	420300	AA258245	Hs.127573	Homo sapiens FKSG41 (FKSG41) mRNA, compl	3.3
	416662	T25853	Hs.7538	ESTs	3.3
	411436	AW846433		gb:CAV0-CT0179-070300-143-b02 CT0179 Homo	3.3
	420851	AA281062	Hs.29493	hypothetical protein FLJ20142	3.3
	428715	AW293716	Hs.53128	ESTs	3.3
55	429318	AW861930	Hs.102500	hypothetical protein dJ511E16.2	3.3
	444246	H83281	Hs.10710	hypothetical protein FLJ20417	3.3
	453973	AI291895	Hs.61993	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	434497	AI821803	Hs.136580	ESTs	3.2
	439306	BE220199		WD40 protein C1a01	3.2
60	420608	BE548277	Hs.103104	ESTs	3.2
	418966	AI123555	Hs.81796	ESTs	3.2
	438118	AW753311	Hs.346690	ESTs	3.2
	447516	W05355	Hs.102971	hypothetical protein FLJ14751	3.2
	449570	AA001793		gb:zh86c05.r1 Soares_fetal_liver_spleen_	3.2
65	424994	AW954525		gb:EST386595 MAGE resequences, MAGC Homo	3.2
	417676	AI808607	Hs.3781	similar to murine leucine-rich repeat pr	3.2
	402145			Target Exon	3.2
	448131	AI675054	Hs.200481	ESTs	3.2
	422352	AA786296	Hs.99200	ESTs	3.2
70	432625	AI243596	Hs.94830	ESTs, Moderately similar to T03094 A-kin	3.2
	447183	AI554733	Hs.173182	ESTs	3.2
	447597	AI888036	Hs.213675	ESTs	3.2
	459535	AV654907		gb:AV654907 GLC Homo sapiens cDNA clone	3.2
	415467	R60891	Hs.260274	ESTs	3.2
75	434408	AI031771	Hs.132586	ESTs	3.2
	456354	X58411	Hs.1219	alcohol dehydrogenase 4 (class II), pi p	3.2
	453789	AA628517	Hs.118502	ESTs	3.2
	412666	AL080116	Hs.74420	origin recognition complex, subunit 3 (y	3.2
	416319	AW611703	Hs.190173	ESTs, Weakly similar to A46010 X-linked	3.2
80	419088	AI538323	Hs.52620	Integrin, beta 8	3.2
	420397	NM_007018	Hs.97437	centrosomal protein 1	3.2
	422165	AL041199	Hs.1481	histidine decarboxylase	3.2
	448044	AA456882		gb:k13a01.x1 NCL_CGAP_Lu24 Homo sapiens	3.2
	454665	AW812866		gb:RC3-ST0186-300100-017-b03 ST0186 Homo	3.1

	405321		Target Exon	3.1	
	429569	AA454993	Hs.138343	ESTs, Weakly similar to I78865 serine/th	3.1
	434512	AW139932	Hs.188941	ESTs	3.1
5	452102	U04343	Hs.27954	CD86 antigen (CD28 antigen ligand 2, B7-	3.1
	433444	AW975324	Hs.129316	ESTs	3.1
	410821	AI114811	Hs.92526	ESTs, Weakly similar to T00365 hypotheti	3.1
	415861	Z43123	Hs.144513	ESTs	3.1
	422289	AK000181	Hs.114556	hypothetical protein FLJ20174	3.1
10	432527	AW975028	Hs.102754	ESTs	3.1
	427773	AA412290	Hs.98124	ESTs	3.1
	441817	AW969705	Hs.293332	ESTs	3.1
	416812	H91010	Hs.44940	ESTs	3.1
	417958	AA767382	Hs.193417	ESTs	3.1
15	407426	AF129533		gb:Homo sapiens F-box protein Fbl3b (FBL	3.1
	416423	H54375	Hs.268921	ESTs	3.1
	418037	AI990212	Hs.86447	ESTs	3.1
	419197	N48921	Hs.27441	KIAA1615 protein	3.1
	420179	N74530	Hs.21168	ESTs	3.1
20	436295	N73895		gb:za62d06.s1 Soares fetal liver spleen	3.1
	405548			Target Exon	3.1
	423595	R82826	Hs.220702	ESTs	3.1
	412533	AA679863	Hs.69906	ESTs	3.1
	434072	H70854	Hs.283059	Homo sapiens PR01082 mRNA, complete cds	3.1
25	405264			NM_030813*:Homo sapiens suppressor of po	3.1
	410869	AW808361		gb:MR1-ST0111-111099-003-r04 ST0111 Homo	3.1
	425354	U62027	Hs.155935	complement component 3a receptor 1	3.1
	441492	AI149998	Hs.146346	ESTs	3.1
	447078	AW885727	Hs.9914	ESTs	3.1
30	436021	AA922182	Hs.54709	ESTs	3.0
	408832	AW065680	Hs.63428	ESTs, Weakly similar to Z195_HUMAN ZINC	3.0
	450580	N40087		ESTs	3.0
	432319	AW510770	Hs.126386	ESTs	3.0
	453713	R20640	Hs.79133	cadherin 8, type 2	3.0
35	445784	AI253155	Hs.146065	ESTs	3.0
	416642	T98118	Hs.226313	ESTs	3.0
	418948	AI217097		gb:qd43h07.x1 Soares_fetal_heart_NbHH19W	3.0
	433796	AA810867	Hs.186997	ESTs	3.0
	439182	AF086030	Hs.21621	hypothetical protein DKFZp762O076	3.0
40	404995			ENSP00000251890*:Monocytic leukemia zinc	3.0
	444794	AI419991	Hs.145225	ESTs	3.0
	443634	H73972	Hs.134460	ESTs	3.0
	420133	AA426117	Hs.155643	ESTs	3.0
	407629	AA045084	Hs.29725	hypothetical protein FLJ13197	3.0
45	426743	AA383833	Hs.245022	ESTs	3.0
	442326	H92962	Hs.124813	hypothetical protein MGC14817	3.0
	449313	AA004696	Hs.333016	ESTs	3.0
	454096	AW062757		gb:CM0-CT0103-120899-037-g07 CT0103 Homo	3.0
	419622	AA452054	Hs.119338	ESTs	3.0
50	449746	AI688593		gb:y138a05.x5 Soares breast 3NvHbAt Homo	3.0
	428412	AA428240	Hs.126083	ESTs	3.0
	428200	AI039524	Hs.98388	ESTs	3.0
	414951	AW794931	Hs.100861	hypothetical protein FLJ14600	3.0
	431869	AA521136	Hs.190176	ESTs	3.0
	451391	AA017410	Hs.40568	ESTs	3.0
55	452959	AI933416	Hs.189674	ESTs	3.0

TABLE 668

60	Key:	Unique Eas probeset identifier number
	CAT number:	Gene cluster number
	Accession:	Genbank accession numbers
65	Key,	CAT Number
	410790	1221131_1
	410869	1225123_1
70	411438	1245660_1
	411479	1247077_1
75	412988	1342150_1
	413081	1348563_1
	413625	1374635_1
	416009	1566378_1
	418948	180808_1
	420111	190755_1
80	420352	192979_1
	424200	236595_1
	424994	245786_1
	428002	285602_1
	AW803357	AW803423
	AW8012233	RD8814
	AW808361	AW808404
	AW808385	AW808422
	AW808401	AW808409
	AW808760	AW808883
	AW808521	AW808539
	AW808609	AW808472
	AW808739	AW808704
	AW808558	AW808714
	AW808420	AW8
	AW846433	AW846159
	AW846377	AW846528
	AW846047	AW848202
	AW848631	AW848142
	AW848702	AW848121
	AW848832	AW848140
	AW848671	AW848009
	AW848067	AW848069
	AW848905	AW848214
	BE046880	BE046738
	BE044958	BE064415
	BE064430	BE064448
	BE145899	BE145848
	BE145849	BE145853
	BE145927	BE145925
	Z43062	R13213
	H14422	AI217097
	AW886090	W38035
	W38792	AA232835
	AW936043	AA255652
	AA280911	AW967820
	AA262684	BE258835
	AW968316	AA258918
	AW843305	R14744
	AI580388	BE071923
	R36260	AA337221
	AA336756	AW966196
	AW954525	AI372685
	AA349501	AI372687
	H10564	AA418703
	AA418711	BE071915
	BE071920	BE071912

428342	290035_2	AI739168 AA426249 AI199636 AW505198 AW977291 AA824583 AA883419 AA724079 AI015524 AI377728 AW293682 AI928140 AA731438
430535	319843_1	AI092404 AI085630 AA731340
432765	353807_1	AW968485 AW968670 AA480922 BE350425
433523	368873_1	AJ003429 AJ003367 AA564825
434763	392847_1	H29882 AW655533 AW149901 AI572917 AA598500 AI086466 AI336390 AW864390 AW864320
436295	41733_1	AA648618 AW974389 H51771
439082	468554_1	N73895 AJ001872
439306	47085_1	AA830149 AW978407 M85983 AW503637
440947	505904_1	BE220199 W01813 AF086118 N70760 BE221405
442481	543588_1	AA910403 AI815593 W58361 AW162520 AI816550
445432	63943_1	N99828 BE079873 AI110738 AF074645
448044	747196_1	AV653771 BE089370
449570	81018_1	AI456682 H24240 R14537 R18426 AW867082
449745	814534_1	AA001793 AA001871
450317	831956_1	AI668593 AI820774 R86205 H39971 H22177 H26241
450580	83929_1	AI692689 R14223 R18395
45082	85933_1	N40087 H12925 AA460779 AA096372 BE160847 AW816890 AW816893 AW816577 AW816891 AW816882 AW816868 AW816889 AW816940
450687	84327_1	AW816892 AW816941 AW816578 AA029183 T83320 H86850 AA010295 BE160823 Z25353 AA150883 AW887764 AW023806 AW022095
452462	918580_1	AA164518 AA730973 W00417 W65303
453682	977454_1	AI339732 AA010300 AW515041 AA768334 N29860 AA425874 AA425118 AA865829 AW936878
454037	996287_1	AA495800 AA496737 AA010736 AA654716 AA640726
454096	1007449_1	BE173515 BE173560 AI902860
454171	1048240_1	T79703 T96307 AL079725
454457	1207274_1	AW998716 AW022148 N68020
454665	1228599_1	AW062757 AW176890 AW062758 AW176895 AW176869 AW176900 AW176897 AW176928 AW176868 AW176892
454860	1237732_1	AW854832 AW854798 AW854857 AW854816 AW854834 AW854817
454968	1247029_1	AW753456 AW753036 AW854868 AW854862
455087	1252050_1	AW812866 AW812746 AW812747 AW812884 AW812763 AW812722
455276	1272541_1	AW835767 AW835537 BE180187
455446	1348557_1	AW849048 AW847956 AW849039 AW847957 AW848279 AW848698 AW849034 AW849033
455710	1352368_1	AW854538 AW854418 AW854412
457374	328758_1	BE176479 BE176678 BE176357 BE176650 AW886079 BE176676 BE176615 BE176555 BE176489 BE176610 BE176362
458012	823104_1	BE084420 BE084436 BE084429 BE084414 BE084400 BE084517
		BE072049 BE069471 BE069489 BE069478 BE069479 BE069492 BE069485 BE072122 BE072124 BE069491 BE069486 BE069464
		AA493662 AW897396 BE154814
		AJ911066 AI933734 AI880888 AJ003599

TABLE 66C

Pkey: Unique number corresponding to an Eos probeset
 Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
 Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
400533	6981826	Minus	277132-277595
400746	7329328	Minus	147703-147896
401132	8705350	Minus	85679-85795
402145	8018280	Plus	113086-114800
403242	7637817	Minus	11287-12511
403481	9965004	Plus	93496-93633
403510	7852047	Plus	81886-82027
403667	6850483	Minus	1344-1442,1545-1697
404003	8655948	Plus	198349-199096
404581	9795980	Minus	59039-70100
404592	9943865	Minus	39067-39225
404848	8248647	Minus	23955-24034,25143-25264
404987	7523744	Minus	89944-90729
404995	6006247	Minus	154015-154123
405264	7329374	Plus	28568-28684
405321	3419846	Minus	44654-45210
405348	2814717	Minus	43310-43452
405510	7630909	Minus	101026-101174
405548	1532158	Plus	11562-11688

TABLE 67A: 689 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

Table 67A lists about 689 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 9009 probesets on the Affymetrix/Eos Hu03 GeneChip array that showed some expression in human xenograft tumors and cell lines. The 689 genes were selected such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" prostate cancer level was set to the 75th percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile values amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigenesID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of tumor to normal body tissue

	Pkey	ExAccn	UnigenelD	Unigene Title	R1
5	448999	AF179274	Hs.22791	transmembrane protein with EGF-like and	73.2
	426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	65.0
	432441	AW292426	Hs.163484	ESTs	56.0
	446057	AJ420227	Hs.149358	Trp-p8 transient receptor potential cati	55.0
10	400302	N48056	Hs.283946	folate hydrolase (prostate-specific memb	48.1
	414569	AF109298	Hs.118258	prostate cancer associated protein 1	41.4
	432240	AI694767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL	40.3
	419526	AI821895	Hs.193481	ESTs	35.9
15	400298	AA032279	Hs.61635	six transmembrane epithelial antigen of	35.7
	400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	34.9
	453370	AI470623	Hs.139336	ATP-binding cassette, sub-family C (CFTR	33.9
	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	32.8
20	424099	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	32.6
	400292	AA250737	Hs.72472	BMP-R1B	28.8
	400267	S39329	Hs.181350	kallikrein 2, prostatic	28.8
	425075	AA506324	Hs.1852	acid phosphatase, prostate	28.6
25	409361	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolo	27.8
	415539	AI733881	Hs.72472	BMP-R1B	27.0
	428819	AL135623	Hs.193914	KIAA0575 gene product	25.7
	409262	AK000631	Hs.52255	hypothetical protein FLJ120624	25.5
30	432374	W68815	Hs.301866	Homo sapiens cDNA FLJ11346 fis, clone PL	24.8
	407168	R45175	Hs.117183	ESTs	24.5
	400296	AA306627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	23.6
	428336	AA503115	Hs.183752	microseminoprotein, beta-	23.5
35	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	23.4
	403047			NM_005656*:Homo sapiens transmembrane pr	23.4
	444484	AK002126	Hs.11260	hypothetical protein FLJ11264	22.0
	423073	BE252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	21.6
40	407709	AA456135	Hs.23023	ESTs	21.5
	401424			NM_001172:Homo sapiens arginase, type II	20.6
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	19.7
	434666	AF151103	Hs.112259	T cell receptor gamma locus	18.5
45	415989	AI267700		ESTs	17.9
	437052	AA861697	Hs.120591	ESTs	17.8
	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	16.8
	431548	AI834273	Hs.9711	novel protein	16.6
50	425628	NM_004476	Hs.283946	folate hydrolase (prostate-specific memb	16.5
	428852	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (ca	16.5
	450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin)-prop	16.5
	413697	AW302885	Hs.117183	ESTs	16.1
55	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	15.7
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	15.3
	419743	AW408762	Hs.5857	Homo sapiens clone 24416 mRNA sequence	15.3
	407122	H20276	Hs.31742	ESTs	15.1
60	427958	AA418000	Hs.98280	potassium intermediate/small conductance	14.1
	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	13.9
	428501	AW043782	Hs.293616	ESTs	13.9
	428898	AB033070	Hs.194408	KIAA1244 protein	13.7
65	418961	AW967646	Hs.23023	ESTs	13.3
	448519	AW175665	Hs.278696	Homo sapiens protein mRNA, complete cds	13.2
	418848	AI820961	Hs.193466	ESTs	13.1
	426398	AI249368	Hs.98558	ESTs	13.0
70	428220	AW207208		ESTs	12.7
	401451			NM_004496*:Homo sapiens hepatocyte nucle	12.4
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	12.4
	419078	M93119	Hs.89584	Insulinoma-associated 1	12.3
75	450382	AA397668	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	11.9
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	11.8
	408826	AF216077	Hs.48378	Homo sapiens clone HB-2 mRNA sequence	11.4
	429918	AW873986	Hs.119383	ESTs	11.3
80	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU 8	11.1
	412446	AI786015		ESTs	11.1
	433404	T32982		ESTs	10.9
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	10.9
	427674	NM_003528	Hs.2178	H2B histone family, member Q	10.6
	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	10.4
	447942	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	10.3
	418278	AK88489	Hs.83937	hypothetical protein	10.3
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	10.2
	433927	AI557019	Hs.116467	small nuclear protein PRAC	10.2
	408000	L11680	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	10.1
	449625	NM_014253		odc (odd Ozten-m, Drosophila) homolog 1	10.1
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	10.0
	439444	AI277652	Hs.54578	ESTs, Weakly similar to I38022 hypotheti	9.8
	437718	AI927288	Hs.196779	ESTs	9.8
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	9.7
	453160	AI263307		H2B histone family, member L	9.7
	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	9.7
	450325	AI935862	Hs.91973	ESTs	9.6
	434170	AA626509	Hs.122329	ESTs	9.6
	428600	AW863261	Hs.138860	hypothetical protein DKFZp434K1421	9.6

	447033	AJ357412	Hs.157601	ESTs	9.5
	401747			Homo sapiens keratin 17 (KRT17)	9.3
	434423	NM_006769	Hs.3844	UIM domain only 4	9.3
5	411887	AW162924	Hs.128790	ESTs	9.2
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S51797 vasodilat	9.2
	415263	AA948033	Hs.130853	ESTs	9.2
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	9.2
	421896	N62293	Hs.45107	ESTs	9.1
10	432101	AI918960	Hs.123642	EphA3	9.1
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	9.0
	428046	AW812795	Hs.337534	ESTs, Moderately similar to I38022 hypot	8.9
	420218	AW958037		ribosomal protein L4	8.8
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	8.6
15	424692	AA429834	Hs.151791	KIAA0092 gene product	8.6
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	8.6
	425294	AU076405	Hs.23981	solute carrier family 26 (sulfate transp	8.5
	446100	AW967109	Hs.13804	hypothetical protein cJ462023.2	8.5
	400294	N95798	Hs.278695	Homo sapiens protein mRNA, complete cds	8.5
20	416182	NM_004354	Hs.79069	cyclin G2	8.5
	431542	H63010	Hs.5740	ESTs	8.4
	447397	BE247676	Hs.18442	E-1 enzyme	8.3
	432674	AA641092	Hs.257339	ESTs, Weakly similar to I38022 hypoteti	8.1
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	8.1
25	443822	AI087412	Hs.143611	ESTs, Weakly similar to 2004399A chromos	8.1
	451684	AF216751	Hs.26813	CDA14	8.1
	437124	AA554458		KIAA0868 protein	8.0
	416239	AL038450	Hs.48948	ESTs	8.0
	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	7.9
	424800	AL035588	Hs.153203	MyoD family inhibitor	7.9
30	428728	NM_016825	Hs.191381	hypothetical protein	7.9
	418564	AA631143	Hs.278695	Homo sapiens protein mRNA, complete cds	7.8
	442049	AA310393	Hs.190044	ESTs	7.8
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	7.8
35	410869	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	7.7
	443180	R15875	Hs.258576	claudin 12	7.6
	433285	AW975944	Hs.237396	ESTs	7.6
	410870	U81599	Hs.66731	homeo box B13	7.4
	418836	AI655499	Hs.161712	ESTs	7.4
40	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	7.3
	431992	NM_002742	Hs.2891	protein kinase C, mu	7.3
	426905	AB032859	Hs.318584	novel C3HC4 type Zinc finger (ring finger	7.3
	432585	AA568548		ESTs	7.3
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	7.3
45	435047	AA454985	Hs.54973	cadherin-like protein VR20	7.3
	447476	BE293466	Hs.20880	ESTs, Weakly similar to I38022 hypoteti	7.3
	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	7.2
	426108	AA622037	Hs.166468	programmed cell death 5	7.1
	433323	AA805132	Hs.159142	ESTs	7.1
50	423349	AF010258	Hs.127428	homeo box A9	7.0
	416816	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	6.9
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	6.9
	438869	AF075009		gb:Homo sapiens full length insert cDNA	6.9
	418329	AW247430	Hs.84152	cystathionine-beta-synthase	6.8
55	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	6.8
	418601	AA279450	Hs.86368	calmegin	6.8
	429769	NM_004917	Hs.218366	kalikrein 4 (protease, enamel matrix, p	6.8
	438962	AW377314	Hs.5364	DKFZP564I052 protein	6.8
	425465	L18984	Hs.1904	protein kinase C, iota	6.6
	450377	AB033091		KIAA1265 protein	6.6
60	451418	BE387780	Hs.26369	hypothetical protein FLJ20287	6.6
	418250	U29926	Hs.83918	adenosine monophosphate deaminase (isofo	6.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A {	6.6
	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	6.5
65	440774	AI420611	Hs.153934	ESTs	6.5
	413992	W26276	Hs.136075	RNA, U2 small nuclear	6.4
	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	6.4
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	6.4
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	6.4
70	451027	AW519204	Hs.40808	ESTs	6.4
	436063	AK000028		ribosomal protein S24	6.3
	440749	W22335	Hs.7392	hypothetical protein MGC3199	6.3
	432103	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), cat	6.3
	431958	X63629	Hs.2877	cadherin 3, type 1, P-cadherin (placenta	6.2
75	411019	AW993087	Hs.48617	Homo sapiens cDNA FLJ12540 fis, clone NT	6.2
	421566	NM_000399	Hs.1395	early growth response 2 (Krox-20) (Drosop	6.2
	452744	AI267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	6.1
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	6.1
	442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	6.1
80	448045	AJ297438	Hs.20166	prostate stem cell antigen	6.0
	428342	AJ739168		Homo sapiens cDNA FLJ13458 fis, clone PL	6.0
	453439	AJ572438	Hs.32976	guanine nucleotide binding protein 4	6.0
	433517	AW022133	Hs.189638	ESTs	6.0
	424036	AA770588		H2A histone family, member L	5.9

	420092	AA814043	Hs.88045	ESTs	5.9
	410268	AA316181	Hs.61635	slx transmembrane epithelial antigen of	5.8
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	5.8
5	441866	BE464341	Hs.21201	nectin 3; DKFZP566B0846 protein	5.8
	450244	AA007534	Hs.125062	ESTs	5.8
	429165	AW009886	Hs.118258	prostate cancer associated protein 1	5.7
	451952	AL120173	Hs.301663	ESTs	5.7
	429084	AJ001443	Hs.195614	splicing factor 3b, subunit 3, 130kD	5.7
10	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-	5.7
	412935	BE267045	Hs.75064	tubulin-specific chaperone c	5.7
	415068	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	5.7
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	5.7
	416621	AI648602	Hs.55468	ESTs	5.7
15	416653	AA768553	Hs.193145	metallothionein 1E (functional)	5.6
	433332	AI367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	5.5
	455497	AA112573	Hs.278695	Homo sapiens protein mRNA, complete cds	5.5
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	5.4
	428593	AW207440	Hs.185973	degenerative spermatocytes (homolog Dros	5.4
20	425211	M18687	Hs.1867	progastricsin (pepsinogen C)	5.4
	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	5.4
	458809	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	5.4
	410762	AF226053	Hs.66170	HSKM-B protein	5.4
	440594	AW445167	Hs.126036	ESTs	5.4
25	413328	Y15723	Hs.75295	guanylate cyclase 1, soluble, alpha 3	5.3
	447805	AW627932	Hs.302421	gemin4	5.3
	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	5.3
	453308	AW959731	Hs.323099	ESTs	5.3
	421470	R27496	Hs.1378	annexin A3	5.3
30	418555	AI417215	Hs.87159	hypothetical protein FLJ12577	5.2
	404632			NM_022490:Homo sapiens hypothetical prot	5.1
	450861	AI523898	Hs.17617	ESTs	5.1
	431583	AI042613	Hs.262476	S-adenosylmethionine decarboxylase 1	5.1
	400303	AA242758	Hs.79136	LV-1 protein, estrogen regulated	5.1
35	400290	H18836	Hs.31608	hypothetical protein FLJ20041	5.1
	410037	AB020725	Hs.58009	KIAA0918 protein	5.1
	410240	AL157424	Hs.61289	synaptotagmin 2	5.0
	403046			NM_006656:Homo sapiens transmembrane pr	5.0
	419647	AA348947	Hs.91816	hypothetical protein	5.0
40	450203	AF097994		L-kynurenine/alpha-aminoadipate aminotra	5.0
	450164	AJ239923	Hs.63931	ESTs	5.0
	417318	AW963937	Hs.240845	ESTs	4.9
	417153	X67010	Hs.81343	collagen, type II, alpha 1 (primary oste	4.9
	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	4.9
45	455088	BE177320	Hs.156148	hypothetical protein FLJ13231	4.9
	433852	AI378329	Hs.128629	ESTs	4.9
	452679	Z42387	Hs.83863	transmembrane, prostate androgen induced	4.9
	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	4.9
	416276	U41060	Hs.79136	LV-1 protein, estrogen regulated	4.8
50	441021	AW578716	Hs.7644	H1 histone family, member 2	4.8
	453171	R76472	Hs.65646	ESTs	4.8
	416795	AI497778	Hs.20509	HBV pX associated protein-8	4.8
	427615	BE410107	Hs.178817	CGI-82 protein, PSOR1	4.8
	419440	AB020689	Hs.90419	KIAA0882 protein	4.8
55	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	4.8
	453082	H18935	Hs.31608	hypothetical protein FLJ20041	4.8
	420948	AB016898	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	4.8
	442592	BE566623	Hs.29899	ESTs, Weakly similar to G02075 transcrip	4.8
	421685	AF189723	Hs.105778	ATPase, Ca transporting, type 2C, member	4.7
60	431724	AA514535	Hs.283704	ESTs	4.7
	423242	AL039402	Hs.125783	DENF-6 protein	4.7
	434485	AI623511	Hs.118567	ESTs	4.7
	407103	AA424881	Hs.258301	hypothetical protein MGC13170	4.6
65	414085	AA114018	Hs.75746	aldehyde dehydrogenase 1 family, member	4.6
	422486	BE514492	Hs.117487	gene near HD on 4p16.3 with homology to	4.6
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	4.6
	439735	AI635386	Hs.142846	hypothetical protein	4.6
	420039	NM_004805	Hs.94581	sulfotransferase family, cytosolic, 2B,	4.6
	448845	AW971183	Hs.6019	DnaJ (Hsp40) homolog, subfamily C, membe	4.5
70	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	4.5
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	4.5
	426006	R49031	Hs.22627	ESTs	4.5
	451982	F13036	Hs.27373	Homo sapiens mRNA; cDNA DKFZp56401763 (f	4.5
75	415082	AA160000	Hs.137396	ESTs, Weakly similar to JC6238 galactosy	4.5
	409799	D11928	Hs.76845	phosphoserine phosphatase-like	4.5
	423683	AL122055	Hs.129836	KIAA1028 protein	4.4
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	4.4
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	4.4
	451468	AW503398	Hs.293663	ESTs, Moderately similar to I38022 hypot	4.4
80	429467	NM_004477	Hs.203772	FSHD region gene 1	4.4
	451752	AB032997		KIAA1171 protein	4.3
	430284	AI538226	Hs.32976	guanine nucleotide binding protein 4	4.3
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	4.3
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	4.3

	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	4.3
	440300	N39760	Hs.8859	Homo sapiens, Similar to RIKEN cDNA 5830	4.3
	427308	D26067	Hs.174905	KIAA0033 protein	4.3
	435706	W31254	Hs.7045	GL004 protein	4.3
5	416854	H40164	Hs.80296	Purkinje cell protein 4	4.2
	451406	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	4.2
	410076	T05387	Hs.7991	ESTs	4.2
	410275	U86558	Hs.61796	transcription factor AP-2 gamma (activat	4.2
10	419239	AA68183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	4.2
	442501	AA315267	Hs.23126	ESTs	4.2
	436761	AI817776	Hs.236557	ESTs	4.2
	420380	AA640891	Hs.102406	ESTs	4.2
	436555	AI364997	Hs.7572	ESTs	4.2
15	458440	AI095468	Hs.135254	Homo sapiens clone 1 thrombospondin mRNA	4.2
	446416	AV658299	Hs.163959	ESTs	4.2
	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA A430	4.2
	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	4.1
	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	4.1
20	429299	AI620463	Hs.347408	hypothetical protein MGC13102	4.1
	407894	AJ278313	Hs.41143	phosphoinositide-specific phospholipase	4.1
	414664	AA687775	Hs.66295	multi-PDZ-domain-containing protein	4.1
	408418	AW963897	Hs.44743	KIAA1435 protein	4.1
	430945	U80669	Hs.55999	NK homeobox (Drosophila), family 3, A	4.1
25	432363	AA534489		gb:nf6g11.s1 NCI_CGAP_Co3 Homo sapiens	4.1
	447574	AF162665	Hs.18895	lousied-like kinase 1	4.0
	447595	AW379130	Hs.18953	phospholipase 9A	4.0
	453857	AL080235	Hs.35861	DKFZP586E1621 protein	4.0
	444108	R55784	Hs.140942	ESTs	4.0
30	422890	Z43784		ankyrin 3, node of Ranvier (ankyrin G)	4.0
	417379	AA196390		gb:zp99b10.s1 Stratagene muscle 937209 H	4.0
	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.0
	410102	AW248508	Hs.279727	ESTs; homologue of PEM-3 (Clona savignyi	4.0
	418821	AA436002	Hs.183161	ESTs	4.0
35	438825	BE327427	Hs.79953	ESTs	4.0
	433233	AB040927	Hs.301804	KIAA1494 protein	4.0
	415276	U88686	Hs.78353	SFRS protein kinase 2	4.0
	440146	AW014231	Hs.50790	Homo sapiens cDNA: FLJ22930 fis, clone K	4.0
	407819	R42185		ESTs	4.0
40	450402	BE218027	Hs.89969	ESTs	4.0
	432527	AW975028	Hs.102754	ESTs	4.0
	419733	AW362955		Homo sapiens cDNA FLJ14415 fis, clone HE	3.9
	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	3.9
45	432435	BE218886	Hs.282070	ESTs	3.9
	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	3.9
	436420	AA443966	Hs.31595	ESTs	3.9
	430122	NM_013342	Hs.233765	TCF3 (E2A) fusion partner (in childhood	3.9
	411031	W37943	Hs.34892	KIAA1323 protein	3.9
	429259	AA420450	Hs.292911	Plakophilin	3.9
50	407813	AL120247	Hs.40109	KIAA0872 protein	3.9
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	3.9
	410227	AB008284	Hs.61152	exocytosis (multiple)-like 2	3.9
	417958	AA767382	Hs.193417	ESTs	3.9
	427176	AW381569	Hs.40534	ESTs	3.9
55	448826	AI580252	Hs.263246	ESTs, Weakly similar to putative p150 IH	3.8
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	3.8
	432875	AI791855		ESTs	3.8
	419713	AW968058	Hs.92391	nudix (nucleoside diphosphate linked mol	3.8
	427479	BE410082	Hs.178471	KIAA0798 gene product	3.8
60	443182	T49951	Hs.9029	DKFZP434G032 protein	3.8
	413950	AA249086	Hs.32793	ESTs	3.8
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	3.8
	419083	AI479580	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	3.8
	448148	NM_016578	Hs.20509	HBV pX associated protein-8	3.8
65	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23068 fis, clone L	3.8
	432274	AK000382	Hs.274251	hypothetical protein FLJ20375; KIAA1797	3.8
	447620	AW230951		ESTs	3.8
	430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	3.8
70	418004	U37619	Hs.87539	aldehyde dehydrogenase 3 family, member	3.8
	416655	AW968613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	3.8
	459284	AF155660	Hs.300496	mitochondrial solute carrier	3.8
	421829	AB018330	Hs.108708	calcium/calmodulin-dependent protein kin	3.7
	437252	AK33833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	437967	BE277414	Hs.5947	mel transforming oncogene (derived from	3.7
75	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	3.7
	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	3.7
	418838	AW385224	Hs.35198	eclonucleotide pyrophosphatase/phosphodi	3.7
	453468	AB014533	Hs.33010	KIAA0533 protein	3.7
	408063	BE086548	Hs.42346	calcineurin-binding protein calsardin-1	3.7
80	422072	AB018255	Hs.111138	KIAA0712 gene product	3.7
	420297	AI628272	Hs.86323	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.7
	420522	AW957137	Hs.98541	hypothetical protein	3.6
	408833	AW612232	Hs.254835	ESTs	3.6
	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	3.6

5	456177	NM_012391	Hs.79414	prostate epithelium-specific Ets transcr	3.6
	425689	W16480	Hs.24283	ESTs, Moderately similar to reduced expr	3.6
	432370	AA308334	Hs.274424	N-acetylneuraminic acid phosphate syntha	3.6
	422424	A186431	Hs.296638	prostate differentiation factor	3.6
	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22582 fis, clone H	3.6
	433339	AFD19226	Hs.8036	glioblastoma overexpressed	3.6
	421887	AW161450	Hs.109201	CGI-86 protein	3.6
	435114	AA775483	Hs.288936	mitochondrial ribosomal protein L9	3.6
10	412520	AA442324	Hs.795	H2A histone family, member O	3.6
	436476	AA326108	Hs.33829	bHLH protein OEC2	3.6
	441224	AU076964	Hs.7753	calumenin	3.5
	404922			NM_003071:Homo sapiens SWI/SNF related,	3.5
	432278	AL137506	Hs.274256	hypothetical protein FLJ23563	3.5
15	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	3.5
	429886	A1871613	Hs.28538	Homo sapiens cDNA: FLJ21086 fis, clone C	3.5
	408001	AA046458	Hs.95296	ESTs	3.5
	428330	L22524	Hs.2256	matrix metalloproteinase 7 (matlysin,	3.5
	418113	A1272141	Hs.83484	SRY (sex determining region Y)-box 4	3.5
20	428055	AA420564	Hs.101760	ESTs	3.5
	418827	BE327311	Hs.47166	HT021	3.5
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	3.5
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (Hs	3.5
	419168	A1336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	3.5
25	409151	AA306105		SEC22, vesicle trafficking protein (S. c	3.5
	439671	AW162840	Hs.6641	kinesin family member 5C	3.4
	452721	A1269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.4
	449933	AW157098	Hs.324104	Human DNA sequence from clone RP1-63M2 o	3.4
	432615	AA557191	Hs.55028	ESTs, Weakly similar to I54374 gene NF2	3.4
30	443884	N20817	Hs.194397	leptin receptor	3.4
	403752			NM_002753:Homo sapiens mitogen-activate	3.4
	427723	A1356260	Hs.279789	histone deacetylase 3	3.4
	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	3.4
	440494	BE618768	Hs.7232	acetyl-Coenzyme A carboxylase alpha	3.4
35	426716	NM_006379	Hs.171921	soma domain, Immunoglobulin domain (Ig),	3.4
	433647	AA603367	Hs.222294	ESTs	3.4
	407137	T97307		gb:53h05.s1 Soares fetal liver spleen	3.4
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	3.4
	427715	BE245274	Hs.180428	KIAA1181 protein	3.3
40	437617	A1026701	Hs.5716	KIAA0310 gene product	3.3
	447818	W79940	Hs.21906	Homo sapiens clone 24670 mRNA sequence	3.3
	414407	AA147026	Hs.76704	ESTs	3.3
	421537	BE363488	Hs.105547	neural proliferation, differentiation an	3.3
	435655	AW105663	Hs.6947	HSPC069 protein	3.3
45	427871	AW992405	Hs.59822	Homo sapiens, clone IMAGE:3507281, mRNA,	3.3
	421882	NM_014141	Hs.106552	cell recognition molecule Caspr2	3.3
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.3
	407908	BE379758	Hs.110853	uncharacterized hematopoietic stem/proge	3.3
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	3.3
50	420588	F08247	Hs.247735	protocadherin alpha 10	3.3
	435873	N23874	Hs.50477	RA827A, member RAS oncogene family	3.3
	411145	BE439553	Hs.250628	Homo sapiens, clone IMAGE:4098694, mRNA,	3.3
	435017	AA336522	Hs.12854	angiotensin II, type I receptor-associat	3.3
	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	3.3
55	443891	NM_002250	Hs.10082	potassium intermediate/small conductance	3.3
	409860	BE261944		hexokinase 1	3.3
	433891	AA813792		gb:nc97k03.s1 NCLCGAP_P12 Homo sapiens	3.3
	430389	AL117429	Hs.240845	DKFZP434D146 protein	3.3
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	3.3
60	419972	AL041465	Hs.182982	polgln-67	3.3
	445707	A1248720	Hs.114390	ESTs	3.3
	412628	A1972402	Hs.306051	hypothetical protein MGC2648	3.3
	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	3.3
65	419879	Z17805	Hs.93564	Horner, neuronal immediate early gene, 2	3.3
	433345	A1681545	Hs.152982	hypothetical protein FLJ13117	3.3
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	3.3
	414922	D00723		glycine cleavage system protein H (amino	3.3
	437898	W81260	Hs.43410	ESTs	3.2
	426126	AL118747	Hs.26691	ESTs	3.2
70	422089	AA523172	Hs.103135	ESTs, Weakly similar to SFR4_HUMAN SPIC	3.2
	450649	NM_001429	Hs.25272	E1A binding protein p300	3.2
	404210			NM_005936:Homo sapiens myeloid/lymphoid	3.2
	434954	AF161455	Hs.284295	Homo sapiens HSPC337 mRNA, partial cds	3.2
75	401519			C15000476*gi142737279[ref XP_012163.1]	3.2
	419577	AF052107	Hs.90797	Homo sapiens clone 23620 mRNA sequence	3.2
	431585	BE242803	Hs.262823	hypothetical protein FLJ10325	3.2
	427461	AA531527	Hs.332040	hypothetical protein MGC13010	3.2
	453288	AW583292	Hs.274412	similar to yeast Upf3, variant A	3.2
	412513	AA322699	Hs.5163	ESTs, Weakly similar to AF151840 1 CGI-8	3.2
80	432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis repressor	3.2
	439583	BE073697	Hs.124863	ESTs	3.2
	451945	BE504055	Hs.211420	ESTs	3.2
	434614	A1249502	Hs.29868	ESTs	3.2
	445625	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.2

	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	3.2
	408101	AW988504	Hs.123073	CDC2-related protein kinase 7	3.2
	425810	AI923627	Hs.31903	ESTs	3.2
5	443123	AA094538	Hs.272908	putative transcription regulation nuclea	3.2
	447439	AA313565	Hs.145020	ESTs, Weakly similar to KIAA1205 protein	3.2
	452167	N75238	Hs.13075	Homo sapiens cDNA: FLJ23013 fis, clone L	3.1
	440789	AB007857	Hs.7416	KIAA0397 gene product	3.1
	436087	BE300296	Hs.5054	CGI-133 protein	3.1
10	414222	AL135173		sorbitol dehydrogenase	3.1
	419749	X73608	Hs.93029	sparc/osteonectin, cwcv and kazal-like d	3.1
	418559	AA225048	Hs.104207	ESTs	3.1
	408784	AW971350	Hs.63386	ESTs	3.1
	424285	BE207188	Hs.144630	nuclear receptor subfamily 2, group F, m	3.1
15	417193	AI922189	Hs.288390	hypothetical protein FLJ22795	3.1
	428738	NM_000380	Hs.192803	xeroderma pigmentosum, complementation g	3.1
	436489	AJ272269	Hs.121429	zinc-binding protein Rbccc728	3.1
	433006	BE242758	Hs.190223	ESTs, Moderately similar to T29285 hypot	3.1
	426991	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.1
20	445943	AW898533	Hs.181574	ESTs	3.1
	434194	AF119847		Homo sapiens PRO1550 mRNA, partial cds	3.1
	432426	AW973152	Hs.31050	ESTs	3.1
	418974	AF010233	Hs.80667	RALBP1 associated Eps domain containing	3.1
	451131	AI267586	Hs.268012	fatty-acid-Coenzyme A ligase, long-chain	3.1
25	423453	AW450737	Hs.126791	CGI-09 protein	3.1
	417215	BE253181	Hs.81687	non-metastatic cells 3, protein express	3.1
	436278	BE396290	Hs.6097	synaptophysin 2	3.1
	432908	AI861896		ESTs	3.1
	432952	AA813887	Hs.188173	Homo sapiens cDNA FLJ12187 fis, clone MA	3.1
30	436705	AI049824	Hs.283390	ESTs, Weakly similar to 2109260A B cell	3.1
	427982	NM_016156	Hs.181325	KIAA1073 protein	3.1
	431576	AB037759	Hs.261587	GCN2 eIF2alpha kinase	3.1
	408767	NM_001898	Hs.123114	cystatin SN	3.1
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	3.1
35	434293	NM_004445	Hs.3796	EphB6	3.1
	410001	AB041036	Hs.57771	kallikrein 11	3.1
	434970	AW272262	Hs.225767	ESTs	3.1
	432800	BE391046	Hs.278862	AIM-1 protein	3.1
	423392	AA195037	Hs.169341	HTPAP protein	3.1
40	432205	AI806593	Hs.125291	ESTs	3.1
	448607	AI571940	Hs.7549	ESTs	3.1
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	3.1
	435661	AA351978	Hs.4943	hepatocellular carcinoma associated prot	3.0
	427315	AA179949	Hs.175683	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	3.0
45	410082	AA061594	Hs.158311	Musashi (Drosophila) homolog 1	3.0
	432621	AI298501	Hs.21192	ESTs, Weakly similar to T46428 hypotheti	3.0
	429538	AI816662	Hs.211577	kinectin 1 (kinasin receptor)	3.0
	452908	AB001451	Hs.30985	neuronal Shc adaptor homolog	3.0
	426030	BE243933	Hs.108642	zinc finger protein 22 (KOX 15)	3.0
50	407688	W25317	Hs.37616	Human D9 splice variant B mRNA, complete	3.0
	434958	T99949	Hs.303428	Homo sapiens cDNA FLJ14832 fis, clone OV	3.0
	418610	AW245993	Hs.223394	hypothetical protein MGC2742	3.0
	451815	AW974911	Hs.184793	Homo sapiens cDNA: FLJ21880 fis, clone H	3.0
	435556	W55321	Hs.111460	calcium/calmodulin-dependent protein kin	3.0
55	413010	AA393273	Hs.75133	transcription factor 6-like 1 (mitochond	3.0
	449459	BE546846	Hs.196048	ESTs	3.0
	438523	H66220	Hs.278177	ESTs	3.0
	434263	N34895	Hs.44648	ESTs	3.0
	446825	BE265822	Hs.344097	filamin A, alpha (actin-binding protein-	3.0
60	408881	AW953853	Hs.282833	ESTs, Weakly similar to I38022 hypotheti	3.0
	429966	BE081342	Hs.283037	HSPC039 protein	3.0
	412552	AI801777		ESTs	3.0
	442409	BE208843	Hs.129544	hypothetical protein MGC15438	3.0
	450832	AW970602	Hs.105421	ESTs	3.0
65	440074	AA863045	Hs.10869	ESTs, Weakly similar to T00060 hypotheti	3.0
	436032	AA150797	Hs.109276	latexin protein	3.0
	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	3.0
	421674	T10707	Hs.296355	hypothetical protein FLJ23138	2.9
	432302	AA345857	Hs.274307	KIAA1442 protein	2.9
70	415172	AF079529	Hs.78108	phosphodiesterase 8B	2.9
	412926	AI879076	Hs.75061	macrophage myristoylated alanine-rich C	2.9
	413142	M81740	Hs.75212	ornithine decarboxylase 1	2.9
	437179	AA393508		serologically defined colon cancer antig	2.9
	418372	AA311833	Hs.84318	replication protein A1 (70kD)	2.9
75	439609	AW971945	Hs.293236	ESTs	2.9
	427398	AW390020	Hs.20415	chromosome 21 open reading frame 11	2.9
	447950	AW796524	Hs.68644	Homo sapiens microsomal signal peptidase	2.9
	409340	BE174629	Hs.321130	hypothetical protein MGC2771	2.9
	420051	AW024937	Hs.29410	ESTs	2.9
80	431663	NM_016669	Hs.267182	TBX3-iso protein	2.9
	417822	AW258163	Hs.82318	WAS protein family, member 3	2.9
	420944	BE463721	Hs.97101	putative G protein-coupled receptor	2.9
	446791	AI632278	Hs.195822	ESTs	2.9
	433313	W20128	Hs.296039	ESTs	2.9

	428465	AW970976	Hs.293653	ESTs	2.9
	457489	AI693815	Hs.127179	cryptic gene	2.9
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	2.9
5	446880	AI811807	Hs.108546	Homo sapiens cDNA FLJ14934 fs, clone PL	2.9
	419829	AI924228	Hs.115185	ESTs, Moderately similar to PC4259 ferri	2.9
	437395	BE140396	Hs.21621	hypothetical protein DKFZp762G076	2.9
	413125	BE244689	Hs.75207	glyoxalase 1	2.9
	401785			NM_002275*Homo sapiens keratin 15 (KRT1	2.9
	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	2.9
10	452099	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to	2.9
	437296	AA350994	Hs.20281	KIAA1700	2.9
	421254	AK001724	Hs.102950	coat protein gamma-cop	2.9
	445109	AF039916	Hs.12330	ecolunucleoside triphosphata diphospholhyd	2.9
	423551	AA327598	Hs.89633	ESTs	2.9
15	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fs, clone PL	2.9
	410193	AJ132592	Hs.59757	zinc finger protein 281	2.9
	435854	AJ278120	Hs.4995	putative ankyrin-repeat containing prote	2.9
	423396	AI382555	Hs.127950	bramodomain-containing 1	2.8
	442202	BE272862	Hs.105534	hypothetical protein FLJ22625	2.8
20	441345	AW068579	Hs.7780	Homo sapiens mRNA; cDNA DKFZp564A072 (fr	2.8
	444367	H54892	Hs.10974	hypothetical protein FLJ22390	2.8
	422522	AI023428	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	2.8
	443337	Y07604	Hs.9235	non-metastatic cells 4, protein expresse	2.8
25	418166	AI754416		Cdc42 effector protein 3	2.8
	448734	BE614070	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	2.8
	413550	W03011	Hs.306981	MSTP043 protein	2.8
	426170	BE161055	Hs.167531	methylcrotonyl-Coenzyme A carboxylase 2	2.8
	444101	R19175	Hs.169793	ribosomal protein L32	2.8
	425320	U29344	Hs.83190	fatty acid synthase	2.8
30	431631	AA548906	Hs.122244	ESTs	2.8
	448804	AW512213	Hs.342849	ADP-ribosylation factor-like 5	2.8
	431416	AA532718		ESTs	2.8
	447881	BE620886		GCN1 (general control of amino-acid synt	2.8
35	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	2.8
	453186	AK001708	Hs.32271	hypothetical protein FLJ10846	2.8
	439778	AL109729	Hs.99364	putative transmembrane protein	2.8
	425010	T16837	Hs.4241	ESTs	2.8
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	2.8
40	450546	AA010200	Hs.175551	ESTs	2.7
	431674	AA098901	Hs.301642	G-protein coupled receptor	2.7
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	2.7
	443181	AI039201	Hs.283316	ESTs	2.7
	448913	AA194422	Hs.22564	myosin VI	2.7
45	440193	AW902312	Hs.7037	Homo sapiens clone 24923 mRNA sequence	2.7
	452941	AL110347	Hs.31074	N-sulfoglucosamine sulfolhydrolase (sulfa	2.7
	451338	AW612322	Hs.19131	transcription factor Dp-2 (E2F dimerizat	2.7
	411190	AA306342	Hs.69171	protein kinase C-like 2	2.7
	434529	AA789081	Hs.4029	glioma-amplified sequence-41	2.7
50	407192	AA809200		gb:af12e02.s1 Soares_testis_NHT Homo sap	2.7
	434747	AA837085		ESTs	2.7
	428171	AA489323	Hs.182825	ribosomal protein L35	2.7
	426657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	2.7
55	447147	AA910353	Hs.75432	ESTs, Weakly similar to T23482 hypotheti	2.7
	452955	AW390282	Hs.31130	transmembrane 7 superfamily member 2	2.7
	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	2.7
	445596	R89543	Hs.12942	vesicle trafficking protein	2.7
	452258	NM_003512	Hs.28777	H2A histone family, member L	2.7
	446494	AA463276	Hs.288906	WW Domain-Containing Gene	2.7
60	436157	AW137011	Hs.49576	ESTs	2.7
	452260	AA453208	Hs.330994	RAB9, member RAS oncogene family	2.7
	409648	AW451449	Hs.57749	ESTs	2.7
	401866			Target Exon	2.7
	400301	X03635	Hs.1657	estrogen receptor 1	2.7
65	453390	AA862496	Hs.28482	ESTs	2.7
	426514	BE616633	Hs.170195	bone morphogenetic protein 7 (osteogenic	2.7
	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	2.7
	405387			NM_022170*Homo sapiens Williams-Beuren	2.7
	441266	H18968	Hs.293845	Homo sapiens, clone IMAGE:3502329, mRNA,	2.7
70	432388	X15218	Hs.2969	v-ski avian sarcoma viral oncogene homol	2.7
	450937	R49131	Hs.26267	ATP-dependent interferon response protal	2.7
	447210	AF035269	Hs.17752	phosphatidylserine-specific phospholipas	2.7
	445098	AL050272	Hs.12305	DKFZP566B183 protein	2.7
	451404	AA480775	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	2.7
75	409550	T08490	Hs.288969	HSCARG protein	2.7
	452707	AI093823	Hs.45070	ESTs	2.7
	451134	AA318315	Hs.25999	hypothetical protein FLJ22195	2.7
	452826	BE245286	Hs.301636	peroxisomal biogenesis factor 6	2.7
	420818	AW969635	Hs.33032	ESTs, Weakly similar to 1207289A reverse	2.7
80	438510	AL080220	Hs.6285	DKFZP585P0123 protein	2.7
	406527	T64904	Hs.163780	ESTs	2.7
	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	2.7
	421717	AF230924	Hs.107187	divalent cation tolerant protela CUTA	2.6
	425910	AA830797	Hs.184760	CCAAT-box-binding transcription factor	2.6

5	440695	AW088363	Hs.246240	ESTs	2.6
	416941	BE000150	Hs.48778	ribon protein	2.6
	422717	AI557623	Hs.119475	cold inducible RNA-binding protein	2.6
	426110	NM_002913	Hs.186563	replication factor C (activator 3) 1 (14	2.6
	422027	AL043100	Hs.306319	fatty acid amide hydrolase	2.6
10	401197			ENSP00000229263:HSPC213.	2.6
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	2.6
	410297	AA148710		lumican	2.6
	447963	AI452973	Hs.165900	ESTs, Weakly similar to ALU1_HUMAN ALU 6	2.6
	433101	AW572317	Hs.12082	Homo sapiens mRNA; cDNA DKFZp566L203 (tr	2.6
15	437546	AW074836	Hs.173984	T-box 1	2.6
	443725	AW245680	Hs.9701	growth arrest and DNA-damage-inducible,	2.6
	436213	AA325512	Hs.71472	hypothetical protein FLJ10774; KIAA1709	2.6
	408157	AA047695	Hs.62946	ESTs	2.6
	420805	L10333	Hs.99947	reticulin 1	2.6
20	454144	BE280478	Hs.182695	hypothetical protein MGC3243	2.6
	426761	AJ015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp59612022 (f	2.6
	428695	AI356647	Hs.189999	purinergic receptor (family A group 5)	2.6
	431725	X66724	Hs.2839	Norrie disease (pseudoglioma)	2.6
	425174	D87450	Hs.154978	KIAA0251 protein	2.6
25	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	2.6
	413435	X51405	Hs.75360	carboxypeptidase E	2.6
	428293	BE250944	Hs.183556	solute carrier family 1 (neutral amino a	2.6
	428180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	2.6
	439580	AW245741	Hs.58461	ESTs, Weakly similar to A35659 knueppel-	2.6
30	424395	AA165082	Hs.146388	microtubule-associated protein 7	2.6
	406870	W79832	Hs.256301	hypothetical protein MGC13170	2.6
	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	2.6
	429922	Z97630	Hs.226117	H1 histone family, member 0	2.6
	449318	BE395253	Hs.30881	ESTs	2.6
35	445919	T53519	Hs.334592	hypothetical protein MGC14141	2.6
	429343	AK000785	Hs.199480	Homo sapiens, Similar to epsin 3, clone	2.6
	438552	AJ245820	Hs.6314	type I transmembrane receptor (seizure-r	2.6
	431472	AK001023	Hs.255649	nucleotide binding protein 2 (E.coli Min	2.6
	409299	AA045650	Hs.53125	small nuclear ribonucleoprotein D2 polyp	2.6
40	434672	AW254020	Hs.117721	ESTs	2.6
	443016	R33261	Hs.6614	ESTs, Weakly similar to A43932 much 2 p	2.6
	452576	AB023177	Hs.28900	KIAA0960 protein	2.6
	412843	AF007555	Hs.74624	protein tyrosine phosphatase, receptor 1	2.6
	430375	AW371048	Hs.93758	H4 histone family, member H	2.6
45	408196	AL034548	Hs.43627	SRY (sex determining region Y)-box 22	2.6
	424339	BE257148		endoglycan	2.6
	416292	AA179233	Hs.42390	nasopharyngeal carcinoma susceptibility	2.6
	451040	AA324743	Hs.40808	ESTs	2.6
	445636	AW105401		ribosomal protein L29	2.6
50	419175	AW270037		KIAA0779 protein	2.6
	422000	M30599	Hs.110637	homeo box A10	2.6
	441128	AA570256		ESTs, Weakly similar to T23273 hypotheti	2.6
	446237	AW270516	Hs.149596	Homo sapiens, Similar to RIKEN cDNA 2310	2.6
	431797	BE169541	Hs.270134	hypothetical protein FLJ20280	2.5
55	406789	AI041403		ribosomal protein L29	2.5
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	2.5
	423115	AA421973	Hs.169119	ESTs, Weakly similar to T25731 hypotheti	2.5
	420460	AA262331	Hs.48378	Homo sapiens clone HB-2 mRNA sequence	2.5
	438185	AI373544	Hs.331328	intermediate filament protein syncoilin	2.5
60	430542	AI557488	Hs.119122	ribosomal protein L13a	2.5
	452827	AI571835	Hs.55468	ESTs	2.5
	431609	AW792792	Hs.264330	N-acylsphingosine amidohydrolase (acid c	2.5
	431108	AA991508	Hs.105317	ESTs	2.5
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	2.5
65	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	2.5
	439864	AI720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	2.5
	438821	AA826425	Hs.192375	ESTs	2.5
	421091	W22821		ribosomal protein L26	2.5
	439414	NM_001183	Hs.6561	ATPase, H transporting, lysosomal (vacuo	2.5
70	400263			Eos Control	2.5
	451428	AW083384	Hs.11067	ESTs, Highly similar to T46395 hypotheti	2.5
	449051	AW981400	Hs.333528	HER2 receptor tyrosine kinase (c-erb-b2,	2.5
	431615	AW295859	Hs.235800	ESTs	2.5
	433037	NM_014168	Hs.279938	HSPC067 protein	2.5
75	409504	AA304961	Hs.699	peptidylprolyl isomerase B (cyclophilin	2.5
	409330	AK001231	Hs.53940	hypothetical protein FLJ10369	2.5
	436299	AK000767	Hs.5111	hypothetical protein FLJ20729	2.5
	450828	AW382884	Hs.204715	ESTs	2.5
	426783	X89867	Hs.172350	HIR (histone cell cycle regulation defec	2.5
80	431122	A267593	Hs.250535	Homo sapiens mRNA; cDNA DKFZp434N2412 (f	2.5
	407236	W79485	Hs.173980	nuclear matrix protein NMP200 related to	2.5
	421109	L32832	Hs.101842	AT-binding transcription factor 1	2.5
	408770	AW270608	Hs.170196	bone morphogenetic protein 7 (osteogenic	2.5
	416737	AF154335	Hs.79691	LIM domain protein	2.5
	414859	AA157291	Hs.21479	tubulein 1	2.5
	431222	X55777	Hs.273790	zona pellucida glycoprotein 3A (sperm re	2.5
	403532			NM_024638:Homo sapiens hypothetical prot	2.5

5	418549	AI096485	Hs.169341	ESTs, Moderately similar to S65657 alpha	2.5
	443804	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypothet	2.5
	407887	AA579668	Hs.41072	serine (or cysteine) proteinase inhibitor	2.5
	414566	AW975063	Hs.343443	ribosomal protein L36	2.5
	446911	N27605	Hs.16492	DKFZP564G2022 protein	2.5
	435126	AI393666	Hs.42315	p10-binding protein	2.5
	421966	M24470	Hs.1435	guanosine monophosphate reductase	2.5
	426788	U66615	Hs.172280	SWI/SNF related, matrix associated, acti	2.5
10	447050	NM_016314	Hs.17200	STAM-like protein containing SH3 and ITA	2.5
	408461	AB037756	Hs.45207	hypothetical protein KIAA1335	2.5
	421594	R45689	Hs.21889	Homo sapiens cDNA FLJ12978 fls, clone NT	2.5
	443837	AI984625	Hs.9884	spindle pole body protein	2.5
	421867	AA481078	Hs.109045	hypothetical protein FLJ10498	2.5
15	435021	AA922182	Hs.73962	ESTs	2.5
	435750	AB029012	Hs.4990	KIAA1089 protein	2.5
	435025	T08990	Hs.4742	anchor attachment protein 1 (Gaelp, yeast	2.5
	407255	AA012992	Hs.256301	hypothetical protein MGC13170	2.5
	425976	C75094	Hs.334514	NG22 protein	2.5
20	440458	AI805078	Hs.208261	ESTs	2.5
	428013	AF151020	Hs.161444	hypothetical protein	2.5
	424369	RB7622	Hs.26714	KIAA1831 protein	2.5
	431604	AF175265	Hs.264190	vacuolar protein sorting 35 (yeast homol	2.5
	452779	AA418775	Hs.47234	ESTs	2.5
25	433585	T85301	Hs.194397	gb:yd78d05.s1 Soares fetal liver spleen	2.5
	436682	AA354489	Hs.222103	EBP50-PDZ Interactor of 64 kD	2.5
	427515	T79528	Hs.179516	integral type I protein	2.5
	418700	AI963808	Hs.86970	ESTs, Moderately similar to ALU5_HUMAN A	2.5

TABLE 67B

Pkey: Unique Eos probe set identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

35	Pkey	CAT Number	Accession
40	415989	10194_1	BC013389 BC017398 AI023543 AA191424 AI267700 AM89633 AW958465 AW953397 AA172056 BE940298 BF909208 BF909980 BF095153 BG285937 AI720344 BF541715 AA355086 AA172235 AW341473 AA448195 AW207206 AI951341 AA969259 BC021735 AI669212 AL120184 AI769949 BE701002 BE184383 BE819031 BG702238 BF090049 BF963318 BF981912 BF943013 AA934514 AA151245 BF980859 AA987807 Z41449 BF908059 BF908053 BF908049 BE689424 BF908060 BF952832 BF952020 BF963134 BI035538 BF908052 BF908057 BF090026 BF943158 AI632924 BF512340 BF952021 BF960776 BF943437 BF942847 AI768015 F09778 F04816 F02721 AA102645 AI633838 AA617829 BF947001 BI035448 BE935876 AW890837 AW898604 BF957405 BF963433 BG704815 BC022980 BF224081 BG149908 AW672842 BE670687 AI702161 AW341832 BE222503 N71836 AI026061 AW953116 AW083132 AI979261 AV725377 AI423298 AI640707 AW975518 AI032611 AI818044 AI299508 AI911386 AI270418 BE219257 BM141826 AA826491 Z25159 AA587421 N59447 Z39436 T32882 R54110 BF115783 F09044 BF808433 BI918168 AW779760 N48674 AI375997 AA235370 BG699146 AI913631 AI498402 AI016320 AA323193 R49021 D69344 BG966750 N45526 BG966917 T81382 R49391 R45432 AI203107 R35004 F07491 R25094 R35360 BC009812 NM_003528 BI597616 AV781592 AV760377 AL601008 BI604131 BE645918 BG187760 BG181625 BG210634 BG192999 AI253307 AA344186 AW952986 AA033609 AA037562 AA722183 R79452 H70775 BF674991 BE769437 BG007856 AA037483 AW572535 AI143991 AA084581 AA033610 AV742510 AV735788 R06338 AW958037 R42557 AI337047 AA948350 AI638005 AA450950 AI624915 AI638047 AI467856 AI521826 AA860305 AI932315 AW009092 AW271756 AW779380 AA609879 AI634791 AI93770 AI558211 Z41145 AI627952 AA303734 BE349457 AW196765 AA256527 BE089727 AI050013 BG939600 AW969191 AA769925 AI377973 AI625545 AA811365 AA521114 N24708 AI379579 AA424899 AI884671 AA829715 AI453010 N35401 AA677452 AA504340 AI209149 AA883574 AI379062 AI084455 AI280147 AA644327 BF432508 N27873 N47364 N34880 AI147024 T86860 AI219716 AA960926 H25544 BI857123 AW960489 AA599099 AA765246 AA328537 BG434703 AA890373 AA424765 AI292318 AA829886 N95742 AI218758 H25588 N35282 AA024987 N36887 BI919187 N49471 AA869870 AW166152 AA468546 AI262504 AI452782 AA554458 AA807080 AA724542 AW102730 AA909978 AW118134 AW827241 W56431 BM127381 BF436987 AI016509 AW953972 BM127686 C15552 N63435 N51744 T98800 N56980 BG108636 N49381 R49886 D51278 BI756812 AA508234 R49885 BF850422 BC022881 AU150944 BG750783 AW754175 AW857737 AI911659 AI050036 AA554053 AI826259 AA568548 AF075009 R63109 R63068 AB033091 AL520743 BE811813 N53332 N99716 AL561910 AA280655 BE710392 AV705100 AW239378 AW444558 AA281459 AI879751 AI873695 BG700891 BI553517 R80518 BG779771 BG534451 AA479402 AW961580 BF061430 AI857643 AI768486 AW512118 AA479302 AW770384 AW072470 AI041696 AI049699 AW592865 AA976261 BE879747 BG114119 AW183811 AA909938 BF571621 BF350794 BF351375 BE925699 AL050294 BC010371 BF982270 AL042656 BF095732 AW812818 BF095731 BG212397 BF678766 BI038602 BG388664 AW675337 BG289398 BE939598 AW805570 AA527097 AW150540 AI693720 AA743364 AI915793 N48185 AI573107 AA043474 AI351615 AI969490 AI910763 R50866 AI699181 N73808 H08164 AK000028 AA494483 AI298674 AA720773 AV761529 AI884670 AI936202 AW294235 D61652 BF881184 AV711384 N27154 AI926970 AV734970 N40094 N28596 AA884747 AA512890 BG436593 AK056315 AI015524 AA724079 BI713619 AI377728 AW293682 AI28140 AI092404 AI085630 AA731340 BM469629 AW968804 AA425658 AA768094 BF446026 AW118719 AI327655 AW500888 AW575556 AI859571 AW495664 AW614573 AW629495 AW505314 W74704 AI358361 AI923640 AW070509 AI521500 AL042095 AA609309 AA761319 AI381489 H45700 AA761333 AW265424 AA909524 AA635311 AA649040 AI392620 Z40708 AI885584 AW263513 AA913892 AI893488 AW263502 AI808164 AW291137 BI061872 BI059498 AA1134476 AW084888 AA036967 AW370823 T55263 BI002756 AA489664 BF827261 W74741 BF953166 NM_033445 BC001193 AI885781 BF794032 AA476620 AA810906 AA810905 AI291244 AI885097 AI359708 AI335629 H97395 AI344589 AA300377 AA457566 AW771833 BE465621 AI364068 AI364452 AI648505 AI918342 AI928670 AA886580 AL531029 AA886344 AI186419 BG329098 BM045465 AL531028 BG437151 BE868021 AA179427 AK055952 BG182168 BG220105 BG191569 BG188964 BG187388 BG220104 BG183714 BE645998 AI819354 AW974068 AI393635 AI580846 AI024796 AW020098 BI491127 AI393644 N74993 AW472959 BM478854 BI597437 H12165 BI458612 BE543182 AB032897 AI141878 AW978722 BE467119 AI761403 BF727385 AW237035 AI934521 BF436248 AI479668 Z40632 AA832081 AW259901 BF067835 BE465977 AI621269 BE465989 BF756369 N74056 AI817896 AA716567 AA934774 H62600 H09497 BF943762 BE395335 BE863333 AW970240 AA534489 AW970323

5	422890	61426_1	AK057805 AW162343 AI190479 AI083318 BE048820 AI198397 AA654667 BE219303 Z39851 F02655 Z28734 T16575 F10145 Z45266 AW572911 AW964435 AW004030 AI632565 BE502630 BI792393 BF056928 AA449241 AI651825 AA805324 AI264863 AW196918 AA948267 AI953735 AI263703 BF056387 AW594171 AI867447 AA319159 AI903440 AW956110 AI368013 AI867923 BG911906 D81142 C15616 AL538687 Z25032 Z43784 R13382 AV746924 AA449369 AA318815 BF364265 H17038 H10064 F04161 T87230 R40898 AW204071 BI819428 AA683393 AA683376 Z43192 T74078 T05103 F12527 T77951 H10118 H17037 BF855407 R19603
10	417379 407819	1610005_1 7392_2	AA196390 AA507837 AA196468 AK056626 AI600896 BF939022 BE644718 AI954754 BE218177 BE348667 AI962406 AW293122 AI968798 AI457321 BE327228 BG913531 AW939055 T30280 R54166 Z43366 BG819153 BF003119 BE646274 BF940881 R18246 R42185
15	419733	7612_3	AK027321 W63676 W63789 BE046412 BF114614 BE646183 BM126230 AW044233 AI951970 AW863548 AI139947 AA514302 AA848232 BM126251 AA789002 AA581966 AA809643 AW188870 BE706664 BE705539 BE153177 BF084925 AI133779 AW961788 AA659693 AA347970 AA295134 AA526037 AA449282 BG190454 H61476 T91396 N20018 T90114 H75644 BE710736 BF887723 H28581 AA249370 BF726698 BE841554 BI045099 T84625 AW129678 BG770826
20	432675 447820 409151	1237917_1 687223_1 4123_1	AW973834 AI791932 AI791855 AI732640 AA558833 AA558987 AI821610 AI973061 AI400921 AI796154 AW241817 AW260951 NM_004892 AF047442 BE275338 BF724683 BI917206 BE276993 AI602308 AA306105 BM152505 BC001364 AW993471 AW993481 AW993283 AW992919 AW992921 AW992980 AW992861 AW993220 BG573124 AA458385 AA234796 AI902726 AA354813 BI092644 BG778400 BI260001 BG007325 AI267455 AA426574 AI160782 AI472186 AA255500 AA434006 BG435520 AI356111 H00525 AV749060 BG944497 BG292831 AA902153 C04925 AA902160 AA383100 AW073533 AA256706 AA150809 R55766 AW958448 BE090972 BF693195 AV738979 R55856 R80136 AA484577
25	409960	39576_1	BE644758 AI082238 BF940027 AI201079 AI436035 AW275966 AI085394 AI291655 AW070441 AI474134 AI268978 AI769279 AI567682 AA693941 BF477668 AW664149 AA283782 BF509538 AW296858 AI268977 AI168133 BM352055 AI262769 BF941976 AI056920 AA481861 BF763697 AI565888 BM352383 AA427768 AA385348 AI186988 AA931831 AA134972 BF217480 BF111012 AI908246 AA319949 AA318136 AL514271 BF364291 AL515057 AV702312 AA377395 AI544217 AI341000 AW193583 AI350789 AA888338 BF945380 AW879092 AA130839 T91066 N92326 AI004389 AA078832 AL572370 W04622 BE314003 AW960808 BM360872 AA319160 AA130778 AL514257
30	433891 414922	647290_1 1563_2	AW182329 AA613792 T05304 AW868385 BG107484 AA632009 AI432670 AI656560 AI650884 AI521919 AI264653 AW150793 AW611894 AI917098 BI091245 AI651454 BF434889 AI580286 AI880735 BE301995 AI392959 AW613965 BM023628 AW515374 AI460102 BM023318 BE328188 AI952820 AI581363 AA557165 AI656577 AL562079 AI700926 AI470561 BF083058 AW196387 AI132984 BI064046 AI970167 R02122 H56924 AI521721 AA808206 AA725223 AI766003 AW339621 AA805951 AI287969 AW654627
35	414222	18695_1	BC021085 AL527872 AL526298 AI557087 BI255090 AU143499 AI560356 BG823170 BE736988 AU141388 AL580262 BI764173 AU120299 AU141755 AU141988 AU142941 AU1411330 AU141784 BI770885 BI911394 BE901426 BI918039 BG760842 BE883026 BI254740 BE732690 BG430761 BE792868 AW326267 AI135173 AA102674 BF726986 AL564735 BE155662 BE155979 BF741679 H67776 H59234 H85665 AW117774 AW274435 L20008 NM_003104 U07361 BF002824 BI222949 AI458045 AW951537 BF196474 AI669049 AI042523 BE463928 AU160125 AU160580 AW058877 AW015214 AI948718 BE219706 AI953605 BE217765 AI991382 AI245005 BF431179 AI521843 BE048908 AI204449 AW275385 AA336950 BE501521 BF740568 AA311404 AA384639 BI772535 BG473076 BE891298 BE246928 BM012896 BE242693 BE901342 BG745358 BF374053 AI564430 AU143835 AI635707 BF195492 AI280559 BF741685 AA385257 BE247655 W94974 BE163702 AI025167 AI827118 N78641 AI581093 AU158954 AU158917 AI282616 AU146399 AA713947 AI285028 AA101228 AI338522 AA832316 AI284986 AA857928 BF372568
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45	434194 432908 412652	62680_1 452541_1 18658_2	AK001536 AK056135 BM474813 BE887303 AK022914 AW581996 AW812945 BE882302 AA134266 BI043873 AA019433 BI862088 BM468657 AU128438 BE384458 AI353967 BI857117 BF686525 BI465223 BM460132 AU129877 Z122283 BG171592 BI043544 BG486295 BG750710 BI256542 BG108520 AU107119 AW510354 AJ554256 AI353968 AA191092 BF132635 AF119847 AA437261 AA438987 AI132985 AF150424 AI861896 AA570057 AV738855
50	437178	12239_1	AI801777 BE577762 AW008210 AW009441 BE350994 BE207949 AI091475 AI802774 AI827533 AI075363 AI659979 AA887855 AI078125 AI090265 AA670058 AA602411 AA683472 AI436058 AA612826 AI039932 BG057726 AI167355 BF449023 AI289476 AW074381 BF927912 AI991780 AA889119 AI537472 Z39730 AI856953 AI192337 BE112978 BE812939 AA115248 H99006 AI915784 F08973 T16748 D20466 AA608989 BF081234 AA115336 BE812876 BE812972 BE812982 BE813006 BE813018 R43883 BE812881
55	418166	18858_1	AK055109 BC019085 AA187684 BG658228 BM023227 AI932311 AW264381 AA398371 BM021483 AI432433 AI375777 AI129680 AW262782 AI134107 BM023515 AA977504 AI859222 AI348454 R69725 AA975268 BM021207 AL080074 AI292918 AW207842 N50581 AA771919 AI092269 AI028416 AI074114 BG656536 BE001677 AW193419 AA917040 W90430 AI342884 AI378957 AL036486 AW020068 BI491093 BF476021 R41226 R99631 F04125 C02343 AA115589 R56480 AI00988 R54266 R31422
60	431416 447881	120918_1 44623_1	AK056915 BE887252 AI523348 AA765350 BF468588 Z43675 R19529 AI133837 BG389444 AW382942 BE702956 AA081961 BE835247 BE835308 BE835295 AA376302 BE645790 AA375690 AA378692 AW964423 N85732 AA249770 AI754418 AA213816 BF592044 AA811729 AW514842 AI633486 AI098810 AW183016 AI635738 N27524 BE45916 AI247842 AW991230 AI754277 H16814 AI766582 BF108422 AI800361 T95129 F11313 R97946 R93989 AA375242 BF109388 AI860939 AI680080 AW953889 BF971486 AI972337 AW953841 AA372437 AI216746 H11384 R38484 AA249043 AA248732
65	407192 434747 410297	2200202_1 117643_1 2990_1	AW969151 AA532718 AA504784 AI791194 AI821930 AI821485 F37127 AA654208 F27874 AK074291 AW293424 BE676135 AI832126 BE019146 BE465019 AI761124 AA617778 AI279232 AW575897 AI672039 F28618 BF824261 AA722184 BF934174 BE004328 AV749301 BE880282 BI019798 BI019389 BF928776 AW813409 AV726804 AA077560 BE272975 BF949119 AW814195 BE879126 AI697926 BF694155 BE205787 BF063513 N35828 AI948557 AI438839 AI379879 BG056182 AI589094 N23123 AA588805 AW318581 AI080272 AI421980 AI493318 BF194630 N87590 AA495993 N32986 AA698844 H96845 H96592 N28741 BI035539 BF747723 BF171056 W01350 H05495 AI243785 Z39522 AA887432 AI350669 R46102
70	424339	50559_1	AA602964 AA609200 AW976537 AI033582 AA837085 AA745261 AA648395 BC013939 BI494690 BI491211 AI928393 AA843546 BG938644 AU185828 BI495842 AW173255 BM052709 AI743999 AI690144 AI922209 AI740907 AW340368 AA828759 AW116737 BF513970 AA707807 BF435295 AI339463 AI373842 AI433809 BE222392 AA502308 AA428261 AI460355 AW652760 AI888087 AI342098 AA722418 W78151 N64382 BE221848 AW025901 AA452120 AI150479 AI016166 AA779515 AA661791 BM474307 BI911169 BG675154 AW953303 T33604 D59141 AA385785 AA148648 BM461961 BG681168 BI602483 BE889592 AW954311 BM052986 BI662693 AI989289 Z42328 BF028504 T35668 BG402602 AU185770 AI023271 AA147719 AI434079 AI568000 AI276488 AA992453 AA342821 AA648303 AI349364 AI051008 AA926941 AA350894 AW071451 N22249 AI784138 AA083847 N22258 AW440825 AA661570 AA376887 AA659125 AI356299 R70463 AI363586 AA827189 BI494972 AW021094 BI494871 AA605500 AA460923 BI492041 AW028965 AI824611 BG271780 AI497723 H88862 D59658 N89979 AA658425 N81154 D62341 AI274437 N66697 H96993 AI370863 AA728850 H05232 R59374 H12223 AI935759 AI362553 D60006 N29572 AI916833 N76273 AA148710 BI597117 BG740471 AA332671 AA333874 AA643052 AW020175 R70550 BG623469 AA452342 AW965441 W19723 R32966 BE883841 R61003 AI910374 AI865262 R55325 AI468927 R34681 H96211 Z39807 BF954388
75			NM_015720 AF219137 AL534420 AL524055 AL537346 AL538442 BG765888 AL530064 AL525377 BG474566 BG473144 BE251553 BG706099 AL530039 BG703131 BE255806 BF080526 F12128 AL568773 BI828686 BF761480 AI204971 BG818818 BI199246 AL534816 BF529841 AA324163 AL523285 BG914330 H07952 AL534815 BE769903 AI867802 BM310135 AL533702 BE254484 BE528852 BE867462 BE740130 AL134164 AL567115 AL533701 AL524054 AL515904 AL523284 AL568203 AL534419 BF981162 BE257149 AL561833
80			

445636 B561_5 BF339388 AI345516 BG391657 BE708967 BG026034 BE261703 H56716 H65572 H93801 T48830 R96953 R96999 R39707 BE857593 AA090310
AA090672

419175 35068_1 AB018322 BC012480 B1524873 AW665564 A1934469 A1479916 BF096179 BF098162 BF096132 AA744972 A1961988 A1858339 BE076331
AA886998 A1570585 A1916688 A1678811 A1693109 A1308135 AA669046 AA961064 A1018062 H80618 BE221942 R52609 A1915164 AA365626
Z44671 B1062776 BF882486 BG286184 A1589558 AA931663 AA534979 A1275392 A1273455 R52553 AA829920 H80662 AA360728 F10618
AW953666 AW176773 H85527 AA765570 AA081927 BF093262 BG743753 AL037576 AA634314 BE814964 BE973713 N49493 BE006634
BE006630 AW270037 AA234765 A1334004 BF057179 A1857450 A1341191 A1434143 A1917449 AW517207 AA256424 AW008334 AA847572
AA994211 AA861901 AA581873 A1580157 A1364363 AW242357 AW235291 N55645 AA319869 R36911 AA256551 AW044188 A1203159 N49403
F02090 A1187299 A1609644 Z40516 AW952314

441128 20932_1 BC014072 BE328850 A1355557 A148171 A1022165 BG149661 BF000571 AA233101 AA573721 AA447991 AW016855 A1005058 AA554071
BF478215 AA906902 AW014761 BE905651 BE512923 BM047129 AA243852 AA232991 AA127550 AA127551 AA570256 A1473237 BF033706
N90525 AW973623 A1359627 BG674574 BE903322

405789 0_0 A1041403 Z49148

421091 24941_2 AK057700 BC015899 BE857108 AL526926 AL527436 BG13023 A1884867 BE858461 A1885227 A1935218 BE645596 A1922406 AA778161
BF345973 AW195853 A1687121 A1336147 A1091364 A1769203 AW627859 BE677432 BF439954 BG820230 AA283686 AAB12396 A1358396
AA932022 BE222881 AW016109 BM352667 BF528089 BG818616 A1935916 AA912295 BG910887 A1568301 AL567278 B1522445 B1754384
BG819375 BF835950 AA323718 AA860955 A1089847 AL520776 AL526045 AL538507 AL567798 A1536876 AL574332 BF834531 BF340116
BF836954 AL573997 AL581252 BF957667 AL580170 AW952324 AL569382 AW148696 AL569234 BG034270 B1913839 A1581327 AL565842
H43568 BF945188 AL559686 AL559326 T15481 AW895092 AL582684 B1519898

400263 18977_1 Z11692 X51466 NM_001961 M19997 B1224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE886804 B1868669 BG337218 AW629935
BM016625 A1560409 AL562866 A109178 BF849556 AA371735 BF038841 BF727115 BC005547 BG757526 A1555664 B1261304 BG770095
B1033486 B1517580 BG876486 B1011828 A1313235 BG831724 BF669852 BG998348 B1011834 BF888337 BF998627 BF092380 AW803215 F01241
BF805719 BG076487 AW498536 BF988866 BG988849 AA248724 BG829202 BG756456 BG032392 B1859287 BM016990 BG332369 BE933685
BE166758 BM452445 A1937808 AW026128 N23684 AW006041 A1337621 F33111 BF344301 BG105450 BG387343 BF568947 BF154671
BM007368 BF669385 BE772007 B1199487 BF761700 B1261519 BF944452 BF698506 A1036390 BM044934 AW361142 BG743618 BE769206
BE893973 B1015047 BF886479 BF761350 BE769768 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180984
BF089940 B1000274 BG255503 BG674499 BG774174 B1015084

TABLE 67C

Key: Unique number corresponding to an Eos probeset.
Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA
sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.
Strand: Indicates DNA strand from which exons were predicted.
NL_position: Indicates nucleotide positions of predicted exons.

Key	Ref	Strand	NL_position
403047	3540153	Minus	59793-59968
401424	8178894	Plus	24223-24428
401451	6634068	Minus	119926-121272
401747	9783672	Minus	118596-118818, 119119-119244, 119609-11976
404632	9795668	Plus	45098-45229
403046	3540153	Minus	55707-55859, 56369-56511
404922	7341893	Plus	13248-13428
403752	7678857	Plus	33704-33828
404210	5006248	Plus	169926-170121
401519	6649315	Plus	157315-157950
401785	7249190	Minus	165776-166996, 166189-166314, 166408-16656
401866	8018105	Plus	73128-73623
405387	6587915	Minus	3769-3833, 5708-5895
401197	9719705	Plus	176341-176452
403532	8076842	Minus	81750-81901

TABLE 68A: 895 GENES UP-REGULATED IN PROSTATE CANCER COMPARED TO NORMAL ADULT TISSUES

Table 68A lists about 895 genes up-regulated in prostate cancer compared to normal adult tissues. These were selected from 9009 probesets on the Affymetrix/Eos Hu03 GeneChip array that showed some expression in human xenograft tumors and cell lines. The 995 genes were selected such that the ratio of "average" prostate cancer to "average" normal adult tissues was greater than or equal to 2.5. The "average" prostate cancer level was set to the 85th percentile amongst prostate cancers. The "average" normal adult tissue level was set to the 85th percentile amongst non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Key: Unique Eos probeset identifier number
ExAccn: Exemplar Accession number, Genbank accession number
UnigeneID: Unigene number
Unigene Title: Unigene gene title
R1: Ratio of tumor to normal body tissue

Key	ExAccn	UnigeneID	Unigene Title	R1
448889	AF179274	Hs.22791	transmembrane protein with EGF-like and	85.6
426747	AA535210	Hs.171995	kallikrein 3, (prostate specific antigen	68.6
446057	A1420227	Hs.149358	Trp-pB transient receptor potential cat	66.6
400302	N48056	Hs.283946	folate hydrolase (prostate-specific memb	61.9
432441	AW292425	Hs.163484	ESTs	60.4
419526	A1821895	Hs.193481	ESTs	45.9
414569	AF109298	Hs.118258	prostate cancer associated protein 1	45.7
424069	AF071202	Hs.139336	ATP-binding cassette, sub-family C (CFTR	45.2
432240	A1694767	Hs.129179	Homo sapiens cDNA FLJ13581 fis, clone PL	44.9
400298	AA032279	Hs.81635	slx transmembrane epithelial antigen of	40.9
453370	A1470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	39.6

5	409731	AA125985	Hs.56145	thymosin, beta, identified in neuroblast	37.7
	400299	X07730	Hs.171995	kallikrein 3, (prostate specific antigen	34.9
	400296	AA305627	Hs.139336	ATP-binding cassette, sub-family C (CFTR	31.7
	400292	AA250737	Hs.72472	BMP-R1B	31.4
	425075	AA506324	Hs.1852	acid phosphatase, prostate	31.4
10	409262	AK000631	Hs.52256	hypothetical protein FLJ20624	31.4
	428819	AL136623	Hs.193914	KIAA0575 gene product	31.2
	409351	NM_005982	Hs.54416	sine oculis homeobox (Drosophila) homolog	30.3
	407168	R45175	Hs.117183	ESTs	29.6
	400287	S39329	Hs.181350	kallikrein 2, prostatic	29.6
15	415539	AI733861	Hs.72472	BMP-R1B	28.8
	432374	W68815	Hs.301885	Homo sapiens cDNA FLJ11346 fis, clone PL	28.8
	433043	W57554	Hs.125019	lymphoid nuclear protein (LAF-4) mRNA	28.1
	423073	9E252922	Hs.123119	MAD (mothers against decapentaplegic, Dr	27.5
	403047			NM_005656*:Homo sapiens transmembrane pr	27.4
20	444484	AK002125	Hs.11260	hypothetical protein FLJ11264	25.7
	428336	AA503115	Hs.183752	microseminoprotein, beta-	25.0
	401424			NM_001172:Homo sapiens arginase, type II	24.9
	407709	AA456135	Hs.23023	ESTs	24.7
	407122	H20276	Hs.31742	ESTs	24.6
25	425628	NM_004476	Hs.283946	folate hydrolase (prostate-specific memb	23.2
	415989	AI257700		ESTs	23.1
	448290	AK002107	Hs.20843	Homo sapiens cDNA FLJ11245 fis, clone PL	22.7
	437052	AA861697	Hs.120591	ESTs	22.6
	411096	U80034	Hs.68583	mitochondrial intermediate peptidase	22.5
30	451939	U80456	Hs.27311	single-minded (Drosophila) homolog 2	21.2
	450096	AI682088	Hs.79375	holocarboxylase synthetase (biotin-prop	20.8
	419743	AW408752	Hs.5957	Homo sapiens clone 24416 mRNA sequence	20.5
	427956	AA418000	Hs.98280	potassium intermediate/small conductance	20.5
	431548	AI834273	Hs.9711	novel protein	19.8
35	434666	AF151103	Hs.112259	T cell receptor gamma locus	19.4
	426501	AW043782	Hs.293616	ESTs	19.3
	413597	AW302885	Hs.117183	ESTs	18.9
	428662	NM_000346	Hs.2316	SRY (sex determining region Y)-box 9 (oa	18.7
	435677	AA694142	Hs.293726	ESTs, Weakly similar to TSGA RAT TESTIS	18.0
40	429220	AW207206		ESTs	17.9
	408826	AF216077	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	17.6
	418961	AW967646	Hs.23023	ESTs	17.3
	428898	AB033070	Hs.194408	KIAA1244 protein	17.3
	420757	X78592	Hs.99915	androgen receptor (dihydrotestosterone r	16.8
45	428398	AI249368	Hs.98568	ESTs	16.3
	419078	M93119	Hs.89584	insulinoma-associated 1	15.8
	450382	AA397658	Hs.60257	Homo sapiens cDNA FLJ13598 fis, clone PL	15.4
	449625	NM_014253		odz (odd Ozten-m, Drosophila) homolog 1	15.2
	401451			NM_004496*:Homo sapiens hepatocyte nucle	14.9
50	447033	AI357412	Hs.157601	ESTs	14.9
	452594	AIJ076405	Hs.29981	solute carrier family 26 (sulfate transp	14.7
	448619	AW175885	Hs.278695	Homo sapiens prostelin mRNA, complete cds	14.6
	418829	AA516531	Hs.55999	NK homeobox (Drosophila), family 3, A	14.5
	430376	AW292053	Hs.12532	chromosome 1 open reading frame 21	14.4
55	418848	AI820981	Hs.193465	ESTs	14.3
	428918	AW873986	Hs.119383	ESTs	14.2
	424012	AW368377	Hs.137569	tumor protein 63 kDa with strong homolog	14.1
	418278	AI088489	Hs.83937	hypothetical protein	14.1
	408000	L11690	Hs.198689	bullous pemphigoid antigen 1 (230/240kD)	13.9
60	443822	AI087412	Hs.143611	ESTs, Weakly similar to 2004398A chromos	13.3
	432101	AI918960	Hs.123642	EphA3	13.3
	447342	AI199268	Hs.19322	Homo sapiens, Similar to RIKEN cDNA 2010	13.1
	412446	AI768015		ESTs	12.7
	437718	AI927288	Hs.196779	ESTs	12.6
65	433404	T32982		ESTs	12.6
	431089	BE041395	Hs.156110	ESTs, Weakly similar to unknown protein	12.6
	427212	AW293849	Hs.58279	ESTs, Weakly similar to ALU7_HUMAN ALU 5	12.6
	429597	NM_003816	Hs.2442	a disintegrin and metalloproteinase doma	12.5
	444151	AW972917	Hs.128749	alpha-methylacyl-CoA racemase	12.4
70	428046	AW812795	Hs.337534	ESTs, Moderately similar to I38022 hypot	12.4
	453160	AI263307		H2B histone family, member L	12.2
	439927	AI557019	Hs.116467	small nuclear protein PRAC	12.1
	431117	AF003522	Hs.250500	delta (Drosophila)-like 1	12.1
	424800	AL035588	Hs.153203	MyoD family inhibitor	11.9
75	427874	NM_003528	Hs.2178	H2B histone family, member Q	11.9
	424692	AA428834	Hs.151791	KIAA0092 gene product	11.7
	415263	AA948033	Hs.130853	ESTs	11.3
	416182	NM_004354	Hs.79069	cyclin G2	11.3
	420218	AW958037		ribosomal protein L4	11.3
80	411887	AW182924	Hs.128790	ESTs	11.2
	425154	NM_001851	Hs.154850	collagen, type IX, alpha 1	11.2
	430226	BE245562	Hs.2551	adrenergic, beta-2-, receptor, surface	11.2
	450325	AI935962	Hs.91973	ESTs	11.1
	439444	AI277852	Hs.54578	ESTs, Weakly similar to I38022 hypothesi	11.1
	440529	AW207640	Hs.16478	Homo sapiens cDNA: FLJ21718 fis, clone C	11.0
	457211	AW972565	Hs.32399	ESTs, Weakly similar to S61797 vasodilat	11.0
	428600	AW863261	Hs.138860	hypothetical protein DKFZp434K1421	11.0

5	422728	AW937826	Hs.103262	ESTs, Weakly similar to ZN91_HUMAN ZINC	11.0
	417333	AL157545	Hs.173179	bromodomain and PHD finger containing, 3	10.7
	434423	NM_006769	Hs.3844	LIM domain only 4	10.6
	434170	AA626509	Hs.122329	ESTs	10.6
	432729	AK000292	Hs.130732	hypothetical protein FLJ20285	10.5
10	446100	AW967109	Hs.13804	hypothetical protein dJ462023.2	10.4
	432715	AA247152	Hs.200483	ESTs, Weakly similar to KIAA1074 protein	10.4
	421896	N62293	Hs.45107	ESTs	10.3
	401747			Homo sapiens keratin 17 (KRT17)	10.1
	451640	AA195601	Hs.26771	Human DNA sequence from clone 747H23 on	10.1
15	431542	H63010	Hs.5740	ESTs	10.0
	447397	BE247876	Hs.18442	E-1 enzyme	10.0
	433285	AW975944	Hs.237396	ESTs	10.0
	431325	AW026751	Hs.5794	ESTs, Weakly similar to 2109260A B cell	9.9
	410889	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalus	9.8
20	432674	AA641092	Hs.257339	ESTs, Weakly similar to 138022 hypotheti	9.6
	434926	BE543269	Hs.50252	mitochondrial ribosomal protein L32	9.6
	442049	AA310393	Hs.180044	ESTs	9.6
	443180	R16875	Hs.258576	claudin 12	9.5
	406864	M21305		FGFES predicted novel secreted protein	9.5
25	426350	NM_003245	Hs.2022	transglutaminase 3 (E polypeptide, prote	9.5
	456660	AA909249	Hs.112282	solute carrier family 30 (zinc transport	9.5
	448045	AJ297436	Hs.20166	prostate stem cell antigen	9.5
	451684	AF216751	Hs.26813	CDA14	9.5
	440594	AW445167	Hs.126036	ESTs	9.4
30	432415	T16971	Hs.289014	ESTs, Weakly similar to A43932 mucin 2 p	9.3
	418601	AA279490	Hs.86368	calmegin	9.3
	433332	AJ367347	Hs.44898	Homo sapiens clone TCCCTA00151 mRNA sequ	9.2
	437124	AA554458		KIAA0665 protein	9.2
	428728	NM_016625	Hs.191381	hypothetical protein	9.2
35	438869	AF075009		gb:Homo sapiens full length insert cDNA	9.1
	431892	NM_002742	Hs.2891	protein kinase C, mu	8.9
	413992	W26276	Hs.138075	RNA, U2 small nuclear	8.9
	428342	AJ739168		Homo sapiens cDNA FLJ13458 fis, clone PL	8.9
	418836	AI655499	Hs.161712	ESTs	8.8
40	409799	D11928	Hs.76845	phosphoserine phosphatase-like	8.8
	400294	N95796	Hs.278695	Homo sapiens protein mRNA, complete cds	8.7
	434826	AF155661	Hs.22265	pyruvate dehydrogenase phosphatase	8.7
	418250	U29928	Hs.83918	adenosine monophosphate deaminase (isofo	8.7
	425905	AB032959	Hs.318684	novel C3HC4 type Zinc finger (ring finger	8.7
45	418329	AW247430	Hs.84152	cystathionine-beta-synthase	8.7
	450203	AF097994		L-lysine/alpha-amino adipate aminotra	8.7
	425465	L16964	Hs.1804	protein kinase C, iota	8.5
	416239	AL038450	Hs.48948	ESTs	8.5
	436962	AW377314	Hs.5364	DKFZP564I052 protein	8.4
50	450164	AI239923	Hs.63931	ESTs	8.4
	452744	AI267652	Hs.246107	Homo sapiens mRNA; cDNA DKFZp434E082 (fr	8.4
	440774	AI420511	Hs.153934	ESTs	8.3
	444922	AI921750	Hs.144871	Homo sapiens cDNA FLJ13752 fis, clone PL	8.3
	410870	U81599	Hs.66731	homeo box B13	8.3
55	435047	AA454985	Hs.54973	cadherin-like protein VR20	8.2
	418564	AA631143	Hs.278695	Homo sapiens protein mRNA, complete cds	8.2
	451027	AW519204	Hs.40808	ESTs	8.2
	445873	AA250970	Hs.251946	poly(A)-binding protein, cytoplasmic 1-I	8.2
	423349	AF010258	Hs.127428	homeo box A9	8.1
60	421928	AF013758	Hs.109643	polyadenylate binding protein-interactin	8.1
	432586	AA568548		ESTs	8.0
	426108	AA622037	Hs.166468	programmed cell death 5	8.0
	417153	X57010	Hs.81343	collagen, type II, alpha 1 (primary oste	8.0
	416653	AA768553	Hs.183145	metallothionein 1E (functional)	7.9
65	447476	BE293456	Hs.20880	ESTs, Weakly similar to 138022 hypotheti	7.9
	450377	AB033091		KIAA1265 protein	7.8
	429769	NM_004917	Hs.218366	kalikrein 4 (protease, enamel matrix, p	7.7
	416815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	7.7
	433323	AA805132	Hs.159142	ESTs	7.7
70	451962	AL120173	Hs.301663	ESTs	7.7
	452367	U71207	Hs.29279	eyes absent (Drosophila) homolog 2	7.7
	421470	R27496	Hs.1378	annexin A3	7.7
	420092	AA814043	Hs.88045	ESTs	7.6
	416111	AA033813	Hs.79018	chromatin assembly factor 1, subunit A (7.6
75	440749	W22335	Hs.7382	hypothetical protein MGC3199	7.6
	441866	BE484341	Hs.21201	nectin 3; DKFZP566B0846 protein	7.6
	411019	AW993097	Hs.48617	Homo sapiens cDNA FLJ12540 fis, clone NT	7.5
	421588	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	7.4
	451418	BE387790	Hs.26369	hypothetical protein FLJ20287	7.4
80	433517	AW022133	Hs.189838	ESTs	7.4
	415621	AI648502	Hs.55468	ESTs	7.4
	442692	BE566623	Hs.29899	ESTs, Weakly similar to G02075 transcrip	7.3
	452340	NM_002202	Hs.505	ISL1 transcription factor, LIM/homeodoma	7.3
	450244	AA007534	Hs.125062	ESTs	7.2
	433293	AF007835	Hs.32417	hypothetical protein MGC4309	7.2
	425259	AL049280	Hs.155397	Homo sapiens mRNA; cDNA DKFZp564K143 (fr	7.2
	434485	AI623511	Hs.118567	ESTs	7.2

5	442772	AW503680	Hs.5957	Homo sapiens clone 24416 mRNA sequence	7.1
	425211	M18667	Hs.1867	progastricsin (pepsinogen C)	7.1
	431868	XG3628	Hs.2877	cadherin 3, type 1, P-cadherin (placenta)	7.0
	408418	AW963897	Hs.44743	KIAA1435 protein	7.0
	438063	AK000028		ribosomal protein S24	7.0
10	412350	AI659306	Hs.73826	protein tyrosine phosphatase, non-recept	6.9
	414664	AA587775	Hs.66295	multi-PDZ-domain-containing protein	6.9
	428465	AW970976	Hs.293653	ESTs	6.9
	436476	AA326108	Hs.33829	bHLH protein DEC2	6.8
	431585	BE242803	Hs.262823	hypothetical protein FLJ10326	6.8
15	434808	AF155108	Hs.256150	Homo sapiens, Similar to RIKEN cDNA 2810	6.7
	432103	T15803	Hs.272458	protein phosphatase 3 (formerly 2B), cat	6.7
	456088	BE177320	Hs.156148	hypothetical protein FLJ13231	6.6
	429084	AJ001443	Hs.195814	splicing factor 3b, subunit 3, 130kD	6.6
	422486	BE614492	Hs.117487	gene near HD on 4p16.3 with homology to	6.6
20	410227	AB009284	Hs.61152	exostoses (multiple)-like 2	6.6
	453439	AI572438	Hs.32976	guanine nucleotide binding protein 4	6.5
	410037	AB020725	Hs.58009	KIAA0918 protein	6.5
	420297	AI628272	Hs.88323	ESTs, Weakly similar to ALU1_HUMAN ALU S	6.4
	405648	AW451449	Hs.57749	ESTs	6.4
25	448148	NM_016578	Hs.20509	HBV pX associated protein-B	6.4
	410268	AA316181	Hs.61635	six transmembrane epithelial antigen of	6.4
	422134	AW179019	Hs.112110	mitochondrial ribosomal protein L42	6.3
	415058	Z19448	Hs.131887	ESTs, Weakly similar to T24396 hypotheti	6.3
	404632			NM_022490:Homo sapiens hypothetical prot	6.3
30	412935	BE267045	Hs.75064	tubulin-specific chaperone c	6.3
	453308	AW959731	Hs.323099	ESTs	6.3
	449048	Z45051	Hs.22920	similar to S68401 (cattle) glucose induc	6.3
	410782	AF226053	Hs.66170	HSKM-B protein	6.3
	436032	AA150797	Hs.109276	latexin protein	6.3
35	456508	AA502764	Hs.123469	ESTs, Weakly similar to AF208855 1 BM-01	6.3
	413328	Y15723	Hs.76285	guanylate cyclase 1, soluble, alpha 3	6.2
	425071	NM_013989	Hs.154424	deiodinase, iodothyronine, type II	6.2
	424036	AA770688		H2A histone family, member L	6.2
	418245	AA088767	Hs.83883	transmembrane, prostate androgen induced	6.2
40	450861	AI523898	Hs.17617	ESTs	6.1
	418821	AA436002	Hs.183161	ESTs	6.1
	458609	AW972512	Hs.20985	sin3-associated polypeptide, 30kD	6.1
	432527	AW975028	Hs.102754	ESTs	6.1
	433730	AK002135	Hs.3542	hypothetical protein FLJ11273	6.1
45	449845	AW971183	Hs.8019	DnaJ (Hsp40) homolog, subfamily C, membe	6.1
	420948	AB016888	Hs.100469	myeloid/lymphoid or mixed-lineage leukem	6.1
	425704	U9293	Hs.159264	Human clone Z3948 mRNA sequence	6.0
	458440	AI095468	Hs.135254	Homo sapiens clone 1 thrombospondin mRNA	6.0
	419647	AA348947	Hs.91816	hypothetical protein	6.0
50	455497	AA112573	Hs.278695	Homo sapiens protein mRNA, complete cds	6.0
	428593	AW207440	Hs.185973	degenerative spermatocytes (homolog Droso	5.9
	400303	AA242758	Hs.79136	LIV-1 protein, estrogen regulated	5.9
	446418	AV658299	Hs.163959	ESTs	5.9
	407819	R42185		ESTs	5.9
55	430387	AW372884	Hs.240770	nuclear cap binding protein subunit 2, 2	5.9
	410102	AW246508	Hs.279727	ESTs; homologue of PEM-3 (Clona savignyl	5.9
	429165	AW006886	Hs.118258	prostate cancer associated protein 1	5.9
	417873	BE266659	Hs.293659	Homo sapiens, Similar to RIKEN cDNA AA30	5.8
	410240	AL157424	Hs.61289	synaptotagmin 2	5.8
60	421305	BE397354	Hs.324830	diphtheria toxin resistance protein requi	5.8
	451406	AI694320	Hs.6295	ESTs, Weakly similar to T17248 hypotheti	5.8
	418795	AA97778	Hs.20509	HBV pX associated protein-B	5.7
	427701	AA411101	Hs.243886	nuclear autoantigenic sperm protein (his	5.7
	451468	AW503398	Hs.283663	ESTs, Moderately similar to I38022 hypot	5.7
65	433852	AJ376329	Hs.126629	ESTs	5.7
	432882	NM_013257	Hs.279696	serum/glucocorticoid regulated kinase-II	5.6
	419440	AB020688	Hs.90419	KIAA0882 protein	5.6
	435706	W31254	Hs.7045	GLD04 protein	5.6
	431583	AL042613	Hs.262476	S-adenosylmethionine decarboxylase 1	5.6
70	442409	BE208843	Hs.129544	hypothetical protein MG315438	5.6
	453171	R76472	Hs.65646	ESTs	5.6
	437252	AM33833	Hs.164159	ESTs, Weakly similar to ALU1_HUMAN ALU S	5.6
	422083	NM_001141	Hs.111256	arachidonate 15-lipoxygenase, second typ	5.6
	425838	AI916662	Hs.211577	kineclin 1 (kinesin receptor)	5.5
75	403046			NM_005656:Homo sapiens transmembrane pr	5.5
	447805	AW627932	Hs.302421	gemin4	5.5
	443162	T49851	Hs.9029	DKFZP434G032 protein	5.4
	418555	AI417215	Hs.87159	hypothetical protein FLJ12577	5.4
	437162	AW005505	Hs.5464	thyroid hormone receptor coactivating pr	5.4
80	419465	AW500239	Hs.21187	Homo sapiens cDNA: FLJ23058 fis, clone L	5.4
	440145	AW014231	Hs.90780	Homo sapiens cDNA: FLJ22930 fis, clone K	5.4
	427308	D26067	Hs.174905	KIAA0033 protein	5.4
	409151	AA306106		SEC22, vesicle trafficking protein (S. c	5.4
	432840	AK001403	Hs.279521	hypothetical protein FLJ20530	5.4
	423242	AL039402	Hs.125783	DEME-6 protein	5.3
	453092	H18835	Hs.31608	hypothetical protein FLJ20041	5.3
	441021	AW578716	Hs.7644	H1 histone family, member 2	5.3

	415276	U88566	Hs.78353	SFRS protein kinase 2	5.3
	400290	H18836	Hs.31608	hypothetical protein FLJ20041	5.3
	432435	BE218886	Hs.282070	ESTs	5.3
5	417318	AW953937	Hs.240845	ESTs	5.3
	429467	NM_004477	Hs.203772	F5HD region gene 1	5.3
	416276	U41050	Hs.79136	LIV-1 protein, estrogen regulated	5.3
	410076	T05387	Hs.7991	ESTs	5.3
	420039	NM_004605	Hs.94581	sulfotransferase family, cytosolic, 2B,	5.2
10	423445	NM_014324	Hs.128749	alpha-methylacyl-CoA racemase	5.2
	436420	AA443966	Hs.31595	ESTs	5.2
	414085	AA114016	Hs.75746	aldehyde dehydrogenase 1 family, member	5.1
	422048	NM_012445	Hs.288126	spondin 2, extracellular matrix protein	5.1
	427176	AW381569	Hs.40334	ESTs	5.1
15	450832	AW970602	Hs.105421	ESTs	5.1
	448807	AJ571940	Hs.7549	ESTs	5.1
	420568	F08247	Hs.247735	protocadherin alpha 10	5.1
	421665	AF189723	Hs.106778	ATPase, Ca transporting, type 2C, member	5.0
	427615	BE410107	Hs.179817	CGI-82 protein, PSDR1	5.0
20	430598	AK001764	Hs.247112	hypothetical protein FLJ10902	5.0
	452578	AB023177	Hs.29900	KIAA0960 protein	5.0
	431724	AA514535	Hs.283704	ESTs	5.0
	409757	NM_001898	Hs.123114	cystatin SN	5.0
	432242	AW022715	Hs.162160	ESTs, Weakly similar to ALU4_HUMAN ALU S	5.0
25	407103	AA424861	Hs.256301	hypothetical protein MGC13170	5.0
	421154	AA284333	Hs.287631	Homo sapiens cDNA FLJ14269 fis, clone PL	5.0
	400301	X03635	Hs.1657	estrogen receptor 1	5.0
	426006	R49031	Hs.22627	ESTs	5.0
	452679	Z42387	Hs.83983	transmembrane, prostate androgen induced	4.9
30	446890	AB111807	Hs.108646	Homo sapiens cDNA FLJ14934 fis, clone PL	4.9
	444108	R56784	Hs.140842	ESTs	4.9
	452259	AA317439	Hs.28707	signal sequence receptor, gamma (translo	4.9
	419083	AI479660	Hs.98613	Homo sapiens cDNA FLJ12292 fis, clone MA	4.9
	416854	H40164	Hs.80296	Purkinje cell protein 4	4.9
35	422890	Z43784		ankyrin 3, node of Ranvier (ankyrin G)	4.9
	428330	L22524	Hs.2255	matrix metalloproteinase 7 (matrilysin,	4.9
	419168	AI336132	Hs.33718	Homo sapiens cDNA FLJ12641 fis, clone NT	4.9
	452017	AF109302	Hs.27495	prostate cancer associated protein 7	4.9
	456362	AW973003	Hs.179909	hypothetical protein FLJ22995	4.9
40	442501	AA315267	Hs.23128	ESTs	4.8
	439735	AI635386	Hs.142846	hypothetical protein	4.8
	451752	AB032987		KIAA1171 protein	4.8
	423583	AL122055	Hs.129836	KIAA1028 protein	4.8
45	446157	BE270828	Hs.131740	Homo sapiens cDNA: FLJ22562 fis, clone H	4.8
	432363	AA534489		gbm176g11.s1 NCL CGAP_Co3 Homo sapiens	4.8
	433313	W20128	Hs.298039	ESTs	4.8
	408101	AW968504	Hs.123073	CDC2-related protein kinase 7	4.8
	453857	AL080236	Hs.35861	DKFZP586E1621 protein	4.8
	451982	F13036	Hs.27373	Homo sapiens mRNA: cDNA DKFZp58401763 f	4.7
50	447574	AF162666	Hs.18896	tousled-like kinase 1	4.7
	429299	AI620483	Hs.347408	hypothetical protein MGC13102	4.7
	420522	AW957137	Hs.98541	hypothetical protein	4.7
	417379	AA196390		gbzps99b10.s1 Striatogene muscle 937209 H	4.7
	411031	W37943	Hs.34892	KIAA1323 protein	4.7
55	431725	X65724	Hs.2839	Nonie disease (pseudoglioma)	4.7
	441224	AJ076964	Hs.7753	calumenin	4.7
	407813	AL120247	Hs.40109	KIAA0872 protein	4.7
	440074	AA630345	Hs.10689	ESTs, Weakly similar to T00050 hypotheti	4.7
	430294	AI638226	Hs.32976	guanine nucleotide binding protein 4	4.7
60	415082	AA180000	Hs.137396	ESTs, Weakly similar to JC5238 galactosy	4.7
	414922	D00723		glycine cleavage system protein H (amino	4.7
	430945	U80669	Hs.55999	NK homeobox (Drosophila), family 3, A	4.7
	438825	BE327427	Hs.79953	ESTs	4.7
	425174	D87450	Hs.154878	KIAA0261 protein	4.7
65	420360	AA640891	Hs.102406	ESTs	4.7
	410193	AJ132562	Hs.69757	zinc finger protein 281	4.7
	440300	N39780	Hs.8659	Homo sapiens, Similar to RIKEN cDNA 5630	4.6
	436761	AI817776	Hs.236557	ESTs	4.6
	410275	U85658	Hs.61796	transcription factor AP-2 gamma (activat	4.6
70	404922			NM_003071:Homo sapiens SWWSNF related,	4.6
	436556	AI364997	Hs.7572	ESTs	4.6
	429302	AJ076674	Hs.198899	eukaryotic translation initiation factor	4.6
	447595	AW379130	Hs.18953	phosphodiesterase 9A	4.6
	433006	BE242758	Hs.190223	ESTs, Moderately similar to T29285 hypol	4.5
75	407894	AJ276313	Hs.41143	phosphoinositide-specific phospholipase	4.5
	418818	AA228899	Hs.101307	Homo sapiens HUT11 protein mRNA, partial	4.5
	433556	W56321	Hs.111460	calcium/calmodulin-dependent protein kin	4.5
	443123	AA094538	Hs.272806	putative transcription regulation, nuclea	4.5
	419991	AJ000098	Hs.94210	eyes absent (Drosophila) homolog 1	4.5
80	419594	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	4.5
	453390	AA862496	Hs.26482	ESTs	4.5
	417061	AI675944	Hs.188691	Homo sapiens cDNA FLJ12033 fis, clone HE	4.5
	419239	AA468183	Hs.184598	Homo sapiens cDNA: FLJ23241 fis, clone C	4.5
	436873	N23874	Hs.50477	RAB27A, member RAS oncogene family	4.5

5	408001	AA046458	Hs.95296	ESTs	4.4
	413950	AA249096	Hs.32793	ESTs	4.4
	416655	AW988613	Hs.79428	BCL2/adenovirus E1B 19kD-interacting pro	4.4
	418004	U37519	Hs.87539	aldehyde dehydrogenase 3 family, member	4.4
	419733	AW362955		Homo sapiens cDNA FLJ14415 fis, clone HE	4.4
10	433233	AB040927	Hs.301804	KIAA1494 protein	4.4
	439979	AW600291	Hs.6823	hypothetical protein FLJ10430	4.4
	430589	AJ002744	Hs.246315	UDP-N-acetyl-alpha-D-galactosamine:polyp	4.4
	417958	AA767382	Hs.193417	ESTs	4.4
	450680	AF131784	Hs.25318	Homo sapiens clone 25194 mRNA sequence	4.4
15	435020	AW505076	Hs.301855	DiGeorge syndrome critical region gene 8	4.4
	437396	BE140396	Hs.21621	hypothetical protein DKFZp782O076	4.4
	425810	AI923627	Hs.31903	ESTs	4.4
	426028	NM_001110	Hs.172028	a disintegrin and metalloproteinase doma	4.3
	452747	BE153855	Hs.61460	Ig superfamily receptor LNIR	4.3
20	429269	AA420450	Hs.292911	Plakophilin	4.3
	452092	BE245374	Hs.27842	hypothetical protein FLJ11210	4.3
	437967	BE277414	Hs.5947	mel transforming oncogene (derived from	4.3
	459284	AF155660	Hs.300496	mitochondrial solute carrier	4.3
	417067	AJ001417	Hs.81086	solute carrier family 22 (extraneuronal	4.3
25	423453	AW450737	Hs.128791	CGI-09 protein	4.3
	407137	T97307		gbv53h05.s1 Soares fetal liver spleen	4.3
	448826	AI580252	Hs.293246	ESTs, Weakly similar to putative p150 [H	4.3
	419713	AW568058	Hs.92381	nudix (nucleoside diphosphate linked moi	4.3
	427359	AW020782	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	4.3
30	450402	BE218027	Hs.89969	ESTs	4.3
	426055	AA420564	Hs.101760	ESTs	4.3
	429441	AJ224172	Hs.204096	lipophilin B (uteroglobin family member)	4.3
	432676	AI791855		ESTs	4.2
	439963	AW247529	Hs.6793	platelet-activating factor acetylhydrola	4.2
35	445707	AJ248720	Hs.114390	ESTs	4.2
	410297	AA148710		kumcan	4.2
	416737	AF154335	Hs.79691	LIM domain protein	4.2
	430255	AK000703	Hs.323822	Homo sapiens mRNA for KIAA1551 protein,	4.2
	421829	AB018330	Hs.108708	calcium/calmodulin-dependent protein kin	4.2
40	447620	AW290951		ESTs	4.2
	426647	AA243464	Hs.294101	pre-B-cell leukemia transcription factor	4.2
	432886	BE159028	Hs.279704	chromatin accessibility complex 1	4.2
	446237	AW270515	Hs.149596	Homo sapiens, Similar to RIKEN cDNA 2310	4.2
	421878	AA299652	Hs.111496	Homo sapiens cDNA FLJ11643 fis, clone HE	4.2
45	423337	NM_004655	Hs.127337	axin 2 (conductin, axil)	4.2
	435854	AJ278120	Hs.4996	putative ankyrin-repeat containing prote	4.2
	427723	AJ355260	Hs.279789	histone deacetylase 3	4.2
	430122	NM_013342	Hs.233765	TCF3 (E2A) fusion partner (in childhood	4.2
	416140	AI918035	Hs.301198	roundabout (axon guidance receptor, Dros	4.2
50	428231	U17989	Hs.183105	nuclear autoantigen	4.2
	447966	AA340605	Hs.105887	ESTs, Weakly similar to Homolog of rat Z	4.1
	432274	AK000382	Hs.274251	hypothetical protein FLJ20375; KIAA1797	4.1
	432621	AI298501	Hs.21192	ESTs, Weakly similar to T46428 hypotheti	4.1
	408063	BE086548	Hs.42346	calcineurin-binding protein calcisarin-1	4.1
55	407192	AA609200		gla:af12c02.s1 Soares_Jesús_NHT Homo sap	4.1
	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	4.1
	427479	BE410092	Hs.178471	KIAA0788 gene product	4.1
	434194	AF119847		Homo sapiens PRO1550 mRNA, partial cds	4.1
	422072	AB018255	Hs.111138	KIAA0712 gene product	4.1
60	411145	BE439553	Hs.250528	Homo sapiens, clone IMAGE:4096694, mRNA,	4.1
	449459	BE546848	Hs.195048	ESTs	4.1
	421662	NM_014141	Hs.106552	cell recognition molecule Caspr2	4.1
	445309	AL157474	Hs.12504	likely ortholog of mouse Arkadia	4.1
	412520	AA442324	Hs.795	H2A histone family, member O	4.0
65	448663	BE614589		hypothetical protein MGC14797	4.0
	425689	W16480	Hs.24283	ESTs, Moderately similar to reduced expr	4.0
	433847	AA803967	Hs.222294	ESTs	4.0
	426030	BE243933	Hs.108842	zinc finger protein 22 (KOX 15)	4.0
	418838	AW385224	Hs.35198	ectonucleotide pyrophosphatase/phosphodi	4.0
70	439820	AL380204	Hs.283853	Homo sapiens mRNA full length insert cDN	4.0
	422634	NM_016010	Hs.118821	CGI-62 protein	4.0
	453469	AB014533	Hs.33010	KIAA0633 protein	4.0
	418827	BE327311	Hs.47166	HT021	4.0
	448791	AF632278	Hs.195922	ESTs	4.0
75	443884	N20617	Hs.194397	tepin receptor	4.0
	418857	AA188775	Hs.292453	ESTs	4.0
	401519			C15000476*.g 12737279[ref]XP_012163.1]	4.0
	407846	AA426202	Hs.40403	Cbp/p300-interacting transactivator, wit	4.0
	431689	AA305688	Hs.267696	UDP-Gal:betaGalNAc beta 1,3-galactosyltr	3.9
80	408784	AW971350	Hs.63386	ESTs	3.9
	435655	AW106663	Hs.6947	HSPC069 protein	3.9
	432615	AA557191	Hs.55028	ESTs, Weakly similar to I54374 gene NF2	3.9
	448804	AW512213	Hs.342849	ADP-ribosylation factor-like 5	3.9
	430389	AL117429	Hs.240846	DKFZP434D146 protein	3.9
	432278	AL137508	Hs.274256	hypothetical protein FLJ23563	3.9
	414869	AA157291	Hs.21479	ubiquitin 1	3.9
	429163	AA884766		gbam20a10.s1 Soares_NFL_T_GBC_S1 Homo s	3.9

	444190	A1878918	Hs.10526	cysteine and glycine-rich protein 2	3.9
	443991	NM_002250	Hs.10082	potassium intermediate/small conductance	3.9
	433339	AF019226	Hs.8036	glioblastoma overexpressed	3.9
	435021	AA922192	Hs.73962	ESTs	3.9
5	412834	R77123	Hs.79881	Homo sapiens cDNA: FLJ23006 fis, clone L	3.9
	442607	AA507576	Hs.288361	Homo sapiens cDNA: FLJ22696 fis, clone H	3.9
	408833	AW612232	Hs.254835	ESTs	3.9
	432652	AA813887	Hs.168173	Homo sapiens cDNA FLJ12187 fis, clone MA	3.9
10	456177	NM_012391	Hs.79414	prostate epithelium-specific Ets transcr	3.8
	433345	A1681545	Hs.152982	hypothetical protein FLJ13117	3.8
	421887	AW161450	Hs.109201	CGI-86 protein	3.8
	434614	A1249502	Hs.29669	ESTs	3.8
	425910	AA830787	Hs.184760	CCAAT-box-binding transcription factor	3.8
15	432370	AA308334	Hs.274424	N-acetylneuraminic acid phosphate syntha	3.8
	413010	AA393273	Hs.75133	transcription factor B-like 1 (mitochond	3.8
	435114	AA776483	Hs.288938	mitochondrial ribosomal protein L9	3.8
	439024	R96696	Hs.35598	ESTs	3.8
	426891	AK001536		Homo sapiens cDNA FLJ10674 fis, clone NT	3.8
20	427871	AW892405	Hs.59622	Homo sapiens, clone IMAGE:3507281, mRNA,	3.8
	439671	AW162840	Hs.6641	kinesin family member 5C	3.8
	418113	A1272141	Hs.83484	SRY (sex determining region Y)-box 4	3.8
	422424	A1186431	Hs.296638	prostate differentiation factor	3.8
	447439	AA313565	Hs.145020	ESTs, Weakly similar to KIAA1205 protein	3.8
25	414178	AW557372	Hs.46791	ESTs, Weakly similar to I38022 hypotheti	3.8
	427099	AB032953	Hs.173560	odd Oz/ten-m homolog 2 (Drosophila, mous	3.8
	407908	BE378758	Hs.110853	uncharacterized hematopoietic stem/proge	3.8
	440695	AW088363	Hs.246240	ESTs	3.8
	429586	A1871613	Hs.28538	Homo sapiens cDNA: FLJ21086 fis, clone C	3.8
30	447533	NM_004786	Hs.18792	thioredoxin-like, 32kD	3.8
	411190	AA306342	Hs.69171	protein Kinase C-like 2	3.8
	426126	AL118747	Hs.26691	ESTs	3.8
	434263	N34895	Hs.44648	ESTs	3.8
	414407	AA147026	Hs.76704	ESTs	3.7
35	432426	AW973152	Hs.31050	ESTs	3.7
	425770	NM_014963	Hs.159482	spastic ataxia of Charlevoix-Saguenay (s	3.7
	432579	AF043244	Hs.278439	nucleolar protein 3 (apoptosis repressor	3.7
	444101	R19175	Hs.169793	ribosomal protein L32	3.7
	432908	A1861896		ESTs	3.7
40	432800	BE391046	Hs.278962	AIM-1 protein	3.7
	429966	BE081342	Hs.283037	HSPC039 protein	3.7
	419972	AL041465	Hs.182982	golgin-67	3.7
	410001	AB041036	Hs.57771	kallikrein 11	3.7
	432205	A1806583	Hs.125291	ESTs	3.7
45	401197			ENSP00000229263*HSPC213.	3.7
	420081	AW024937	Hs.28410	ESTs	3.7
	431103	M57399	Hs.44	pleiotrophin (heparin binding growth fac	3.7
	433577	AW007080	Hs.284182	ESTs	3.7
	435017	AA336522	Hs.12854	angiotensin II, type I receptor-associat	3.7
50	420805	L10333	Hs.99947	reticulon 1	3.7
	401866			Target Exon	3.7
	457183	H91882	Hs.118569	Dyf-binding protein IDAX (inhibition of	3.7
	427982	NM_016156	Hs.181326	KIAA1073 protein	3.7
	405387			NM_022170*Homo sapiens Williams-Beuren	3.7
55	449933	AW157098	Hs.324104	Human DNA sequence from clone RP1-63M2 o	3.7
	432388	X15218	Hs.2969	v-ski avian sarcoma viral oncogene homol	3.7
	438157	AW137011	Hs.49576	ESTs	3.7
	451845	BE504066	Hs.211420	ESTs	3.7
	452721	AJ269529	Hs.301871	solute carrier family 37 (glycerol-3-pho	3.6
60	454229	AW957744	Hs.278469	lacrimal proline rich protein	3.6
	416974	AF010233	Hs.80667	RALBP1 associated Eps domain containing	3.6
	421537	BE383488	Hs.105547	neural proliferation, differentiation an	3.6
	428738	NM_000380	Hs.192803	xeroderma pigmentosum, complementation g	3.6
	440484	BE518768	Hs.7232	acetyl-Coenzyme A carboxylase alpha	3.6
65	407748	AL079409	Hs.38176	KIAA0606 protein; SCN Circadian Oscillat	3.6
	453049	BE537217	Hs.30343	ESTs	3.6
	422089	AA523172	Hs.103135	ESTs, Weakly similar to SFRA_HUMAN SPUC	3.6
	408096	BE250162	Hs.63765	dihydrofolate reductase	3.6
	407204	R41933	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.6
70	450649	NM_001429	Hs.25272	E1A binding protein p300	3.6
	436489	AJ272289	Hs.121429	zinc-binding protein Rboe728	3.6
	447818	W75940	Hs.21906	Homo sapiens clone 24670 mRNA sequence	3.6
	424285	BE207168	Hs.144630	nuclear receptor subfamily 2, group F, m	3.6
	452280	AA453208	Hs.330994	RAB9, member RAB oncogene family	3.6
75	420344	BE463721	Hs.97101	putative G protein-coupled receptor	3.6
	427716	BE245274	Hs.180428	KIAA1181 protein	3.6
	426793	X89887	Hs.172350	HIR (histone cell cycle regulation defec	3.6
	419879	Z17806	Hs.93584	Homer, neuronal immediate early gene, 2	3.6
80	403762			NM_002753*Homo sapiens mitogen-activate	3.6
	418559	AA225048	Hs.104207	ESTs	3.6
	438523	H66220	Hs.278177	ESTs	3.6
	438705	A1048624	Hs.283390	ESTs, Weakly similar to 2108260A B cell	3.6
	443960	A1093577	Hs.255416	hypothetical protein FLJ21986	3.5
	412513	AA322599	Hs.5163	ESTs, Weakly similar to AF151840 1 CGI-8	3.5

5	428695	AJ355647	Hs.189999	purinergic receptor (family A group 5)	3.5
	419517	AF052107	Hs.90797	Homo sapiens clone 23620 mRNA sequence	3.5
	446494	AA463276	Hs.288906	VW Domain-Containing Gene	3.6
	417515	L24203	Hs.82237	ataxia-telangiectasia group D-associated	3.5
	433891	AA613792		gbmo97h03.s1 NC1_CGAP_Py2 Homo sapiens	3.5
10	427315	AA179949	Hs.175563	Homo sapiens mRNA; cDNA DKFZp564N0763 (f	3.5
	445525	BE149866	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.5
	434672	AW294020	Hs.117721	ESTs	3.5
	453288	AW583292	Hs.274412	similar to yeast Upf3, variant A	3.5
	434970	AW272262	Hs.225767	ESTs	3.5
15	417183	AI922189	Hs.288390	hypothetical protein FLJ22795	3.5
	437617	AI026701	Hs.5716	KIAA0310 gene product	3.5
	445943	AW688533	Hs.181574	ESTs	3.5
	412628	AI972402	Hs.306061	hypothetical protein MGC2648	3.5
	452167	N75238	Hs.13075	Homo sapiens cDNA: FLJ23013 fis, clone L	3.5
20	410467	AF102546	Hs.63931	dachshund (Drosophila) homolog	3.5
	440193	AW902312	Hs.7037	Homo sapiens clone 24923 mRNA sequence	3.5
	451816	AW974911	Hs.184793	Homo sapiens cDNA: FLJ21880 fis, clone H	3.5
	429170	NM_001394	Hs.2359	dual specificity phosphatase 4	3.5
	410082	AA081594	Hs.158311	Musashi (Drosophila) homolog 1	3.5
25	436087	BE300296	Hs.5054	CG1-133 protein	3.5
	437898	W81260	Hs.43410	ESTs	3.5
	451131	AI267586	Hs.268012	fatty acid-Coenzyme A ligase, long-chain	3.5
	439609	AW971945	Hs.293236	ESTs	3.5
	443555	N71710	Hs.21398	ESTs, Moderately similar to A Chain A, H	3.5
30	418610	AW245993	Hs.223394	hypothetical protein MGC2742	3.5
	409960	BE261944		hexokinase 1	3.5
	425263	NM_001197	Hs.155419	BCL2-interacting killer (apoptosis-induc	3.5
	404210			NM_005936:Homo sapiens myeloid/lymphoid	3.5
	442323	AW018669	Hs.29190	ESTs	3.5
35	452707	AI093823	Hs.45070	ESTs	3.5
	421437	AW821252	Hs.104336	hypothetical protein	3.5
	426514	BE816633	Hs.170195	bone morphogenetic protein 7 (osteogenic	3.4
	450628	AW382884	Hs.204715	ESTs	3.4
	446825	BE266822	Hs.344097	filamin A, alpha (actin-binding protein-	3.4
40	421867	AA481078	Hs.109045	hypothetical protein FLJ10498	3.4
	434954	AF181455	Hs.284295	Homo sapiens HSPC337 mRNA, partial cds	3.4
	452908	AB001451	Hs.30955	neuronal Shc adaptor homolog	3.4
	429922	Z97630	Hs.226117	H1 histone family, member 0	3.4
	448734	BE614070	Hs.326416	Homo sapiens mRNA; cDNA DKFZp564H1916 (f	3.4
45	434293	NM_004445	Hs.3796	EphB6	3.4
	414222	AL135173		sorbitol dehydrogenase	3.4
	421674	T10707	Hs.296355	hypothetical protein FLJ23138	3.4
	438279	AA805168	Hs.154762	HIV-1 rev binding protein 2	3.4
	411078	AI222020	Hs.182364	CocoonCrisp	3.4
50	419749	X73608	Hs.93029	sparsiboneocitin, cwcw and kazal-like d	3.4
	432302	AA345857	Hs.274307	KIAA1442 protein	3.4
	407944	R34008	Hs.239727	desmocollin 2	3.4
	431674	AA088901	Hs.301642	G-protein coupled receptor	3.4
	408291	AB023191	Hs.44131	KIAA0974 protein	3.4
55	431578	AB037759	Hs.261587	GCN2 epsilon kinase	3.4
	440789	AB007857	Hs.7416	KIAA0397 gene product	3.4
	434958	T99949	Hs.303428	Homo sapiens cDNA FLJ14632 fis, clone OV	3.4
	452295	BE378935	Hs.28866	programmed cell death 10	3.4
	417229	AA975096	Hs.19522	hypothetical protein PRO2849	3.4
60	439593	BE073597	Hs.124083	ESTs	3.4
	407136	T64896	Hs.287420	Homo sapiens cDNA FLJ11533 fis, clone HE	3.4
	421044	AF061871	Hs.101302	Human DNA sequence from clone RP1-238D15	3.4
	427461	AA531527	Hs.332040	hypothetical protein MGC13010	3.3
	417315	AI080042	Hs.180450	ribosomal protein S24	3.3
65	423392	AA195037	Hs.169341	HTPAP protein	3.3
	412662	AI801777		ESTs	3.3
	415172	AF079529	Hs.78106	phosphodiesterase 8B	3.3
	418372	AA311833	Hs.84318	replication protein A1 (70kD)	3.3
	447958	AW796524	Hs.88644	Homo sapiens microsomal signal peptidase	3.3
70	426010	T18837	Hs.4241	ESTs	3.3
	420460	AA262331	Hs.48376	Homo sapiens clone HB-2 mRNA sequence	3.3
	443181	AI039201	Hs.283316	ESTs	3.3
	442064	AI422867	Hs.88594	ESTs	3.3
	431663	NM_018569	Hs.267182	TBX3-iso protein	3.3
75	412926	AI879076	Hs.75081	macrophage myristoylated alanine-rich C	3.3
	420818	AW969635	Hs.33032	ESTs, Weakly similar to 1207289A reverse	3.3
	408829	NM_006042	Hs.48384	heparan sulfate (glucosamine) 3-O-sulfat	3.3
	408681	AW963853	Hs.282833	ESTs, Weakly similar to 138022 hypotheti	3.3
	436278	BE396290	Hs.5097	synaptogyrin 2	3.3
80	424560	AA158727	Hs.150555	protein predicted by clone 23733	3.3
	417215	BE253181	Hs.81687	non-metastatic cells 3, protein expresse	3.3
	418188	AI754418		Cdc42 effector protein 3	3.3
	434629	AA769081	Hs.4029	glioma-amplified sequence-41	3.2
	427398	AW380020	Hs.20416	chromosome 21 open reading frame 11	3.2
	457489	AI693815	Hs.127179	cryptic gene	3.2
	434747	AA837085		ESTs	3.2
	413125	BE244589	Hs.75207	glyoxalase 1	3.2

5	435561	AA351978	Hs.4943	hepatocellular carcinoma associated prot	3.2
	447210	AF035289	Hs.17752	phosphatidylserine-specific phospholipase	3.2
	422522	A023428	Hs.34549	ESTs, Highly similar to S84541 1 clone 4	3.2
	423396	A1382555	Hs.127950	bromodomain-containing 1	3.2
	401785			NM_002275: Homo sapiens keratin 15 (KRT1	3.2
	441345	AW068579	Hs.2780	Homo sapiens mRNA; cDNA DKFZp564A072 (fr	3.2
	451404	AA480775	Hs.6295	ESTs, Weakly similar to T17248 hypothe	3.2
	422173	BE385828	Hs.250619	phorboln-like protein MDS019	3.2
10	452099	BE612992	Hs.27931	hypothetical protein FLJ10607 similar to	3.2
	452826	BE245286	Hs.301636	peroxisomal biogenesis factor 6	3.2
	419829	A924228	Hs.115185	ESTs, Moderately similar to PC4259 ferri	3.2
	407688	W25317	Hs.37616	Human D9 splice variant B mRNA, complete	3.2
	406214			NM_016371: Homo sapiens hydroxysteroid (1	3.2
15	416292	AA179233	Hs.42380	nasopharyngeal carcinoma susceptibility	3.2
	438714	AA814859	Hs.160074	ESTs	3.2
	433213	AW685130	Hs.137190	ESTs	3.2
	412170	D16532	Hs.73729	very low density lipoprotein receptor	3.2
	409340	BE174629	Hs.321130	hypothetical protein M3C2771	3.2
20	413142	M81740	Hs.75212	ornithine decarboxylase 1	3.2
	451338	AW612322	Hs.19131	transcription factor Dp-2 (E2F dimerizat	3.2
	437179	AA393508		serologically defined colon cancer anti	3.2
	418700	A1653808	Hs.86970	ESTs, Moderately similar to ALUS_HUMAN A	3.2
	438361	AA805566	Hs.146217	Homo sapiens cDNA: FLJ23077 fs, clone L	3.2
25	450546	AA010200	Hs.175551	ESTs	3.2
	409995	AW960597	Hs.129206	ESTs	3.2
	408739	W01555	Hs.44685	ESTs, Moderately similar to I38022 hypot	3.2
	438821	AA826425	Hs.192375	ESTs	3.2
	403532			NM_024638: Homo sapiens hypothetical prot	3.2
30	452941	AL110347	Hs.31074	N-sulfoglucosamine sulfohydrolase (sulfa	3.1
	414341	D80004	Hs.75809	KIAA0182 protein	3.1
	423044	AA320829	Hs.97266	protocadherin 18	3.1
	429716	R25885	Hs.211933	collagen, type XIII, alpha 1	3.1
	444367	H54892	Hs.10974	hypothetical protein FLJ22390	3.1
	423551	AA327598	Hs.89633	ESTs	3.1
35	453186	AK001708	Hs.32271	hypothetical protein FLJ10846	3.1
	413560	W03011	Hs.305881	MSTP043 protein	3.1
	431933	A1187057	Hs.132554	ESTs	3.1
	439778	AL109729	Hs.99384	putative transmembrane protein	3.1
40	446044	AA58682		gbcl13e01.x1 NCL CGAP_Lu24 Homo sapiens	3.1
	422017	NM_003877	Hs.110776	STAT induced STAT inhibitor-2	3.1
	421254	AK001724	Hs.102950	coat protein gamma-coop	3.1
	442339	BE257148		endoglycan	3.1
	445109	AF039916	Hs.12330	ecolnucleoside triphosphate diphosphohyd	3.1
45	425320	U29344	Hs.83190	fatty acid synthase	3.1
	426170	BE181085	Hs.167531	methylcrotonyl-Coenzyme A carboxylase 2	3.1
	408770	AW270608	Hs.170195	bone morphogenetic protein 7 (osteogenic	3.1
	442202	BE272862	Hs.108534	hypothetical protein FLJ22625	3.1
	417622	AW298183	Hs.82318	WAS protein family, member 3	3.1
50	438664	AJ720078	Hs.291997	ESTs, Weakly similar to A47582 B-cell gr	3.1
	433038	AA574091	Hs.105854	ESTs	3.1
	447050	NM_016314	Hs.17200	STAM-like protein containing SH3 and ITA	3.1
	436299	AK000767	Hs.5111	hypothetical protein FLJ20729	3.1
	408380	AF123050	Hs.44532	diubiquitin	3.1
55	407910	AA650274	Hs.41296	fibronectin leucine rich transmembrane p	3.1
	445098	AL050272	Hs.12305	DKFZP566B183 protein	3.1
	431797	BE169641	Hs.270134	hypothetical protein FLJ20280	3.1
	437295	AA350994	Hs.20281	KIAA1700	3.1
	452827	AJ122843	Hs.184319	ESTs, Weakly similar to KIAA1006 protein	3.1
60	448913	AA194422	Hs.22564	myosin VI	3.1
	415079	R43179	Hs.22895	hypothetical protein FLJ23548	3.0
	408157	AA047685	Hs.62946	ESTs	3.0
	443337	Y07604	Hs.9235	non-metastatic cells 4, protein expresse	3.0
	410310	J02931	Hs.62192	coagulation factor III (thromboplastin,	3.0
65	437546	AW074836	Hs.173984	T-box 1	3.0
	451134	AA318315	Hs.25999	hypothetical protein FLJ22195	3.0
	423932	T95633	Hs.189703	ESTs	3.0
	433495	AW373784	Hs.71	alpha-2-glycoprotein 1, zinc	3.0
	453293	AA382267	Hs.10653	ESTs	3.0
70	428171	AA489323	Hs.182825	ribosomal protein L35	3.0
	428293	BE250944	Hs.183558	solute carrier family 1 (neutral amino a	3.0
	428657	NM_015865	Hs.171731	solute carrier family 14 (urea transport	3.0
	406627	T64904	Hs.163780	ESTs	3.0
	418259	AA215404		ESTs	3.0
75	426110	NM_002913	Hs.168563	replication factor C (activator 1) 1 (14	3.0
	411089	AA458454		cell division cycle 2-like 1 (PITSLRE pr	3.0
	431416	AA532718		ESTs	3.0
	431631	AA548908	Hs.122244	ESTs	3.0
	409251	R10723	Hs.20573	ESTs	3.0
80	434974	AA778711		eukaryotic translation initiation factor	3.0
	447147	AA910353	Hs.75432	ESTs, Weakly similar to T23482 hypothe	3.0
	450937	R49131	Hs.26267	ATP-dependant Interferon response protei	3.0
	432728	NM_006979	Hs.278721	HLA class II region expressed gene KE4	3.0
	433037	NM_014158	Hs.279938	HSPC057 protein	3.0

5	411598	BE336654	Hs.70937	H3 histone family, member A	3.0
	430268	AK000737	Hs.237480	hypothetical protein FLJ20730	3.0
	443725	AW245680	Hs.9701	growth arrest and DNA-damage-inducible,	3.0
	431155	AW971213		gb:EST383301 MAGE resequences, MAGL Homo	3.0
	407355	AA846203	Hs.193974	ESTs, Weakly similar to ALU1_HUMAN ALU 6	3.0
10	438209	AL120559	Hs.6111	aryl-hydrocarbon receptor nuclear trans	3.0
	434392	AW963709	Hs.250824	Homo sapiens cDNA: FLJ23436 fis, clone H	3.0
	432810	AA863400	Hs.23054	ESTs	3.0
	430333	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	3.0
	445686	R89543	Hs.12942	vesicle trafficking protein	3.0
15	406670	W79632	Hs.256301	hypothetical protein MGC13170	3.0
	452779	AA418775	Hs.47234	ESTs	3.0
	439880	AW245741	Hs.58461	ESTs, Weakly similar to A35659 knueppel-	3.0
	408298	AI745325	Hs.271923	Homo sapiens cDNA: FLJ27785 fis, clone K	3.0
	424395	AA165082	Hs.146388	microtubule-associated protein 7	2.9
20	423472	AF041260	Hs.129057	breast carcinoma amplified sequence 1	2.9
	425920	AL049977	Hs.162209	claudin 8	2.9
	409827	T69981		gb:yc19d03.r1 Stratagene lung (937210) H	2.9
	447681	BE620886		GCM1 (general control of amino-acid synt	2.9
	439584	AA838114	Hs.221612	ESTs	2.9
25	417601	NM_014735	Hs.82292	KIAA0215 gene product	2.9
	452268	NM_003512	Hs.28777	H2A histone family, member L	2.9
	422576	BE548555	Hs.118554	CGI-83 protein	2.9
	438510	AL080220	Hs.6285	DKFZP586P0123 protein	2.9
	423217	NM_000094	Hs.1640	collagen, type VII, alpha 1 (epidermolys	2.9
30	427581	NM_014788	Hs.179703	KIAA0129 gene product	2.9
	447953	AI452973	Hs.165900	ESTs, Weakly similar to ALU1_HUMAN ALU 5	2.9
	443015	R33261	Hs.6614	ESTs, Weakly similar to A43632 mucin 2 p	2.9
	429351	AK001490	Hs.200016	hypothetical protein FLJ10628	2.9
	425294	AF033827	Hs.155553	HNK-1 sulfotransferase	2.9
35	452955	AW390282	Hs.31130	transmembrane 7 superfamily member 2	2.9
	416439	AA180363	Hs.118769	ESTs	2.9
	442315	AA173992	Hs.7956	ESTs, Moderately similar to ZN91_HUMAN Z	2.9
	446911	N27605	Hs.16492	DKFZP584G2022 protein	2.9
	428801	AW277121	Hs.254881	ESTs	2.9
40	430482	AI584156	Hs.105640	Homo sapiens, clone IMAGE:4139775, mRNA,	2.9
	420552	AK000492	Hs.98906	hypothetical protein	2.9
	428180	AI129767	Hs.182874	guanine nucleotide binding protein (G pr	2.9
	418222	AI675881	Hs.86538	ESTs	2.9
	433009	AA761668		gb:z24c08.s1 NCL_CGAP_GCB1 Homo sapiens	2.9
45	432140	AK000404	Hs.272888	hypothetical protein FLJ20397	2.9
	434517	AA635690	Hs.337251	hypothetical protein MGC2487	2.9
	448718	AA220235	Hs.153959	hypothetical protein MGC15436	2.9
	408196	AL034548	Hs.43627	SRY (sex determining region Y)-box 22	2.9
	419849	BE041436	Hs.93379	eukaryotic translation initiation factor	2.9
50	452258	AK000933	Hs.28661	Homo sapiens cDNA FLJ10071 fis, clone HE	2.9
	430375	AW371049	Hs.93758	H4 histone family, member H	2.9
	409660	T08490	Hs.288969	HSCARG protein	2.9
	413588	AA971014	Hs.75432	IMP (inosine monophosphate) dehydrogenas	2.9
	412719	AW016610		ESTs	2.9
55	438552	AJ245820	Hs.6314	type I transmembrane receptor (seizure-r	2.9
	439621	AI200281	Hs.123910	ESTs, Highly similar to B34087 hypotheti	2.9
	437050	AA768420		ESTs	2.9
	414256	AW410035	Hs.75862	MAD (mothers against decapentaplegic, Dr	2.9
	429343	AK000765	Hs.199480	Homo sapiens, Similar to epsin 3, clone	2.9
60	416841	BE000150	Hs.48778	ribon protein	2.9
	421594	R45689	Hs.21889	Homo sapiens cDNA FLJ12978 fis, clone NT	2.9
	438213	AA325512	Hs.71472	hypothetical protein FLJ10774; KIAA1709	2.9
	435823	AW749885		ESTs, Weakly similar to I38022 hypotheti	2.8
	441266	H15868	Hs.293845	Homo sapiens, clone IMAGE:3502329, mRNA,	2.8
65	428761	AI015709	Hs.172089	Homo sapiens mRNA; cDNA DKFZp586i2022 (f	2.8
	413748	AA133243	Hs.171553	ESTs, Moderately similar to CLC3_HUMAN C	2.8
	457733	AW974812		ESTs	2.8
	400860			Target Exon	2.8
	438185	AI373544	Hs.331328	intermediate filament protein syncoilin	2.8
70	433312	AI241331	Hs.131765	ESTs, Moderately similar to I38937 DNAR	2.8
	431604	AF176265	Hs.264190	vacuolar protein sorting 35 (yeast homol	2.8
	421717	AF230924	Hs.107187	divalent cation tolerant protein CUTA	2.8
	453912	AL121031		SWI/SNF related, matrix associated, acti	2.8
	436703	AW630133	Hs.83313	GK003 protein	2.8
75	431108	AA991508	Hs.105317	ESTs	2.8
	451040	AA324743	Hs.40808	ESTs	2.8
	443837	AI984625	Hs.9884	spindle pole body protein	2.8
	418196	AJ745649	Hs.26548	KIAA1708 protein	2.8
	450447	AF212223	Hs.25010	hypothetical protein P15-2	2.8
80	409330	AK001231	Hs.53940	hypothetical protein FLJ10369	2.8
	413762	AW411479	Hs.848	FK506-binding protein 4 (59kD)	2.8
	433586	T85301	Hs.194397	gb:yd78d06.s1 Soares fetal liver spleen	2.8
	424720	M89907	Hs.152292	SWI/SNF related, matrix associated, acti	2.8
	422027	AL043100	Hs.306319	fatty acid amide hydrolase	2.8
	422717	AJ557623	Hs.119475	acid inducible RNA-binding protein	2.8
	412843	AF007655	Hs.74624	protein tyrosine phosphatase, receptor t	2.8
	434237	AF119908	Hs.235518	hypothetical protein PRO2955	2.8

	407255	AA012992	Hs.256301	hypothetical protein MGC13170	2.8
	431472	AK001023	Hs.255549	nucleotide binding protein 2 (E.coli Min	2.8
	423318	AW467064	Hs.5740	ESTs	2.8
5	454144	BE280478	Hs.182695	hypothetical protein MGC3243	2.8
	452827	AI571635	Hs.55468	ESTs	2.8
	452040	AW973242	Hs.293690	ESTs, Weakly similar to I38022 hypotheti	2.8
	418830	BE513731	Hs.88959	hypothetical protein MGC4616	2.8
	417517	AF001175	Hs.82238	POP4 (processing of precursor, S. cerev	2.8
10	419286	AA236005	Hs.128764	ESTs	2.8
	430287	AW182459	Hs.125759	ESTs, Weakly similar to LEU5_HUMAN LEUKE	2.8
	420911	U77413	Hs.100293	O-linked N-acetylglucosamine (GlcNAc) tr	2.8
	428054	AI948688	Hs.266519	ESTs	2.8
	409504	AA304961	Hs.699	peptidylprolyl isomerase B (cyclophilin	2.8
15	440080	AW051597		ESTs	2.8
	431609	AW792792	Hs.264330	N-acylsphingosine amidohydrolase (acid c	2.8
	447896	AA36124	Hs.294069	Homo sapiens cDNA FLJ13384 fis, clone PL	2.8
	431525	AA506656	Hs.6185	KIAA1557 protein	2.8
	442995	AA532511	Hs.288455	Homo sapiens cDNA: FLJ23270 fis, clone C	2.8
20	433101	AW572317	Hs.12082	Homo sapiens mRNA; cDNA DKFZp566L203 (tr	2.8
	449052	AW029507	Hs.161102	ESTs	2.8
	418663	AK001100	Hs.41690	desmocollin 3	2.8
	442013	AA506476	Hs.10500	Human DNA sequence from clone RP11-353C1	2.8
	449051	AW961400	Hs.333526	HER2 receptor tyrosine kinase (c-erb-b2,	2.8
25	453038	AW292415	Hs.20509	HBV pX associated protein-8	2.8
	419175	AW270037		KIAA0779 protein	2.8
	426788	U66816	Hs.172280	SWI/SNF related, matrix associated, acti	2.8
	421091	W22821		ribosomal protein L26	2.8
	413435	X51405	Hs.75380	carboxypeptidase E	2.8
30	432651	AW973744	Hs.293100	ESTs	2.8
	452700	AI859390	Hs.288940	five-span transmembrane protein M83	2.8
	454148	AW732837	Hs.42390	nasopharyngeal carcinoma susceptibility	2.8
	419452	U33635	Hs.80572	PTK7 protein tyrosine kinase 7	2.8
	425491	AA883316	Hs.255221	ESTs	2.8
35	414556	AW975053	Hs.343443	ribosomal protein L36	2.8
	435126	AI393666	Hs.42315	p10-binding protein	2.8
	435602	AF217515	Hs.283532	uncharacterized bone marrow protein BM03	2.7
	441128	AA570256		ESTs, Weakly similar to T23273 hypotheti	2.7
	440340	AW895503	Hs.125276	ESTs	2.7
40	410339	AI916499	Hs.296258	ESTs	2.7
	430542	AI557486	Hs.119122	ribosomal protein L13a	2.7
	406789	AI041403		ribosomal protein L29	2.7
	424130	AI050136	Hs.140945	Homo sapiens mRNA; cDNA DKFZp566L141 (tr	2.7
	449518	BE395253	Hs.30861	ESTs	2.7
45	410099	AA081630		KIAA0036 gene product	2.7
	422000	AG0599	Hs.110637	homeo box A10	2.7
	407110	AA018042	Hs.252085	Prader-Willi/Angelman syndrome-5	2.7
	415443	T07353	Hs.7948	ESTs	2.7
	432745	AI821926		gbn17805.x5 NCL_CGAP_Pr3 Homo sapiens	2.7
50	409299	AA045850	Hs.53125	small nuclear ribonucleoprotein D2 polyp	2.7
	424369	R87622	Hs.26714	KIAA1831 protein	2.7
	417831	H16423	Hs.82685	CD47 antigen (Rb-related antigen, integr	2.7
	424723	BE408113	Hs.152337	protein arginine N-methyltransferase 3 (tr	2.7
	451428	AW083384	Hs.11057	ESTs, Highly similar to T46395 hypotheti	2.7
55	400263			Eos Control	2.7
	436750	AB028012	Hs.4990	KIAA1089 protein	2.7
	443804	AL135352	Hs.255883	ESTs, Weakly similar to I38022 hypotheti	2.7
	421709	AA159394	Hs.107058	CED-5 protein	2.7
	421077	AK000081	Hs.101590	hypothetical protein	2.7
60	416359	AL042210	Hs.16493	hypothetical protein DKFZp762N2316; KIAA	2.7
	442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	2.7
	411605	AW006831		ESTs	2.7
	437133	AB018319	Hs.5460	KIAA0776 protein	2.7
	407236	W79485	Hs.173980	nuclear matrix protein NMP200 related to	2.7
65	432125	AW972667	Hs.183006	Homo sapiens cDNA FLJ12300 fis, clone MA	2.7
	427657	AV652249	Hs.180107	polymerase (DNA directed), beta	2.7
	445636	AW105401		ribosomal protein L29	2.7
	443801	AW208942	Hs.253594	Intron of trichorhinophthalangeal syndro	2.7
	420223	NZ7807		ribosomal protein L4	2.7
70	427515	T79526	Hs.179516	integral type I protein	2.7
	447673	AI823987	Hs.182285	ESTs	2.7
	411980	R77776	Hs.181103	ESTs	2.7
	433212	BE218049	Hs.121820	ESTs	2.7
	448244	BE613418	Hs.336425	Homo sapiens, clone MGC:17296, mRNA, com	2.7
75	441551	AA318224	Hs.298141	ESTs	2.7
	421883	X55079	Hs.1437	glucosidase, alpha; acid (Pompe disease,	2.7
	411552	AL050201	Hs.70769	hypothetical protein DKFZp586E1923	2.7
	434851	AA808184	Hs.116502	ESTs	2.7
	442875	BE623003	Hs.23625	Homo sapiens clone TCOCCTA00142 mRNA sequ	2.7
80	421109	L32832	Hs.101842	AT-binding transcription factor 1	2.7
	432450	AI990739	Hs.158184	ORF	2.7
	426174	AA547959	Hs.115838	ESTs	2.7
	445919	T53519	Hs.334692	hypothetical protein MGC14141	2.7
	423116	AA421973	Hs.169119	ESTs, Weakly similar to T25731 hypotheti	2.7

	431222	X56777	Hs.273790	zona pellucida glycoprotein 3A (sperm ra	2.7
	451558	NM_001089	Hs.28630	ATP-binding cassette, sub-family A (ABC1	2.7
	431615	AW295859	Hs.235860	ESTs	2.7
5	418549	AK06485	Hs.189341	ESTs, Moderately similar to S65657 alpha	2.7
	431122	AI267593	Hs.250535	Homo sapiens mRNA; cDNA DKFZp434N2412 (f	2.7
	438882	AA354489	Hs.222103	EBP50-PDZ Interactor of 64 kD	2.7
	424954	NM_000546	Hs.1846	tumor protein p53 (Li-Fraumeni syndrome)	2.7
	458082	AW878811	Hs.314451	ESTs, Weakly similar to ALU1_HUMAN ALU S	2.7
10	427087	BE073913	Hs.173515	uncharacterized hypothalamus protein HT0	2.7
	412524	AA417813	Hs.44208	hypothetical protein FLJ23153	2.7
	435176	AA744875	Hs.189413	ESTs	2.7
	419390	AI701162	Hs.90207	hypothetical protein MGC11138	2.7
	428013	AF151020	Hs.181444	hypothetical protein	2.7
15	441094	U33819	Hs.7647	MYC-associated zinc finger protein (puri	2.7
	451356	AA748418	Hs.164577	ESTs	2.7
	408481	AB037756	Hs.45207	hypothetical protein KIAA1335	2.7
	418516	NM_005218	Hs.85701	phosphoinositide-3-kinase, catalytic, al	2.7
	423476	AL036633		Human DNA sequence from clone RP6-1046G1	2.7
20	444034	AL161957	Hs.10177	pleckstrin homology domain Interacting p	2.7
	404913			NM_024408*:Homo sapiens Notch (Drosophil	2.7
	407378	AA299284	Hs.57776	ESTs, Moderately similar to I38022 hypot	2.7
	441054	AA913591		ESTs	2.6
	428500	AB15395	Hs.184641	fatty acid desaturase 2	2.6
25	430512	AF182294	Hs.241578	UG snRNA-associated Sm-like protein LSM8	2.6
	433301	AW296280	Hs.152016	Homo sapiens cDNA: FLJ22140 fis, clone H	2.6
	444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypotheti	2.6
	443666	AA58179	Hs.41628	ESTs, Weakly similar to neuronal thread	2.6
	427378	BE515037	Hs.177556	melanoma antigen, family D, 1	2.6
30	439414	NM_001183	Hs.8551	ATPase, H transporting, lysosomal (vacuo	2.6
	421866	M24470	Hs.1435	guanosine monophosphate reductase	2.6
	421605	BE440108	Hs.106127	RNA polymerase I 16 kDa subunit	2.6
	428797	AW936258	Hs.342849	ADP-ribosylation factor-like 5	2.6
	410835	BE067395	Hs.66881	dynein, cytoplasmic, intermediate polype	2.6
35	407887	AA579668	Hs.41072	serine (or cysteine) proteinase inhibitor	2.6
	430341	NM_006348	Hs.239631	golgi transport complex 1 (90 kDa subun)	2.6
	424956	AW198103	Hs.18724	ESTs, Weakly similar to granule cell mar	2.6
	452748	AB011128	Hs.30512	Homo sapiens mRNA for KIAA0558 protein,	2.6
	408212	AA297667	Hs.43728	hypothetical protein	2.6
40	407893	BE408359	Hs.43621	Homo sapiens, Similar to hypothetical pr	2.6
	425976	C75094	Hs.334514	NG22 protein	2.6
	448424	AW008692	Hs.31924	ESTs	2.6
	420184	AW339037	Hs.24508	ESTs	2.6
	443444	AW652619	Hs.17235	Homo sapiens clone TCCCA00176 mRNA sequ	2.6
45	412774	AA120865	Hs.23136	ESTs	2.6
	445922	AI337316	Hs.147998	ESTs	2.6
	428925	NM_000786		cytochrome P450, 51 (lanosterol) 14-alpha	2.6
	419222	AD001528	Hs.89718	spermine synthase	2.6
	417327	NM_004822	Hs.81954	SEC24 (S. cerevisiae) related gene famil	2.6
50	420337	AW295840	Hs.14555	Homo sapiens cDNA: FLJ21513 fis, clone C	2.6
	408743	AL110248	Hs.47367	KIAA1785 protein	2.6
	434011	AW853437	Hs.5486	clone FLB5214	2.6
	434976	AI963821		ESTs	2.6
	417454	NM_000202	Hs.172458	iduronate 2-sulfatase (Hunter syndrome)	2.6
55	448789	BE539108	Hs.22051	hypothetical protein MGC15548	2.6
	441049	W88920	Hs.29341	hypothetical protein FLJ22376	2.6
	437271	AL137445	Hs.28846	Homo sapiens mRNA; cDNA DKFZp566O134 (fr	2.6
	425017	AL119305	Hs.26409	ESTs	2.6
	440333	AI378424	Hs.288761	hypothetical protein FLJ21749	2.6
60	434551	BE387162	Hs.280858	ESTs, Highly similar to A35661 DNA excis	2.6
	413132	NM_006823	Hs.75209	protein kinase (cAMP-dependent, catalyti	2.6
	409619	AK001015	Hs.55220	BCL2-associated athanogene 2	2.6
	444550	BE250716	Hs.87614	ESTs	2.6
	448258	AI283476	Hs.263478	ESTs	2.6
65	440191	AI990417		tubulin, beta 5	2.6
	453187	AI181383	Hs.34549	ESTs, Highly similar to S94541 1 clone 4	2.6
	412133	U83460	Hs.73614	solute carrier family 31 (copper transpo	2.6
	426841	AI052358	Hs.193726	ESTs	2.6
	435937	AA830893	Hs.119769	ESTs	2.6
70	425960	AW410845	Hs.164649	hypothetical protein DKFZp434H247	2.6
	456161	BE264645	Hs.282093	hypothetical protein FLJ21918	2.6
	455236	AF045229	Hs.82280	regulator of G-protein signalling 10	2.6
	435025	T08990	Hs.4742	anchor attachment protein 1 (Gaap1, yeas	2.6
	416751	T48130	Hs.6897	Homo sapiens mRNA; cDNA DKFZp586P1622 (f	2.6
75	458948	AA009716	Hs.42311	ESTs	2.6
	424762	AL119442	Hs.183584	eukaryotic translation initiation factor	2.6
	449458	AB05078	Hs.208261	ESTs	2.6
	432409	AA806538	Hs.130732	KIAA1575 protein	2.6
	425184	BE278288	Hs.155048	Lutheran blood group (Auberger b antigen	2.6
80	442336	AW340958	Hs.7572	ESTs	2.6
	445622	AF106697	Hs.12971	thioredoxin reductase beta	2.6
	440409	AW294316		ESTs	2.6
	444610	AI174783		gb:HA2501 Human fetal liver cDNA library	2.6
	425983	U43604	Hs.159901	Human unidentified mRNA, partial sequenc	2.6

5	436972	AA284679	Hs.25640	claudin 3	2.6
	426809	BE313114	Hs.29706	ESTs	2.6
	431183	NM_006855	Hs.250696	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	2.6
	457638	AI792670	Hs.144405	ESTs	2.6
	442821	BE391929	Hs.8752	transmembrane protein 4	2.5
	435522	N54214	Hs.9774	synovial sarcoma translocation gene on c	2.5
	406764	AA429825	Hs.343443	ribosomal protein L36	2.5
	422032	AA476966	Hs.110857	polymerase (RNA) III (DNA directed) poly	2.5
10	409125	R17268	Hs.343567	axonal transport of synaptic vesicles	2.5
	416801	X98834	Hs.79971	sal (Drosophila)-like 2	2.5
	446091	AW022192		ESTs	2.5
	419848	AA251242	Hs.103238	ESTs	2.5
	415015	NM_002109	Hs.77798	histidyl-tRNA synthetase	2.5
15	431836	AF178532	Hs.271411	beta-site APP-cleaving enzyme 2	2.5
	414987	AA524394	Hs.294022	hypothetical protein FLJ14950	2.5
	447087	AW403870	Hs.301872	hypothetical protein MGC4840	2.5
	458050	R79445	Hs.76230	ribosomal protein S10	2.5
	426178	AA371409	Hs.105664	hypothetical protein FLJ22294	2.5
20	414528	AA148950	Hs.188836	ESTs	2.5
	426494	AL119528	Hs.170098	KIAA0372 gene product	2.5
	407656	AW747986	Hs.37443	Homo sapiens mRNA; cDNA DKFZp434B2119 (f	2.5
	437330	AL353944	Hs.50115	Homo sapiens mRNA; cDNA DKFZp761J1112 (f	2.5
	449139	BE268315	Hs.23111	phenylalanine-tRNA synthetase-like	2.5
25	448153	Y10805	Hs.20521	HMT1 (hnRNP methyltransferase, S. cerevi	2.5
	417386	AL037228	Hs.82043	D123 gene product	2.5
	409420	Z15008	Hs.54451	laminin, gamma 2 (nicotin (100kD), kalni	2.5
	406795	AA688282	Hs.170345	ESTs	2.5
	407627	AI419020	Hs.62820	chromosome 6 open reading frame 1	2.5
30	421535	AB002359	Hs.105478	phosphoribosylformylglycinamide synth	2.5
	415862	R51034	Hs.144513	ESTs	2.5
	426418	M90464	Hs.169825	collagen, type IV, alpha 5 (Alport syndr	2.5
	436557	W15673	Hs.5027	ESTs, Weakly similar to A47582 B-cell gr	2.5
	413517	N76712	Hs.44829	ESTs, Weakly similar to I38022 hypothei	2.5
35	449500	AW556345	Hs.12926	ESTs	2.5
	457090	AL080243	Hs.180920	ribosomal protein S9	2.5
	445389	NM_016631	Hs.12592	period (Drosophila) homolog 3	2.5
	410006	AW732308	Hs.57783	eukaryotic translation initiation factor	2.5
	452906	BE207039	Hs.306123	MAGEF1 protein	2.5
40	450341	N90956	Hs.17230	hypothetical protein FLJ22087	2.5
	418430	AI878942	Hs.90336	ATPase, H transporting, lysosomal (vacuo	2.5
	440099	AL080058	Hs.6909	DKFZP564G202 protein	2.5
	452518	AA280722	Hs.24758	ESTs, Weakly similar to I38022 hypothei	2.5
	431843	AA516420		ESTs, Weakly similar to I38022 hypothei	2.5
45	424795	AW102850	Hs.153177	ribosomal protein S28	2.5
	448019	AW947164	Hs.195641	ESTs, Moderately similar to I38022 hypot	2.5
	450704	H85157	Hs.40686	ESTs	2.5
	400262			Eos Control	2.5
	435266	AK001942	Hs.4863	hypothetical protein DKFZp566A1524	2.5
50	418039	R08859	Hs.193172	ESTs, Weakly similar to I38022 hypothei	2.5
	429491	NM_012111	Hs.204041	chromosome 14 open reading frame 3	2.5
	456844	AI264155	Hs.152981	CDP-diacylglycerol synthase (phosphatida	2.5
	413781	J05272	Hs.850	IMP (inosine monophosphate) dehydrogen	2.5
	437450	AL390154	Hs.26954	Homo sapiens mRNA; cDNA DKFZp762G123 (fr	2.5
55	424005	AB033041	Hs.137507	vang (van gogh, Drosophila)-like 2	2.5
	429332	AF030403	Hs.199263	Sta-20 related kinase	2.5
	438572	BE267017	Hs.6315	acetylserotonin O-methyltransferase-like	2.5
	425692	D90041	Hs.155956	N-acetyltransferase 1 (arylamine N-acety	2.5
	431188	W09856	Hs.169755	ESTs	2.5
60	408803	AF248953	Hs.24049	golgi autoantigen, golgin subfamily a, 2	2.5
	414482	S57498	Hs.76252	endothelin receptor type A	2.5
	437782	T78028	Hs.154579	synaptotagmin I	2.5
	425722	AI559076	Hs.97031	hypothetical protein MGC13047	2.5
	433681	AI004377	Hs.200360	Homo sapiens cDNA FLJ13027 fls, clone NT	2.5
65	451585	AK001171	Hs.326422	hypothetical protein MGC4549	2.5
	424959	NM_005781	Hs.153537	activated p21cdc42Hs kinase	2.5
	407151	H25836	Hs.301527	ESTs, Moderately similar to unknown [Hs	2.5
	446054	AB014537	Hs.13804	KIAA0637 gene product	2.5
	452556	H78517	Hs.33905	ESTs	2.5
70	421026	AL047332	Hs.101057	GCN5 (general control of amino-acid synt	2.5
	407687	AK002011	Hs.37558	hypothetical protein FLJ11149	2.5
	433883	AI817723	Hs.22678	hypothetical protein FLJ21832	2.5

TABLE 68B

75	Pkey:	Unique Eos probeset identifier number		
	CAT number:	Gene cluster number		
	Accession:	Genbank accession numbers		
80	Pkey	CAT Number	Accession	
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	429220	15103_7	AW341473 AA448195 AW207206 AI951341 AA969259	

449625	249224_1	BI918168 AW779780 N48674 AI375997 AA235370 BG699146 AI913631 AI498402 AI016320 AA323193 R49021 D59344 BG986750 N45526 BG986917 T61362 R49391 R45432 AI203107 R35004 F07491 R25094 R35360
412446	63467_1	BC021735 AI669212 AI120184 AI769949 BE701002 BE184363 BE819031 BG702238 BF090049 BF963318 BF961912 BF943013 AA934514 AI151245 BF960659 AA987907 Z14449 BF908059 BF008053 BF908049 BE699424 BF908050 BF962832 BF962020 BF963134 BI035538 BF908052 BF908057 BF090026 BF943158 AI632924 BF512340 BF952021 BF980776 BF943437 BF942847 AI768015 F09778 F04816 F02721
433404	7392_1	AA102645 AI633838 AA817829 BF947001 BI035448 BE335876 AW980837 AW988604 BF957405 BF963433 BG704816 BC022980 BF224081 BG149908 AW672842 BE570687 AI702161 AW341832 BE222503 N71836 AI026061 AW953116 AW083132 AI979261 AV725377 AI423298 AI640707 AW675518 AI032611 AI818044 AI299508 AI911386 AI270418 BE219257 BM141626 AA26491 Z25159 AA587421 N59447 Z39435 T32982 R54110 BF115783 F09044 BF808433
453160	6028_5	BC009512 NM_003526 BI587616 AV781592 AV780377 AI601008 BI604131 BE645918 BG187760 BG181525 BG210634 BG192999 AI263307 AA344186 AW952966 AA033609 AA037562 AA722183 R79452 H70775 BF674991 BE769437 BG007856 AA037483 AW572535 AI143391 AA084581 AA033610 AV742510 AV735788 R08336
420218	191547_1	AW958037 R42557 AI337047 AA948360 AI638005 AA459950 AI624915 AI638047 AI467856 AI521826 AA860305 AI932315 AW003082 AW271756 AW779380 AA609879 AI634791 AI493770 AI565211 Z41145 AI627952 AA303734 BE349457 AW156765 AA256527 BE089727
437124	59408_1	AL050013 BG939500 AW969191 AA769925 AI377973 AI625545 AA811385 AA521114 N24705 AI379579 AA424699 AI684671 AA829715 AI453010 N35401 AA877452 AA504340 AI209149 AA883574 AI379052 AI084455 AI280147 AA644327 BF432508 B27873 N47364 N34880 AI147024 T86860 AI219716 AA960626 H25544 BI857123 AW960469 AA599099 AA765246 AA328537 BG434703 AA890373 AA424765 AI292318 AA829888 N95742 AI218758 H25588 N36282 AA024987 N36687 BI919187 N49471 AA889970 AW166152 AA468546 AI262504 AI452782 AA554458 AA807080
438869	52134_1	AA724542 AW102730 AA909978 AW118134 AW827241 W56431 BM127381 BF436987 AI016509 AW863972 BM127686 C15552 N63435 N51744 T98800 N56980 BG108638 N49381 R49888 D81276 BI756612 AA508234 R49885 BF850422
428342	6712_1	AF075009 R63109 R63068 AK056315 AI015524 AA724079 BI713619 AI377728 AW293682 AI28140 AI092404 AI085630 AA731340 BM469629 AW968804 AA425658 AA769094 BF446026 AW118719 AI332765 AW500888 AW576556 AI859571 AW499664 AW614573 AW829495 AW505314 W74704 AI356361
450203	19008_1	AI923640 AW070509 AI521500 AI042095 AA608309 AA781319 AI381489 H45700 AA761333 AW265424 AA908524 AA835311 AA649040 AI392620 Z40703 AI985564 AW263513 AA913892 AI693486 AW263502 AI806164 AW291137 BI081872 BI059498 AA134476 AW084688 AA036967 AW370823 T65263 BI002756 AA489664 BF827261 W74741 BF963166
432586	6633_1	AK065952 BG182168 BG220105 BG181569 BG188954 BG187388 BG220104 BG183714 BE645998 AI819354 AW974068 AI393635 AI580846 AI024788 AW020098 BI491127 AI393644 N74993 AW472959 BM478854 BI597437 H12165 BI458612 BE543192
450377	12109_1	BC022881 AU150944 BG750783 AW754175 AW857737 AI911659 AI050036 AA554063 AI826259 AA568548 AB033091 AL520743 BE811813 N53332 N99716 AI561910 AA280656 BE710392 AV705100 AW253978 AW444556 AA281459 AI679751 AI873695 BG700891 BI553517 R80518 BG779771 BG534451 AA794042 AW961580 BF051430 AI857643 AI768486 AW512118 AA479302 AW770384
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424036	6226_1	AE699181 N73808 H08164 AK000028 AA494483 AI288674 AA720773 AV761529 AI684670 AI938202 AW294235 D61652 BF881184 AV711384 N27154 AI926970 AV734970 N40094 N28596 AA884747 AA512890 BG436593
407819	7392_2	NM_033445 BC001193 AI885781 BF794032 AA476520 AA810906 AA810905 AI291244 AI885097 AI369708 AI335629 H97396 AI344688 AA300377 AA457666 AW771833 BE485621 AI364068 AI364452 AI648505 AI918342 AI928670 AA865580 AL531029 AA866344 AI186419 BG329096
409151	4123_1	BM045465 AL531028 BG437151 BE868021 AA175427 AK056628 AI800898 BF939022 BE844718 AI954754 BE218177 BE348557 AI852405 AW293122 AI988798 AI457321 BE327228 BG913531 AW939055 T30280 R54166 Z43388 BG919153 BF003119 BE546274 BF940881 R18246 R42185
422890	61426_1	NM_004892 AF047442 BE275338 BF724863 BI917208 BE276993 AL602308 AA306106 BM152505 BC001394 AW993471 AW993481 AW993283 AW992919 AW992921 AW992980 AW992981 AW993220 BG573124 AA456385 AA234796 AI902728 AA354813 BI092644 BG778400 BI260001 BG007325 AI267455 AA426574 AI160782 AI472186 AA255500 AA434006 BG435520 AI356111 H00525 AV749060 BG944497 BG292031
451752	10408_5	AA902163 C04925 AA902160 AA383100 AW073533 AA256708 AA150809 R65766 AW958448 BE090972 BF693795 AV738979 R65855 R60136 AA484677
432363	1234917_1	AK057805 AW162343 AI190479 AI083318 BE048820 AI196397 AA654667 BE219303 Z39851 F02655 Z28734 T16575 F10145 Z45266 AW572911 AW964438 AW004030 AI632656 BE602530 BI792363 BF058928 AA449241 AI651825 AA805324 AI264883 AW196918 AA948257 AI953735
417379	1610005_1	AI263703 BF056387 AW594171 AI867447 AA319159 AI903440 AW956110 AI366013 AI867923 BG911906 D81142 C15616 AL536697 Z25032 Z43784 R13382 AV745924 AA449398 AA318816 BF9364265 H17038 H10084 F04161 T87230 R40898 AW204071 BI819428 AA683393 AA683376
414922	1563_2	Z43192 T4078 T05103 F12527 T77951 H10118 H17037 BF855407 R19603 AB032987 AI141678 AW978722 BE467119 AI761408 BF727385 AW237035 AI934521 BF436248 AI479668 Z40632 AA832081 AW295801 BF057835 BE465977 AI621269 BE465983 BF766369 N74056 AI817895 AA716587 AI934774 H82600 H09497 BF943762 BE395335 BE883333
419733	7612_3	AW970240 AA534488 AW970323 AA196390 AA507837 AA196468 BG107484 AA632009 AA32670 AI656650 AI650884 AI521919 AI264653 AW150793 AW611894 AI917098 BI031245 AI651454 BF434889 AI580286
432675	1237917_1	AI880735 BE301995 AI392959 AW613965 BM023628 AW515374 AI480102 BM023318 BE328188 AI952820 AI81383 AA557165 AI695677 AI562079 AI700926 AI700561 BF063058 AW196367 AU132984 BI054046 AI970157 R02122 H55924 AI521721 AA808206 AA725223 AI766003
410297	2990_1	AW339821 AA805951 AI287969 AW664827 AK027321 W83676 W83789 BE046412 BF114614 BE846183 BM126230 AW044233 AI951970 AW663548 AI139947 AA514302 AA846232 BM126251 AA789002 AA581966 AA809643 AW198870 BE706664 BE709539 BE153177 BF084925 AL133779 AW951788 AA658683 AA347970
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448553	16112_4	AW340368 AA826758 AW118737 BF513970 AA707807 BF436296 AI339463 AI373842 AI433809 BE222392 AA602308 AA428261 AI460365 AW682760 AI888087 AI342098 AA722418 W78151 N64382 BE221848 AW025901 AA452120 AI160479 AI018168 AA779515 AA661791 BM474307
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		AJ349364 AI051008 AA926941 AA350894 AW071451 N22249 AI784138 AA083847 N22258 AW440825 AA651570 AA376687 AA669125 AI356239 R70463 AI383588 AA827189 BI494872 AW021094 BI494871 AA905500 AA460823 BI482041 AW028965 A626411 BG271780 AI497723 H88862
		D58858 N89979 AA658425 N81154 D62341 AI274437 N66597 H96993 AI370863 AA728850 H05322 R59379 H12223 AI935759 AI362553 D6006 N29572 AI916833 N75273 AI148710 BI597117 BG740471 AA332671 AA333874 AA643052 AW020175 R70550 BG623469 AA452342 AW965441
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		AA602964 AA809200 AF119847 AA437261 AA436987 AI132965
		BE666763 AA659765 AI961658 AI520918 AA761743 AA261477 N66431 BE463652 AA281329 AW272944 AA058687 BM145087 AA045516
		AW341820 AA112515 AA258786 AI886539 AA714133 AA768245 AA035533 AK530459 T20165 AW971268 BE965269 AA522722
		AW974271 AA592975 AA447312 AA884766

426991	29771_1	AK001536 AK055135 BM474813 BE887303 AK022914 AW581996 AW812945 BE882302 AA134266 B1043873 AA019433 B1862088 BM468657 AU128438 BE384458 AL353967 B1857117 BF686526 B1465223 BM460132 AU129877 B1222283 BG171592 B1043544 BG495296 BG760710 B1255542 BG108620 AU150719 AW510354 A1554256 AL353988 AA191092 BF132636
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418166	18858_1	AK055915 BE867252 A1523348 AA765350 BF448858 Z43675 R19529 A1133837 BG989444 AW382942 BE702956 AA081961 BE835247 BE835308 BE835295 AA376302 BE845790 AA375590 AA376692 AW954423 N85732 AA249770 A1754416 A1213816 BF692044 AA811729 AW514842 A1933486 A1096810 AW183016 A1635738 N27524 BE645916 A1247842 AW991230 A1754277 H16814 A1766892 BF108422 A1003031 T95129 F11313 R97948 R93889 AA375242 BF109388 A1860939 A1680060 AW953899 BF971485 A1872337 AW953841 AA372437 A1216746 H11384 R38484 AA249043 AA249732
434747	117643_1	AW976537 A1033582 AA837085 AA745261 AA648385
437179	12239_1	AK055109 BC019085 AA187684 BG966226 BM023227 A1532311 AW264381 AA398371 BM021483 A1432433 A1375777 A1129580 AW262782 AA134107 BM023515 AA977504 A1858222 A1348454 R69725 AA957268 BM021207 A1080074 A1129218 AW207842 N90581 AA771919 A1092259 AA028416 A1074114 BG665636 BE601677 AW193419 AA917040 W90430 A1342884 A1378957 A1036486 AW020068 B1491093 BF476021 R41226 R69631 F04125 C02343 AA115589 R58480 A1400988 R54288 R31422
448044	1111791_1	AW867082 A1458682 H24240 R18426 R14537
424339	50569_1	NM_016720 AF219137 AL534420 AL524055 A1537346 AL538442 BG765888 AL530054 AL625377 BG474596 BG473144 BE251553 BG706089 AL538039 BG703131 BE255806 BF806256 F12128 AL566773 B1828686 BF761480 A1204971 BG818818 B1199246 AL534816 BF529941 AA324163 AL523285 BG914330 H07952 AL534815 BE769903 A1867802 BM310135 AL533702 BE254484 BF528852 BE867462 BE740130 AL134164 AL567115 AL533701 AL524054 AL515804 AL523284 A1568203 AL534419 BF981182 BE257148 AL561833
418259	133853_1	BM310925 AA426110 BM310629 BF434286 AW015091 BF475996 AW118867 BE675186 A1698568 A1435394 AW590689 A1652425 A1827969 BF089946 A1802866 A1393380 A1476224 AW590639 AW138271 A458252 A1524726 AA843768 AA782158 A1336058 A1097532 AW451563 AA459408 AA455633 AA418444 W23607 BG940150 A1493445 AW054728 A1221929 A1868744 AA215405 AA766713 AA621546 BF928317 BE464132 A1890909 AW271459 A1262061 AA215404 N74332 BG940151 BG952281 AA972115 W96315 AA689686 R69057 BF766886 BE769254 W05240
411089	6597_6	B1009308 B1009893 BF922023 BF922909 BF922913 BF922086 BF857733 BE701791 AA456454 AA579876 BF933710 AA091294 B1007291 AW930577 AW975593 AA713730 AW836781 AA666384 AA551106 BF594608 A1082382 A1955808 A1879895 A1679396 BF435555 AA586369 AA551351 AA595822 AA565188 BF808855 AA584921 N86077 AA601031 AA633186 AA514764 AA464562 AA551297 AA936109 B1009389 AW897806 BE815442 BF739374 B1008310 BF825422 BF933709 BF922034 BF925465 B1009680
431418	120918_1	AW669161 AA532718 AA504784 A1791194 A1821930 A1821485 F37127 AA654200 F27974
434974	77302_1	AL079283 BF792538 AA744861 A1871888 A178580 A1720775 A1880937 A1808966 BE483436 BF725510 AW675767 BF689111 BE855951 AW187232 AW272173 A1480335 BF589044 AA443540 A1420128 A1056029 A1650756 AW274589 AW183510 A1440196 A1271801 AW080345 AW189506 AW080293 AA894731 AA579802 A1968845 A1620822 A1222117 AA677146 A1346236 B1792788 AA46615 A1183488 AA897113 AW271851 AW241299 W90134 AA82921 A1049496 AA492010 A1464639 AA983603 A1696293 A1890036 B1254992 AA453513 AA476859 AW673442 AL557763 AA868312 H28885 AA778711 AA081839 A1989340 A1557762 N99654 Z28545 N28874 AA442388 AW887818 AW663158 BG252539 BG501262 BG714174 BG499052 AA058524 BE861198 C75278 R59648 A1829311 AA037656 AW026747 N64518 AW103253 BF529731 AW241677 AW194865 AA917531 R96578 H94036 AA856685 T10342 AW439112 A1090044 AA661591 N71704 A1474828 AU152235 D53426 N21634 R59590 R51072 R96601 H06171 AA084440 H84172 AW118714 C04928 W90082 AA039267 AA136445 R52391 T68024 BG778916
431156	1235742_1	AA428153 N41394 AA283839 R06600 H94122 BF743684 AA147009 T65867 Z19487 BF697478
409927	2333801_1	AW971213 AA493825 AA493567 AA876839 AA934462
447881	44623_1	T69961 T69024 AA078476
433009	2142268_1	AK074291 AW293424 BE876135 A1832125 BE019146 BE465019 A1761124 AA617778 A1279232 AW575897 A1672039 F28618 BF924261
412719	1634_2	AA722184 BF934174 BE004328 AV749301 BE880282 B019798 B1019389 BF928776 AW813409 AV726604 A1077580 BE272875 BF949119 AW814185 BE878126 A1697926 BF504155 BE205787 BF063513 N35828 A1948557 A1438339 A1378679 BG066182 A1589094 N23123 AA588805 AW316581 A1080272 A1421980 A1493318 BF194830 N87590 AA495899 N32698 A1699844 H06845 H95592 N28741 B1035539 BF747723 BF171086 W01350 H05495 A1243785 Z39622 AA867432 A1350659 R46102
437050	1240141_1	AA761688 AA573621 R09570 R92814
436823	MH1680_153	B1918715 BF594193 A1073494 A1363077 A1658855 AA121979 BF983131 AA491795 B6152545 A1350401 BF939121 A1479401 B1493099 BF057693 A1970550 BF111919 BF448282 B1493100 AW043768 AW006202 A1564010 BF433292 A1458202 A1954746 BE220982 A1375411 A11361048
457733	119180_1	AA115853 A1364474 A1668815 AA133407 A1928647 AW016610 AA133334 AA504348 A1291629 A1161208 AA837042 A1887138 AA987255 A1830219
453912	32562_3	AU150404 A1880674 AW369901
440080	517737_1	AW978442 AA743319 A1765420
419175	35068_1	BG180003 AW975741 AW749865 AA731828 AA731829
		AW974812 A1821822 A1821820 A1821075 A1821073 AA651643 AA551862
		BM472224 B1966849 B196735 AW873032 B1962894 B1963048 AA548765 A1928504 AA041561 AW043754 A1066702 AW008105 AA974849
		AW614893 AA553737 AA918995 AW262982 A1580891 BF726843 A1693312 W35325 AA039927 BG460936 AW308482 AW389420 BF374777
		W01350 N94710 H87967
		AW051597 A1733052 A1167287 A1732989 A1565918 A1476787 A1791542 AA887204 AW025394 AA863338 A1240285 A1791393
		AB018322 BC012480 BE524873 A19665554 A1934469 A1479918 BF096162 BF096132 AA744972 A1951988 A1858339 BE076331
		AA886998 A1570585 A1916688 A1678611 A1663109 A1308135 AA669046 AA961064 A1018062 H08018 BE221942 R52809 A1915164 AA365626
		Z44571 B1052776 BF882486 BG286184 A1589558 AA331663 AA5434979 A1275392 A1273455 R52553 AA829920 H80652 AA360728 F10618

			AW953666 AW176773 H85527 AA765570 AA081927 BF093262 BG743753 AL037576 AA534314 BE814964 BE973713 N49493 BE006634 BE006630 AW270037 AA234765 AI334004 BF057179 AI057450 AI341191 AI634143 AI917449 AW517207 AA255424 AW008334 AA847572 AA994211 AA861901 AA581873 AI580157 AI354363 AW242357 AW235291 N56645 AA319869 R36911 AA256551 AW044188 AI203159 N49403 F02090 AI187299 AI609644 Z40516 AW852314
5	421091	24941_2	AK057700 BC015899 BE867108 AL526926 AL527438 BG913023 AI884867 BE858461 AI885227 AI935218 BE645595 AJ922406 AA778161 BF345973 AW195853 AI687121 AI338147 AD91364 AI769203 AW627859 BE677432 BF439954 BG820230 AA283686 AA812306 AI358395 AA932022 BE222881 AW016109 BM352687 BF528099 BG818618 AI935916 AA912295 BG910887 AI568301 AL567278 BI522445 BI754384 BG819375 BF835850 AA323718 AA860955 AI089847 AL520776 AL526045 AI538507 AL567788 AL536876 AL574332 BF834531 BF340116 BF835854 AL573997 AL581252 BF957687 AL580170 AW952324 AL569382 AW148695 AL559234 BG034270 BI913839 AL581327 AL565842 H43668 BF945188 AL559686 AL539326 T15481 AW895092 AL582684 BI519896 BC014072 BE328850 AI356567 AI148171 AI022165 BG149661 BF000671 AA233101 AA573721 AA447991 AW016855 AI005068 AA554071 BF478215 AA906902 AW014761 BE905651 BE512923 BMD47129 AA243852 AA232891 AA127550 AA127551 AA570256 AI473237 BF033706 N90525 AW973623 AI359827 BG674574 BE903322 AI041403 Z49148
10	441128	20932_1	AK055674 AW965247 AV751598 AA290926 R53043 AA331387 AK056148 BI917678 BG819395 BG911971 BG820167 AI174254 AA348720 AA364503 BG714279 AW993230 AA081774 H24222 AV727176 BF875715 AA081638 BE000634 AA334880 AI567337 BG029708 W52892 AI439558 BE551237 AA283724 BF109530 AI457096 AI085992 BE467736 AA693467 AI697583 AI887863 AI167419 AW801980 AW901788 BE702179 AA484549 Z23811 BE327043 AA716027 AA917004 AA167714 BF338675 AA084618 AI186534 T31586 AA436630 AI368472 AA706191 AI422304 AI204899 AI041169 AA211402 AW827081 AI788593 T32736 AI767935 AA747914 T09534 AW959843 AI119527 BE327037 AW901982 AW993370 AW901977 AW902071 W60090 N79908 D52685 T07735 BE702069 BE702172 T08671 BE767117 BE767113 AA658826 AI821926 AI791191 AA635129 AA564492 Z11692 X51466 NM_001861 M19997 BI224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE868804 BI868669 BG337216 AW829935 BMD16625 AI580409 AI582866 AI909178 BF849556 AA371735 BF038841 BF727115 BC006547 BG757526 AL555664 BI261304 BG770095 BI033486 BI517580 BG876486 BI011828 AI313235 BG831724 BF658862 BG998348 BI011834 BF888337 BF898627 BF092380 AW803216 F01241 BF805718 BG876487 AW498536 BF998666 BG998849 AA248724 BG829202 BG756456 BG032392 BI859287 BM016990 BG332369 BE933685 BE166758 BM452445 AI937808 AW026128 N23684 AW006041 AI337621 F33111 BF344301 BG105450 BG387343 BF659847 BF154671 BM007368 BF659385 BE772007 BI199487 BF761700 BI261519 BF944452 BF888506 AI038390 BMD44934 AW381142 BG743618 BE769206 BE893973 BI015047 BF886479 BF761350 BE769789 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964 BF089940 BI000274 BG255503 BG874499 BG774174 BI015084 BG256892 H10532 N46614 R52610 AW977696 BM460488 W56819 BI042183 BG977498 BE767451 BF870009 BG477472 R61137 R14274 R20259 R09686 BI838226 BF034269 AA429173 BE741829 AW867495 AI123883 AW006831 BE831162 AW452753 AV742717 W88152 BF115102 AI633815 BF921562 AA094230 BE092587 W88151 AA526153 AI672156 BF914466 R12579 BF852352 AA899780 T57386 BF903022 R09933 AA578298 BF339388 AI345516 BG391857 BE708957 BG026034 BE261703 H56716 H85572 H93601 T48830 R96593 R96989 R39707 BE867593 AA090310 AA090072
15	406789 410099	Q_0 16732_1	NZ7807 AA258634 BE276324 AF263306 BF951698 T66089 F11794 H29379 R19493 H18042 AL133995 AW134660 AI299437 AA057405 AA817450 AI002692 T09262 R43839 H29280 T65008 N78357 AI221207 AI659856 AA913581 AI220302 NM_000786 U23942 BI601080 BG771947 BG773455 BI581558 BM460208 BG714348 BM126447 AU129411 AU129401 AI119303 AV724389 AU099323 AU127089 BG701614 BM150364 D55653 AV702235 BE090408 AU151526 AW149661 BG054754 W42624 W52098 AV709923 V79867 W74235 AV709052 AI217688 AA399409 BE182318 BM128040 AI893998 AW616411 AW070426 AI124550 AW778736 AA477781 AW263013 AA59819 AA860513 BF809648 AA643635 AA864975 H42020 AW901189 AA904786 BF432722 BI918393 BM470755 BI333211 AA095636 BI256415 U47727 BG773392 N58531 AA226450 BG679564 AA292178 W56683 BE813131 C03646 BG287974 AA386261 H47580 R48658 T91611 H42019 BI889421 BG502073 BG425943 W37200 W31363 BE004451 BF208311 BI048717 N78122 AA228597 AI525334 AI953821 AA657925 AA935436 AW976088 BC000222 AI136871 NM_032261 BC009497 BM461705 BG470749 BG826905 BG285127 BI253235 BE397026 BG704967 AW961225 BM352817 BI227161 BG820180 AA454463 AA256885 N31549 AA326504 BC019924 BG257230 BI082368 BI869896 BG251883 BF034444 BG286577 BE260391 AA599912 BF666779 AI755222 AW241170 AU156565 F28259 T16319 AA362506 N64153 BMD16416 BM458863 BG739972 AV725655 BE288285 BE867433 BI001110 BG285856 AI922439 BE270975 AL119339 BF956085 AI565178 AL554305 AL573240 AL572917 AI129627 AL548640 BE392285 AI092843 AI371057 BE302410 AI050763 AW874261 AI750057 AI052649 N47822 AL516249 AI589903 BG256439 AI123662 AI126014 AA778101 AA243218 AW498837 AA748311 AI754395 T15728 AA776369 AA858195 W73625 AA216784 AW513778 AW243958 AI051112 AI783806 AL569622 AA070466 BF229336 N58159 H80288 N32598 H80293 H80279 AL581253 AW571884 AI361698 AW073321 AA878464 H95640 T34421 AA331419 N99697 H80274 BI26120 AA205826 AA070716 AA653206 AA653483 BG389811 W20432 AA670295 AA653197 D51888 AA382527 BG056668 AW118162 AW073071 BE293888 BF792321 BF792258 BG107176 T66604 BM193568 H03238 AA818045 AA908004 BI086688 AA664566 AI221630 D52045 C14510 AA029390 W60153 H88743 AI882641 H28485 AA723093 AI081730 AA641309 AA687083 BI224818 AW204722 AI309186 AI216122 AI200785 BE457373 BM352502 AI304400 AI193071 AI742463 AW003408 AI400201 AI585740 AI474637 AI284448 AI695909 BE704420 AA989278 AA918266 AA830866 AA989425 AA911829 AA282588 BE740563 BE727592 BE781003 BG030940 BE256750 W23528 AL517059 H95714 W00970 H74304 W32684 H38210 BE617658 AW593584 AA580593 H94853 N69544 AA181782 D20132 T55734 T60692 R76888 AA022948 AW770291 R50934 AA206816 R97811 H40328 R65252 AA936029 AI813809 AA933607 AA129695 AA548261 AA714393 AA776006 AA853439 AA983808 AA743251 AA401150 AA581651 AA555005 AA554408 D51494 C13991 D51478 D52007 AA489663 D52138 D51695 D55942 D52740 AI000118 AL516304 AL534259 N54940 AL579194 AI689399 AI342925 BE938201 AA633000 BI222963 AI619676 AW190306 BF035010 AW087897 AI864989 T57243 R48211 AA113880 R26594 C14467 C14444 AI94549 BE896346 BE270780 AL580073 BG389833 BE891549 BI223147 AW381001 AA448464 AW709744 AA412194 AA848107 AA927157 AA883841 BF752571 BE731304 AI174783 R12271 R83669 AI274757 AI559500 AW022182 AW970134 AA516420 AA543007 BG057526 BI001430 AI498371 D50181 D81004 D60382 C15876 N91070 C14815 C15068 D80763 C14818 C15161 D60184 D60656
20	432745 400263	112643_1 18977_1	Z11692 X51466 NM_001861 M19997 BI224253 BG830478 AU122147 AU123437 BG113591 BG752624 BE868804 BI868669 BG337216 AW829935 BMD16625 AI580409 AI582866 AI909178 BF849556 AA371735 BF038841 BF727115 BC006547 BG757526 AL555664 BI261304 BG770095 BI033486 BI517580 BG876486 BI011828 AI313235 BG831724 BF658862 BG998348 BI011834 BF888337 BF898627 BF092380 AW803216 F01241 BF805718 BG876487 AW498536 BF998666 BG998849 AA248724 BG829202 BG756456 BG032392 BI859287 BM016990 BG332369 BE933685 BE166758 BM452445 AI937808 AW026128 N23684 AW006041 AI337621 F33111 BF344301 BG105450 BG387343 BF659847 BF154671 BM007368 BF659385 BE772007 BI199487 BF761700 BI261519 BF944452 BF888506 AI038390 BMD44934 AW381142 BG743618 BE769206 BE893973 BI015047 BF886479 BF761350 BE769789 BG766117 BF847365 BE397834 AW371121 BF089125 BE082996 BF183193 BG180964 BF089940 BI000274 BG255503 BG874499 BG774174 BI015084
25			
30	411606	10026_3	
35	445836	8561_5	
40	441064 429925	2641480_1 33135_1	
45	434976 440191	121716_1 MH790_2	
50			
55			
60			
65	440409 444810 446091 431843	588375_1 2145282_1 519091_1 445334_1	
70	400262	18977_1	
75			
80			

TABLE 68C

Pkey: Unique number corresponding to an Eos probe set

Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham I. et al." refers to the publication entitled "The DNA sequence of human chromosome 22." Dunham I. et al., Nature (1999) 402:489-495.

Strand: Indicates DNA strand from which exons were predicted.
 Nt_position: Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	Nt_position
403047	3540153	Minus	59793-59968
401424	8176894	Plus	24223-24428
401451	6634068	Minus	119926-121272
401747	9789672	Minus	118596-118816, 119119-119244, 119609-11976
404632	9796868	Plus	45095-45229
403046	3540153	Minus	55707-55859, 56369-56511
404922	7341893	Plus	13248-13428
401519	6649315	Plus	157315-157950
401197	9719706	Plus	176341-176452
401966	8018106	Plus	73126-73623
405387	6587915	Minus	3769-3833, 5708-5895
403752	7678857	Plus	33704-33828
404210	5006246	Plus	169926-170121
401785	7249190	Minus	165778-165996, 166189-166314, 166408-16656
406214	7342036	Plus	86320-86523
403632	8076842	Minus	81750-81901
400860	9757499	Minus	151830-152104, 152649-152744
404913	7341740	Plus	97717-97976

Table 69A lists about 200 genes that are upregulated in human umbilical vein endothelial cells (HUVEC) compared to normal body tissues. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting the relative level of mRNA expression.

Table 70A lists about 148 genes that are downregulated using the mean of vessels (veins and arteries) compared to the mean of HUVEC. These genes were selected from 59680 probesets on the Eos/Affymetrix Hu03 Genechip array. Gene expression data for each probeset obtained from this analysis was expressed as average intensity (AI), a normalized value reflecting relative level of mRNA expression.

TABLE 69A:

Pkey: Unique Eos probeset identifier number
 ExAccn: Exemplar Accession number, Genbank accession number
 UnigeneID: Unigene number
 Unigene Title: Unigene gene title
 R1: Ratio of the mean of HUVEC AI's to the mean of the normal body tissue AI's

Pkey	ExAccn	UnigeneID	Unigene Title	R1
424806	AA382523	Hs.105689	MSTP031 protein	1.51
418036	Z37978	Hs.83337	latent transforming growth factor beta b	1.94
444381	BE387335	Hs.283713	ESTs, Weakly similar to S64054 hypothet	1.60
442802	AL133035	Hs.8728	hypothetical protein DKFZp434G171	1.73
417944	AJ077199	Hs.82885	collagen, type V, alpha 2	1.48
410480	R97457	Hs.63584	cadherin 13, H-cadherin (heart)	1.91
452516	AA058630	Hs.29759	RNA POLYMERASE I AND TRANSCRIPT RELEASE	1.69
425139	AW530488	Hs.25338	protease, serine, 23	1.63
402483			NM_014624: Homo sapiens S100 calcium-bind	1.50
423798	AF047033	Hs.132904	solute carrier family 4, sodium bicarbon	1.31
412568	AI878826	Hs.74034	caveolin 1, caveolae protein, 22kD	1.53
419948	AB041035	Hs.93947	NM_016931: Homo sapiens NADPH oxidase 4 (2.08
447526	AL048763	Hs.303649	small inducible cytokine A2 (monocyte ch	2.10
448500	U78093	Hs.15154	sushi-repeat-containing protein, X chrom	1.67
441457	AW956651	Hs.43838	ESTs	1.30
408296	AL117452	Hs.44155	DKFZP586G1517 protein	1.61
418994	AA298520	Hs.89548	selectin E (endothelial adhesion molecu	1.87
413785	AL040178	Hs.142003	ESTs	1.64
441689	AI123705	Hs.289068	ESTs	1.44
412567	AF750979	Hs.74034	Homo sapiens clone 24651 mRNA sequence	1.75
424432	AB037821	Hs.146858	protocadherin 10	1.65
432573	AB028859	Hs.278605	DnaJ (Hsp40) homolog, subfamily B, membe	1.31
418683	U90908	Hs.87241	hypothetical protein from clones 23549 a	1.42
453085	AW854243		KIAA0251 protein	1.47
438887	R68867	Hs.265499	ESTs	1.49
436729	BE521807		transmembrane 4 superfamily member 1	1.91
400494			ENSP00000238970:CIG30 (Fragment).	1.34
442506	BE566411		ESTs	1.54
425023	AW956889	Hs.154210	endothelial differentiation, sphingolip	1.55
414476	AA301867	Hs.76224	EGF-containing fibulin-like extracellular	2.65
452933	AW391423	Hs.288555	Homo sapiens cDNA: FLJ22425 fis, clone H	1.62
422389	AF240635	Hs.115897	protocadherin 12	1.38
417124	BE122762	Hs.25338	ESTs	2.13
433681	AI004377	Hs.200350	Homo sapiens cDNA FLJ13027 fis, clone NT	1.31
419933	W55956	Hs.94030	Homo sapiens mRNA; cDNA DKFZp586E1624 (f	1.54
414776	AA155598	Hs.212839	hypothetical protein FLJ14195; KIAA1714	1.51
450534	AI570189	Hs.25132	KIAA0470 gene product	1.43
449618	AI076459	Hs.15978	KIAA1272 protein	1.42
446098	AW072215	Hs.208470	ESTs	1.53
413281	AA861271	Hs.222024	transcription factor BMAL2	1.40
448574	W31178	Hs.154140	ovary-specific acidic protein	1.47
407061	X97748		gb:Haapiens PTX3 gene promoter region.	1.33

	434846	AW295389	Hs.119768	ESTs	1.29
	408570	AL046406	Hs.103483	KIAA1798 protein	1.47
	436772	AW975688		metallothionein 1E (functional)	1.81
5	453789	AA628517	Hs.118502	ESTs	1.41
	424259	AK001776	Hs.143954	hypothetical protein FLJ10914	1.35
	441020	W79283	Hs.35962	ESTs	1.82
	401234			mitogen-activated protein kinase 8 Inter	1.48
	420174	AI824144	Hs.199749	ESTs	1.75
10	445684	AK001696	Hs.13109	Ran binding protein 11	1.49
	418693	AI750878	Hs.87409	thrombospondin 1	1.89
	426535	AU077012	Hs.289592	ESTs, Weakly similar to ubiquitous TPR m	1.77
	412330	NM_005100	Hs.788	A kinase (PRKA) anchor protein (gravin)	2.02
	412646	NM_006825	Hs.74368	transmembrane protein (63kD), endoplasmic	1.64
15	434523	AA703709	Hs.23410	translocase of inner mitochondrial membr	1.26
	433376	AI249361	Hs.74122	caspace 4, apoptosis-related cysteine pr	1.49
	422099	AA158022	Hs.111518	hypothetical protein	1.56
	449394	AA004368	Hs.18160	Homo sapiens cDNA FLJ11550 fis, clone HE	1.54
	446119	AF035121	Hs.12337	kinase insert domain receptor (a type II	1.40
20	438142	T90309	Hs.259651	ESTs	1.45
	437478	AL390172	Hs.317432	branched chain aminotransferase 1, cytos	1.44
	422809	AK001379	Hs.121028	hypothetical protein FLJ10549	1.42
	453459	BE047032	Hs.257789	ESTs	1.51
	442711	AF151073	Hs.8645	hypothetical protein	1.42
25	428428	AL037544	Hs.184298	cyclin-dependent kinase 7 (homolog of Xe	1.32
	400288	X06256	Hs.149609	integrin, alpha 5 (fibronectin receptor,	2.67
	417640	D30857	Hs.82353	protein C receptor, endothelial (EPCR)	2.47
	407252	AA659037	Hs.163780	(AB075832) KIAA1952 protein (Homo sapien	1.78
	418825	AA226881	Hs.22394	hypothetical protein FLJ10893	1.40
30	417805	U38545	Hs.82587	phospholipase D1, phosphatidylcholine-spe	1.35
	425828	NM_000020	Hs.172670	activin A receptor type II-like 1	1.55
	415714	NM_002290	Hs.78672	laminin, alpha 4	1.90
	446984	AB020722	Hs.16714	Rho guanine exchange factor (GEF) 15	1.71
	421778	AA428000	Hs.283072	actin related protein 2/3 complex, subun	1.88
35	421218	NM_000499	Hs.72912	cytochrome P450, subfamily I (aromatic c	1.75
	452298	AI039243	Hs.278585	NM_024756; Homo sapiens hypothetical pro	1.86
	434596	T59538		gb:cyb65g12.s1 Stratagene ovary (937217)	1.52
	412351	AL135960	Hs.73828	T-cell acute lymphocytic leukemia 1	1.61
	433374	AI821409	Hs.304471	EST	1.45
40	429113	D28235	Hs.195384	prostaglandin-endoperoxide synthase 2 (p	2.14
	423099	NM_002837	Hs.123641	protein tyrosine phosphatase, receptor t	1.50
	435705	AA782114	Hs.28043	ESTs	1.53
	456999	AA319798	Hs.298581	eukaryotic translation elongation factor	1.62
	453983	H94997	Hs.16450	ESTs	1.94
	406506			Target Exon	1.87
45	424603	NM_002205	Hs.149609	integrin, alpha 5 (fibronectin receptor,	2.32
	452924	AW568939	Hs.97199	complement component C1q receptor	2.36
	426596	AW363332	Hs.171844	NM_006505 Homo sapiens poliovirus recept	1.61
	418941	AA452970	Hs.239527	EB-55kDa-associated protein 5	1.41
50	450152	AI138635	Hs.22968	intron of VEGFR	1.70
	437269	AA334384	Hs.149420	ESTs	1.60
	445279	R41900	Hs.22245	ESTs	1.59
	409509	AL036923	Hs.322710	ESTs	1.52
	410240	AL157424	Hs.61289	synaptotagmin 2	1.61
55	424711	NM_005795	Hs.152175	calcitonin receptor-like	1.96
	449318	AW236021	Hs.78531	Homo sapiens, Similar to RIKEN cDNA 5730	1.81
	407882	BE548267	Hs.337988	Homo sapiens cDNA FLJ10934 fis, clone OV	1.91
	410057	R66634	Hs.268107	multimerin	1.85
	446727	AB011095	Hs.16032	KIAA0523 protein	1.67
60	412584	X83703		cardiac ankyrin repeat protein	1.51
	414786	AI246482	Hs.243010	Homo sapiens ras homolog gene family, me	1.71
	410276	AI554545	Hs.71832	angiotensin-2	1.91
	406627	T64804	Hs.163780	ESTs	1.78
	405025			Bone morphogenetic protein 6	1.69
65	422548	D85983	Hs.118693	Melanoma associated gene	2.33
	452852	AK001972	Hs.30822	hypothetical protein FLJ11110	1.78
	427912	AL022310	Hs.181097	tumor necrosis factor (ligand) superfamily	1.79
	432004	BE018302	Hs.2894	placental growth factor, vascular endoth	2.02
	430129	BE301708	Hs.233955	hypothetical protein FLJ20401	1.93
70	429276	AF056085	Hs.198612	G protein-coupled receptor 51	1.85
	407704	BE315072	Hs.78768	malignant cell expression-enhanced gene/	1.48
	448694	AA478766	Hs.184477	E3 ubiquitin ligase SMURF2	2.01
	434398	AA121098	Hs.3838	serum-inducible kinase	1.83
	416851	AW963951	Hs.85618	ESTs	1.65
75	412420	AL035658	Hs.73853	bone morphogenetic protein 2	1.69
	416179	R19015	Hs.78067	MAD (mothers against decapentaplegic, Dr	1.71
	450589	AI369275	Hs.243010	Homo sapiens cDNA FLJ14445 fis, clone HE	1.86
	416658	U03272	Hs.79432	fibrillin 2 (congenital contractural ara	1.65
	425235	AA353113	Hs.112497	Homo sapiens cDNA: FLJ22743 fs, clone H	1.83
80	428206	AB020643	Hs.183006	KIAA0836 protein	1.77
	412765	BE144306	Hs.179891	ESTs, Weakly similar to P4HA_HUMAN PROLY	2.00
	456977	AK000262	Hs.169758	hypothetical protein FLJ20245	1.81
	456977	AK000262	Hs.169758	hypothetical protein FLJ20245	1.61
	427897	NM_017413	Hs.303084	apelin; peptide ligand for APJ receptor	1.94

	425234	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	1.74
	444409	AI792140	Hs.49265	ESTs	1.88
	421340	F07783	Hs.1359	decay accelerating factor for complement	1.74
5	445701	AF055581	Hs.13131	lymphocyte adaptor protein	2.18
	444009	AI380792	Hs.135104	ESTs	1.90
	409220	BE243323	Hs.51233	tumor necrosis factor receptor superfam	2.16
	418940	N75620	Hs.43157	ESTs	2.03
	418922	AW956580	Hs.42699	ESTs	2.09
10	431548	AI834273	Hs.9711	novel protein	1.81
	434927	H46612	Hs.293815	Homo sapiens HSPC285 mRNA, partial cds	2.14
	434558	AW264102	Hs.39168	ESTs	1.93
	438183	BE263252	Hs.6101	hypothetical protein MGC3178	2.05
	428438	NM_001955	Hs.2271	andohelin 1	2.46
15	453365	AA035211	Hs.17404	SOX7 SRY (sex determining region Y)-box	2.20
	418058	AW161552	Hs.83381	guanine nucleotide binding protein 11	2.26
	439410	AA632012	Hs.188746	ESTs	1.93
	453457	AI535997	Hs.30089	ESTs	2.39
	420209	AA256444	Hs.126485	hypothetical protein FLJ12604; KIAA1692	1.84
20	417933	X02308	Hs.82962	thymidylate synthetase	1.70
	436420	AA443966	Hs.31595	ESTs	1.97
	414430	AI346201	Hs.76118	ubiquitin carboxyl-terminal esterase L1	1.93
	412140	AA219691	Hs.73625	RAB8 Interacting, kinesin-like (raklines	1.80
	442104	L20971	Hs.188	phosphodiesterase 4B, cAMP-specific (dun	2.03
25	425397	J04088	Hs.156346	topoisomerase (DNA) II alpha (170kD)	1.58
	418506	AA084248	Hs.85339	G protein-coupled receptor 39	1.81
	413745	AW247252	Hs.75514	nucleoside phosphorylase	1.59
	405121			mitogen-activated protein kinase 8 Inter	2.99
30	425811	AL039104	Hs.158557	karyopherin alpha 2 (RAG cohort 1, impor	1.76
	415765	NM_005424	Hs.78824	tyrosine kinase with immunoglobulin and	2.13
	431089	BE041395	Hs.156110	ESTs, Weakly similar to unknown protein	2.71
	421937	AI878857	Hs.108706	hematological and neurological expressed	1.65
	408669	AI93591	Hs.78146	platelet/endothelial cell adhesion molec	2.39
	418815	U41514	Hs.80120	UDP-N-acetyl-alpha-D-galactosamine:polyp	1.77
35	418203	X54942	Hs.83758	CDC28 protein kinase 2	1.67
	408243	Y00787	Hs.624	interleukin 8	2.09
	418054	NM_002318	Hs.83354	lysyl oxidase-like 2	2.42
	407891	AA485820	Hs.41135	endomucin-2	2.34
	407891	AA485820	Hs.41135	endomucin-2	2.34
40	436032	AA160797	Hs.109276	latexin protein	2.24
	439382	BE247684	Hs.103070	ESTs	2.07
	419172	AW338625	Hs.22120	ESTs similar to TRANSMEMBRANE 4 SUPERF	2.00
	442006	AW975183		ESTs, Weakly similar to S72482 hypotheti	2.33
45	447560	AF065214	Hs.18858	phospholipase A2, group IVC (cytosolic,	2.11
	432128	AA127221	Hs.298502	ESTs	2.27
	417426	NM_002291	Hs.82124	laminin, beta 1	2.11
	434217	AW014795	Hs.23349	ESTs	2.03
	439285	AL134430	Hs.6906	Homo sapiens cDNA: FLJ23197 fs, clone R	2.08
	442923	AW248322	Hs.95835	ESTs, Weakly similar to unnamed protein	1.57
50	433001	AF217513	Hs.279905	clone HQ0310 PRO0310p1	1.60
	418741	H83265	Hs.8881	ESTs, Weakly similar to 841044 chromosom	2.37
	442573	H93356	Hs.7587	branched chain aminotransferase 1, cytos	2.55
	422544	AB018259	Hs.118140	KIAA0716 gene product	2.09
	449722	BE260074	Hs.23960	cyclin B1	1.76
55	413794	AF234532	Hs.61638	myosin X	2.01
	422803	BE242587	Hs.118651	hematopoietically expressed homeobox	2.15
	406964	M21305		gb:Human alpha satellite and satellite 3	3.08
	448231	AI701916	Hs.202509	ESTs	2.27
	408989	AW381666	Hs.49500	KIAA0746 protein	1.43
60	429653	M68874	Hs.211587	phospholipase A2, group IVA (cytosolic,	2.67
	418738	AW386533	Hs.6682	solute carrier family 7, (cationic amino	2.18
	418185	AW958272	Hs.347326	intercellular adhesion molecule 2	2.60
	417308	H60720	Hs.81892	KIAA0101 gene product	1.86
	407975	X89426	Hs.41716	endothelial cell-specific molecule 1	2.92
65	420256	U84722	Hs.76206	cadherin 5, type 2, VE-cadherin (vascula	2.92
	400668			NM_002425:Homo sapiens matrix metallopro	2.59
	431728	NM_007351	Hs.268107	multimerin	2.72
	440086	NM_005402	Hs.288767	v-rel simian leukemia viral oncogene hom	2.25
	413132	NM_008823	Hs.75209	protein kinase (cAMP-dependent, catalyti	1.78
70	451979	FD6972	Hs.27372	endothelial tyrosine kinase (Etk) (BMX),	3.37
	416138	C18355	Hs.295844	tissue factor pathway inhibitor 2	3.11
	414577	AI056548	Hs.72116	hypothetical protein FLJ20992 similar to	3.11
	444330	AI697655	Hs.49265	ESTs	3.08
	422424	AI186431	Hs.296538	prostate differentiation factor	2.96
75	400289	X07820	Hs.2258	matrix metalloproteinase 10 (stromelysin	4.84
	418007	M13509	Hs.83189	matrix metalloproteinase 1 (interstitial	11.91

TABLE 69B

Pkey: Unique Eos probasel identifier number

CAT number: Gene cluster number

Accession: Genbank accession numbers

Pkey CAT Number Accession

5	453085	10017_1	BC017336 BG716430 BG501286 BI458528 AI582223 N98532 AI338138 AI273442 AW102617 AA831177 AA745642 AA412583 AA355375 BG547492 AW954243 BI766546 BG057641 AI192435 AI338935 AI312651 AI708679 AI191125 AI206832 AA676899 AI078010 AI888718 AA452830 BF445542 N69930 AA715017 BF446713 BE046852 AW771909 AA907729 AI143749 AI761290 AA890233 BF925759 AI783713 AI767267 AA814538 W56778 AA918481 BG743526 BE645242 AI026328 AI298436 AI290445 H27710 AI475034 BG740023 AI090348 AI340003 BI602481 W38495 AI183314 AI927418 BG397181 AA878310 W19369 W56507 C05571 AW380760 AW380770 AW380790 BF930729 H28425 AA037326 AA375805 X75684 AL573167 AA45481 AI453743 AI983655 AI564644 AA977180 AI694111 AI591358 AW071625 AI567812 AI720939 AI927769 BE439796 AI963432 AA292956 AW192593 AI865838 AI696905 AI424384 AI161312 AI911921 AI597801 BI494959 AI240988 AI492554 AW262737 BE044033 AW008570 AW629505 BI494958 AA088439 AA708057 BF222820 BF593608 BE501957 AA524526 BE044134 AW572531 AW015724 BE349186 AA043217 BE219784 AI798814 AA129575 AI671727 AI470033 BE648195 AW779725 AA903050 AA147228 AA404570 AI075878 W38161 AI927399 AW673152 AA723200 C06123 BF057147 AA627686 AA157944 AI990245 AA662517 T32487 AI800106 AI333170 AI859160 W45410 AI990827 AW275048 AA182640 AA478328 AI298935 AW085158 AW471421 AW103470 AW300456 AW191997 AI823466 AA562397 AA136658 AI251817 AW339104 AA724739 AA411100 AA191349 AA757735 AA037696 AI769516 AW772283 AA010631 AI692848 AI061086 H80983 F79933 AI950693 AI245632 AI349380 AA148284 AI798502 AA487893 AI621320 AW194272 C06365 AA953883 BE858936 AI918523 AI872828 AI927217 AI453453 AI189366 AW338678 AI261369 AI500576 BF477735 AK032569 AI972899 AI985583 Z28771 AI353829 AI693030 AA603586 BE773488 AW339301 BE773489 BE773482 BE773495 AI650338 BE773499 AI457117 BE811475 BE811470 BE811464 BE811418 BE811415 BE811400 BE811398 BE811388 BE811352 BE773501 BE773494 BE773486 BE773474 BE773473 BE773470 BE773461 BE811350 BE811337 BF593847 BG055071 AW675302 BF003068 AA719173 BE811348 AI582462 AI686240 BE773500 AI244845 AI585439 AI918453 AI472527 AA46740 AA035576 AA191414 AW674145 C05782 AI589264 D67558 AI468237 AI432033 AA989682 R21752 BF002457 AA988297 AL574085 AL576200 AL571074 AL574525 AL578810 BC498381 AI28364 BE879732 AA479834 AA479712 C17732 BM091258 BF843901 AW620230 C17476 BE327120 AA129574 AA136646 BF843900 AW805193 AA502832 AA549494 AI688520 AL547960 BE706937 BE811360 BE773498 BE811401 BE773484 BE811437 BE811380 BE811389 BF997171 BF757734 BE926037 AI377598 C08111 AW088968 BE811404 BE811472 AI865912 AI925607 AI871950 AI093510 BE905927 BE811435 AA191387 AW772000 BE811453 BE814379 BF844522 BI044896 AI744233 AW984527 C17504 BF843883 AI246307 BE773483 AI567995 W60075 BF941183 AI738944 BE811458 BE773481 AI262930 AA948565 BE706942 BE156380 T65026 AW242658 AW197954 BE905184 AA722206 AI344943 AI348877 AI334860 BE621857 BE156280 AA454099 AA037722 BF843897 AW805183 AA043216 BG482896 AA182734 AA877242 AW372926 H27252 R38114 BF851858 BE166214 AA190427 T91762 AA035067 AA837326 T10930 BF908587 BI755027 BG056731 BC008442 BC010166 AL550134 AL553096 AL548700 AL550751 AL547978 AL545286 AL540643 AU118527 AL601379 BI259821 BG741786 BI808522 AU135868 BI552770 BI259210 BI255620 BI255669 BG485098 BI258228 BG496501 BM044512 AU133884 AI556586 BE745111 BI226333 AU133917 BG288151 BI260715 BI550550 BG500773 BI551761 BG707601 BI818593 BF891383 BG721129 BG541678 BE906666 BG761098 BI224135 BG400746 BG478065 BE790436 AW080238 AU137549 BG429986 BE392485 AW961686 BG721056 BE908365 BE546656 BG541235 AW583735 BG528290 BI280895 AW651691 BM048974 BM043805 BG142185 AA315188 AI446615 C06300 BG497644 AA088644 AI815887 BG528531 BE619182 AW239185 AW062910 AW062902 AA347236 F11933 AA488005 AA301631 AA378800 D58120 AA343532 AA308636 F00242 AA376086 AA316968 AA343759 BI870221 BE910282 BG538748 AW960564 AV732879 D16854 AA192519 BF822148 AA216013 BG624091 BE544387 BG507008 AW176446 BF790033 BE088925 BE888854 AA921353 R21800 AA011222 T97525 NM_002640 L40377 BG227962 AI925897 W60100 BG980023 AA653496 AA360401 AW955168 W61361 AI074846 AA373798 BG193973 BG499418 BF816267 AI675932 BG611734 BG777123 AW449485 BF912016 BE566411 BM068728 AW976385 AL121194 AI767324 BM054718 AW366882 AA166151 Z25109 C05177 AW975688 AA731063 N67084 AF147374 T59538 T59589 T59598 T59542 X83703 NM_014391 BC018657 AU139209 BE924924 BE824899 BE924977 BE924985 BE924947 BF229055 BE924917 BE924938 BE812621 BE924937 AA989184 BE924898 BF229086 BF229054 BF081177 BE924934 BF229040 BE925037 BE925011 BG943778 AA488072 AA488364 Z36249 AW455806 AW582753 BF081131 BE924910 BF229058 BF081172 BE924956 AW378093 BF081132 BF081168 BE812736 BE812738 BF081165 C04160 C04483 BF229048 AW975183 AA973583 AI365103 AI699495 AI301787
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45	TABLE 69C
50	Key: Unique number corresponding to an Eos probaset
	Ref: Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.
	Strand: Indicates DNA strand from which exons were predicted.
	Nt_position: Indicates nucleotide positions of predicted exons.

55	Key	Ref	Strand	Nt_position
	402463	9796895	Minus	8818-8952
	400494	9714719	Plus	165845-170272
	401234	9929542	Plus	120173-120337
	406506	7711374	Minus	6843-8077
	405025	7107727	Plus	105267-105343, 106184-106294, 106387-10653
	405421	8102330	Minus	35816-36004, 36587-36684
	400666	8118496	Plus	17982-18115, 20297-20456

60	TABLE 70A:
65	Key: Unique Eos probaset identifier number
	ExAccn: Exemplar Accession number, Genbank accession number
	UnigeneID: Unigene number
	Unigene Title: Unigene gene title
	R1: Ratio of the mean of the vessel A1's to the mean of the HUVEC A1's

70	Key	ExAccn	UnigeneID	Unigene Title	R1
	428928	BE400838	Hs.194657	cadherin 1, type 1, E-cadherin (epitheli	0.99
	439180	AI393742	Hs.199067	v-erb-b2 avian erythroblastic leukemia v	1.06
	412636	NM_004415		desmoplakin (DPI, DPL)	1.25
	428158	NM_001982	Hs.199087	v-erb-b2 avian erythroblastic leukemia v	1.36
75	414320	U13816	Hs.75893	ankyrin 3, node of Ranvier (ankyrin G)	1.50
	417878	U90916	Hs.82845	Homo sapiens cDNA: FLJ21830 fs, clone H	1.55
	414572	AU077174	Hs.288181	cathepsin H	1.64
	415314	N88802	Hs.5422	glycoprotein M6B	1.70
	431103	M57389	Hs.44	pleiotrophin (heparin binding growth fac	1.75
80	408973	M34996	Hs.198253	major histocompatibility complex, class	1.88
	456874	M12529	Hs.169401	apolipoprotein E	1.90
	430560	Z28942	Hs.243960	N-myc downstream-regulated gene 2	1.91
	406828	AA419202	Hs.84298	CD74 antigen (invariant polypeptide of m	1.97
	422048	NM_012445	Hs.288125	spandin 2, extracellular matrix protein	1.99

5	406826	AW516005	Hs.84298	CD74 antigen (Invariant polypeptide of m	2.02
	453023	AW028733	Hs.31439	serine protease inhibitor, Kunitz type,	2.03
	413391	AJ232338	Hs.75335	glycine amidinotransferase (L-arginine:g	2.12
	406824	AW516981	Hs.84298	CD74 antigen (Invariant polypeptide of m	2.15
	418299	AA279530	Hs.83968	integrin, beta 2 (antigen CD18 (p95), ly	2.17
	437535	X91221	Hs.144465	ESTs	2.21
	442402	NM_000954	Hs.8272	prostaglandin D2 synthase (21kD, brain)	2.28
	446945	AI93115	Hs.16611	tumor protein D52-like 1	2.27
10	422639	AI929377	Hs.173724	creatine kinase, brain	2.29
	427451	AI690816	Hs.178137	transducer of ERBB2, 1	2.31
	454042	H22570		hypothetical protein FLJ20093	2.37
	418283	S79895	Hs.83942	cathepsin K (pseudosclerosis)	2.38
	424247	X14008	Hs.234734	lysosome (renal amyloidosis)	2.39
15	422103	AA984330	Hs.111676	protein kinase H11; small stress protein	2.41
	415894	NM_002923	Hs.78944	regulator of G-protein signalling 2, 24k	2.43
	427393	AB028018	Hs.177635	KIAA1095 protein	2.47
	414217	AJ309298	Hs.279898	Homo sapiens cDNA: FLJ23166 fls, clone L	2.49
	414063	H26904	Hs.75736	apolipoprotein D	2.50
20	426716	NM_006379	Hs.171921	sema domain, immunoglobulin domain (Ig),	2.51
	414803	X03100	Hs.914	Human mRNA for SB class II histocompatib	2.51
	410532	T53088	Hs.155376	hemoglobin, beta	2.56
	431369	BE184455	Hs.251754	secretory leukocyte protease inhibitor (2.58
	437852	D63209	Hs.5944	soluble carrier family 11 (proton-coupled	2.58
25	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	2.59
	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	2.59
	453655	AW960427	Hs.342874	transforming growth factor, beta recepto	2.59
	427980	AA418305	Hs.303205	EST	2.59
	442695	AC002425	Hs.8603	pB protein (candidate of metastasis 1)	2.62
	425751	T19239	Hs.1940	crystallin, alpha B	2.63
30	414194	BE175494	Hs.75811	N-acylphosphatidylesterase (acid c	2.63
	443907	AJ076484	Hs.9963	TYRO protein tyrosine kinase binding pro	2.66
	453464	AI684911	Hs.32989	receptor (calcitonin) activity modifying	2.67
	410577	NM_003278	Hs.65424	tetranectin (plasminogen-binding protein	2.67
35	452685	AI634851	Hs.30250	v-maf musculoaponeurotic fibrosarcoma (a	2.67
	425869	AA524547	Hs.160318	FXRD domain-containing ion transport reg	2.73
	406643	N77976	Hs.347939	hemoglobin, alpha 2	2.73
	453787	AB011792	Hs.35094	extracellular matrix protein 2, female o	2.74
	424614	X54486	Hs.151242	serine (or cysteine) proteinase inhibito	2.80
40	444195	AB002351	Hs.10587	KIAA0353 protein	2.81
	417233	W26005	Hs.24395	small inducible cytokine subfamily B (Cy	2.86
	442498	U54617	Hs.8364	Homo sapiens pyruvate dehydrogenase kina	2.92
	412810	M21574	Hs.74615	platelet-derived growth factor receptor,	2.93
	440820	AL031846		plekophlin 4	2.94
45	428123	AB011099	Hs.196847	KIAA0527 protein	2.97
	411529	AA430348	Hs.317595	Homo sapiens cDNA FLJ12927 fls, clone NT	3.01
	413305	NM_000426	Hs.323511	Homo sapiens cDNA: FLJ23176 fls, clone L	3.01
	425622	AW390847	Hs.18578	ESTs	3.01
	420195	W44348	Hs.251385	Homo sapiens cDNA FLJ11177 fls, clone PL	3.04
50	445584	U53445	Hs.15432	downregulated in ovarian cancer 1	3.04
	407869	AI827976	Hs.24391	hypothetical protein FLJ13612	3.06
	423815	AF038018	Hs.135281	alpha-actinin-2-associated LIM protein	3.07
	410036	R57171	Hs.57975	caldesmon 2 (cardiac muscle)	3.10
	412047	AA934589	Hs.49696	ESTs	3.12
55	414840	R27319	Hs.23823	hairy/enhancer-of-split related with YRP	3.14
	424651	AW93208		ESTs	3.17
	443932	AW688222	Hs.9973	tensin	3.18
	420859	AW468397	Hs.100000	S100 calcium-binding protein A8 (calgran	3.20
60	434025	AF114264	Hs.216381	Homo sapiens clone HH409 unknown mRNA	3.20
	421834	BE543205	Hs.288771	DKFZP586A0522 protein	3.20
	423961	D13666	Hs.136348	periostin (OSF-2os)	3.24
	447384	AJ377221	Hs.40528	ESTs	3.24
	425383	D83407	Hs.156007	Down syndrome critical region gene 1-lik	3.25
	447023	AA356764	Hs.17109	integral membrane protein 2A	3.25
65	420136	AW801090	Hs.195861	actin, alpha 2, smooth muscle, aorta	3.25
	406972	M32053		gb:Human H19 RNA gene, complete cds.	3.28
	410132	NM_003460	Hs.300946	Microfibril-associated glycoprotein-2	3.27
	430998	AF128847	Hs.204038	Indolethylamine N-methyltransferase	3.28
	456898	NM_001928	Hs.155597	D component of complement (adipin)	3.29
70	443623	AA345519	Hs.9641	complement component 1, q subcomponent,	3.33
	410614	AI081195	Hs.65029	growth arrest-specific 1	3.35
	451529	AI917901	Hs.208641	ESTs	3.36
	430310	U60115	Hs.235069	four and a half LIM domains 1	3.37
	424897	D63216	Hs.153684	fizzled-related protein	3.37
75	427111	AA351026	Hs.173594	serine (or cysteine) proteinase inhibito	3.38
	443604	C03577	Hs.9615	myosin regulatory light chain 2, smooth	3.41
	421913	AI934385	Hs.108439	osteoglycin (osteoclast-inductive factor, mime	3.43
	451331	AK002039	Hs.251385	Homo sapiens cDNA FLJ11177 fls, clone PL	3.44
	416908	AA333990	Hs.80424	coagulation factor XIII, A1 polypeptide	3.46
80	407938	AA905087	Hs.85050	phospholamban	3.48
	418005	AI186220	Hs.83164	collagen, type XV, alpha 1	3.51
	452877	AI250789	Hs.32478	ESTs	3.52
	419577	L35531	Hs.91295	integrin, alpha 8	3.52
	404277			NM_018111*Homo sapiens major histocompa	3.54

5	407815	AW373860	Hs.183860	hypothetical protein FLJ20277	3.58
	421853	AL117472	Hs.108924	SH3-domain protein 5 (pou5in)	3.64
	447111	AJ017574	Hs.17409	cysteine-rich protein 1 (intestinal)	3.68
	426935	NM_000088	Hs.172928	collagen, type I, alpha 1	3.70
	418371	M13560	Hs.84298	CD74 antigen (invariant polypeptide of m	3.71
	440274	R24595	Hs.7122	scrapie responsive protein 1	3.73
	427818	AW511222	Hs.193765	ESTs	3.73
	433465	AV857778	Hs.3314	selenoprotein P, plasma, 1	3.75
10	458568	AI769067	Hs.127824	ESTs, Weakly similar to T28770 hypotheti	3.77
	459290	NM_001546	Hs.34853	inhibitor of DNA binding 4, dominant neg	3.80
	424206	NM_003734	Hs.198241	amine oxidase, copper containing 3 (vasc	3.83
	453874	AW591783	Hs.36131	collagen, type XIV, alpha 1 (mdulin)	3.86
	428957	NM_003881	Hs.194679	WNT1 inducible signaling pathway protein	3.89
15	434868	R50032	Hs.159263	collagen, type VI, alpha 2	3.90
	417043	NM_004369	Hs.80988	collagen, type VI, alpha 3	3.95
	417512	X76534	Hs.82225	glycoprotein (transmembrane) nmb	3.95
	452669	AA216363	Hs.262958	hypothetical protein DKFZp434B044	3.97
	421314	BE440002	Hs.180324	Homo sapiens, clone IMAGE4183312, mRNA,	4.01
	449925	AJ342493	Hs.24192	Homo sapiens cDNA FLJ20767 fis, clone CO	4.03
20	453600	AI478427	Hs.43125	esophageal cancer related gene 4 protein	4.07
	430572	U33114	Hs.245168	tissue inhibitor of metalloproteinase 3	4.09
	418223	N40850	Hs.28625	ESTs	4.17
	422550	BE297626	Hs.296049	microfibrillar-associated protein 4	4.25
25	443060	D78874	Hs.8944	procollagen C-endopeptidase enhancer 2	4.25
	450912	AW939251	Hs.25847	v-fos FBJ murine osteosarcoma viral onco	4.29
	432306	Y18207	Hs.303090	protein phosphatase 1, regulatory (inhibi	4.34
	419938	AJ076772	Hs.1279	complement component 1, r subcomponent	4.37
	415165	AW887604	Hs.78085	complement component 7	4.37
30	414176	BE140538	Hs.75794	endothelial differentiation, lysophospha	4.41
	452114	N22887	Hs.8236	ESTs	4.43
	406850	AI624300	Hs.172928	collagen, type I, alpha 1	4.43
	428411	AW291464	Hs.10338	ESTs	4.48
	412802	U41518	Hs.74602	aquaporin 1 (channel-forming integral pr	4.51
35	406849	AA454809	Hs.172928	collagen, type I, alpha 1	4.54
	453064	R40334	Hs.89463	potassium large conductance calcium-acti	4.57
	429500	X78565	Hs.289114	hexabrachion (tenascin C, cytactin)	4.57
	433336	AF017986	Hs.31386	secreted frizzled-related protein 2	4.68
	421814	L12350	Hs.108623	thrombospondin 2	4.73
40	427373	AB007972	Hs.130760	myosin phosphatase, target subunit 2	4.76
	414290	AI588801	Hs.71721	ESTs	4.98
	415274	AF001548	Hs.78344	myosin, heavy polypeptide 11, smooth mus	5.13
	417130	AW276853	Hs.81256	S100 calcium-binding protein A4 (calcium	5.14
	416784	AA334592	Hs.79914	tumican	5.20
45	453356	AW285374	Hs.31412	Homo sapiens cDNA FLJ11422 fis, clone HE	5.50
	408221	AA912183	Hs.47447	ESTs	5.85
	430223	NM_002514	Hs.235835	nephroblastoma overexpressed gene	5.87
	416585	X54182	Hs.79385	leiomodulin 1 (smooth muscle)	6.47
	422737	M26939	Hs.119571	collagen, type III, alpha 1 (Ehlers-Danl	6.65
50	426405	AI742501	Hs.189756	complement component 1, s subcomponent	7.94
	448429	D17408	Hs.21223	calponin 1, basic, smooth muscle	9.90
	413624	BE177019	Hs.76445	SPARC-like 1 (nast9, hev9)	9.91

TABLE 70B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

Pkey	CAT Number	Accession
55		
60	412636	1438_1
65		
70		
75		
80		

M77830 NM_004415 AF139065 BG681115 BG740377 B1712964 BG000856 AA128470 BM438324 H27408 BE316330 BE167165 AW370827
 AW370813 J05211 BG688865 BG740734 BG680618 BG739778 B1705807 BM353403 BM353248 AW177784 AW205789 AW951576 AW248552
 BE182184 BF149266 BE940187 B1060445 B1060444 BF360983 BE720095 BE720089 BE715154 BE082584 BE082578 BE004047 AA857316
 B1039774 BE713818 BE713548 AW170253 BE160433 B1039776 AW888475 BM462504 BE931734 BF149284 AA340777 BF381183 BG621737
 AU127260 AW364859 BF983352 BG223489 BE819009 BF381184 BE715956 R68704 AA852212 AW366566 B1090356 BF087707 BE819046
 BE819005 AA377127 BE073467 BE819069 BE819048 B1036308 BG990973 B1040954 BF199111 AU140165 A1851768 A1434518 AW804874
 BF752969 BE637009 BE925826 BF149265 AW995815 BE814264 B1039782 AU140407 BE144243 BE709883 BF085642 BE001923 BF833510
 AW265328 BG436319 BE182166 AW365175 AW847688 BE818280 AW177933 BF873679 AW178000 BE082526 BF476868 BF086594 BF582276
 BE082507 BE082514 BE082505 BF873683 AW068840 AW847678 BF804153 AW365157 BE813830 BE002030 AW365153 BE184941 BF749421
 BE184920 BF839562 BE184933 BF842254 BE698470 BE931048 BF999889 BF368816 BE184924 BE155646 BE714632 BE184948 BG886845
 AA131128 AA099891 W39488 C04715 BF096124 BE888341 AW799304 AL803116 BE149760 BE705967 BE705966 BE705968 AW848723
 AW376699 AW376817 AW376697 BG005097 BF761115 BE688084 AW848371 AW376782 AW848789 AW849074 AW381413 BF927725 BF094211
 AW997139 BE865474 BE185187 BE156621 BE715089 BE713287 BE713298 BE179915 AW799309 BF872345 BF088676 BE705939 AW752599
 BG005197 BF350086 BE715196 BE715155 BF752396 BF093817 BF831180 BF752409 BE006561 BG959922 BF094833 BF094748 BF094583
 AW377699 AW607238 BE082519 AW377700 BF349467 A190590 A1554403 A1392926 AU158477 B1467252 AU158919 A1760816 BF082516
 A1438101 AA451923 A1340326 A1590975 B1791653 A1700963 A1142882 AA039975 AA946936 AA544381 BM314884 AA702424 A1417612
 AW190555 A1220573 A1304772 A1270345 A1627383 AA552300 A1911702 AW166807 A1346078 W95070 AA149191 AA026864 A1830049 AW780435
 AU078449 A1819984 A1858282 B1468568 A1860684 A1025932 AA026047 AA703232 AA658154 AA515500 AW192085 AA918281 T77861 A1927207
 A1205263 BF082491 AW021347 A1588096 BE938862 A1088888 D12062 AA066527 AA782109 W19287 W02156 AW150038 AA022701 T87181
 HA4405 A1910434 BF082513 A1494069 A1270027 A1358678 A1128330 BG681425 BE708078 R20904 BG880059 BG676647 BF764409 AA026654
 AV745530 B1762796 BG287391 AW798780 BE706045 BE926470 AW798118 BF087996 BE002273 AW879451 A1571075 BE067786 AV721320
 A1022862 N29754 C03378 N84767 AA131077 H30146 BE714290 A1686869 A1558892 A1915596 AW105614 A1887258 A1538577 BE926474
 BE067737 BG319486 AA247685 AW798883 AW103621 BF989173 AW880878 BE939707 BE185750 BE714064 BE713903 BE713858 BE713763
 BG950164 BE713810 AW365151 BG955489 BE006272 BF915937 AW365148 A1905927 BF992780 AW853812 BG954443 B1770853 BG679408

5	454042	30254_1	BG740832 BG681087 BG698430 AA455100 T87267 BE696209 BE696210 BI089483 BE006273 BE872225 AW391912 BE925515 BG677012 BG741970 AA026480 BE705959 BG877157 BE009090 BG681378 BE712291 BG961498 BG678984 BI040941 AA337270 AW384371 AW847442 BI068659 BE813665 W95048 W25458 AW177788 AA025851 BE931733 BF154837 BG949393 BE714441 AW996245 BE711801 AI284090 BE664323 BE719390 BE940148 BG991212 BF375714 BF349522 BG996267 T48793 BI013292 BE001925 AW365156 AW365154 AW606653 BF763109 BE931637 BE167181 BE713879 BF354008 BF878726 H90899 AW365145 W38382 AI498487 AJ420458 AI018523 AA708686 BF949633 AL119553 BF945950 AI081305 AA041432 AI821013 AI684910 AI654847 AW874199 AI206120 AW241428 R43035 T66767 AW103715 W28478 BF963052 H45926 BF807568 AW903943 BE170143 BI040435 BF931989 BI600000 AV722350 W27787 H45331 BI549781 R63955 BI549855 BG991583 BI491075 AW020049 AW129293 H45263 AA410309 AA340613 R42410 AA707199 AI431587 BE858679 AW292267 AI421678 AA041195 BE466753 AI243913 AI358894 AW137298 AI366488 N64360 AA779107 AW025969 R49056 AA347011 R55722 AW771106 F04969 Z38381 F01659 H17396 BI493714 AI880103 AW771447 AI202551 AA788851 AI494438 BF856114 H22570 AW954381 BG007409 BM314056 AA465642 T30861 T33111 Z42834 C04542 BF948152 BF944325 BF858895 AA935284 AI267360 N64249 W67500 F07962 AA322394 BI489987 BE644865 BM313782 AA910364 AI809246 AA836750 BF115228 AA829730 N27413 BM141766 AI742325 AA455261 AA938708 AI420241 AI130039 BF222341 BF941301 AA771807 Z41034 BF447457 BF447426 AW515347 T03874 F02360 F02302 N34898 AI678586 AA807824 AA948556 AW204638 BM142045 BF446775 AV848364 AI801368 AA971739 AI017351 AA760722 AI460007 AI458383 AI694152 AA226536 BE467282 N47808 BE348825 BE830581 BE830583 N53009 N59351 N41056 W67501 AA016246 H43293 F21282 R59121 R56280 BG435302 BM083687 AA904035 AA488889 W76175 AA781874 H28767 AA910081 AA837085 AJ521825 BG986378 AI478562 AA743152 AA746092 H88863 BG986375 AA35644 AI493206 AA699979 BE245127 BG986430 BG986529 BF665873 BG030157 BG622575 AA766495
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TABLE 70C

Pkey:	Unique number corresponding to an Eos probeset
Ref:	Sequence source. The 7 digit numbers in this column are Genbank Identifier (GI) numbers. "Dunham, et al." refers to the publication entitled "The DNA sequence of human chromosome 22" Dunham, et al. (1999) <i>Nature</i> 402:489-495.
Strand:	Indicates DNA strand from which exons were predicted.
NL_position:	Indicates nucleotide positions of predicted exons.

Pkey	Ref	Strand	NL_position
404277	1834458	Minus	91655-91946

TABLE 71A: 774 GENES UP-REGULATED IN EWING SARCOMA COMPARED TO NORMAL ADULT TISSUES

Table 1A lists 774 genes up-regulated in Ewing Sarcoma compared to normal adult tissues. These were selected from 35371 probesets on the Affymetrix/Eos Hu03 GeneChip array such that the ratio of "average" Ewing Sarcoma to "average" normal adult tissues was greater than or equal to 2.1. The "average" Ewing Sarcoma level was set to the 75th percentile amongst numerous Ewing sarcomas. The "average" normal adult tissue level was set to the 85th percentile amongst various non-malignant tissues. In order to remove gene-specific background levels of non-specific hybridization, the 10th percentile value amongst the non-malignant tissues was subtracted from both the numerator and the denominator before the ratio was evaluated.

Pkey:	Unique Eos probeset identifier number
ExAccn:	Exemplar Accession number, Genbank accession number
UnigeneID:	Unigene number
Unigene Title:	Unigene gene title
R1:	75th percentile of ewing sarcoma to 85th percentile of body map

Pkey	ExAccn	UnigeneID	Unigene Title	R1
104659	AW968769	Hs.105201	ESTs	70.3
101447	M21305		gkHuman alpha satellite and satellite 3	64.7
105782	H09748	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	50.5
115881	NM_005756	Hs.184942	G protein-coupled receptor 64	48.8
121792	AW969726	Hs.98381	ESTs, Weakly similar to serine protease	46.7
101104	AW882258	Hs.169268	neuropeptide Y receptor Y1	48.8
110278	AF061573	Hs.19452	protocadherin 8	46.1
126645	AA316181	Hs.61635	six transmembrane epithelial antigen of	41.4
116752	AL008583	Hs.91622	neuronal pentadactin receptor	40.9
119717	AA918317	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	39.6
104691	U29690	Hs.37744	Homo sapiens beta-1 adrenergic receptor	36.9
110728	AA737106	Hs.32250	ESTs, Moderately similar to T78885 serin	35.5
121362	AF050147	Hs.97932	chondromodulin I precursor	34.7
131291	NM_004350	Hs.170019	nunt-related transcription factor 3	33.0
101063	D54745	Hs.80247	cholecystokinin	31.7
121619	AA528339	Hs.178052	ESTs, Weakly similar to phosphatidyseri	28.7
122651	AW975398	Hs.293836	ESTs	28.0
100299	D49483	Hs.2171	growth differentiation factor 10	26.5
129977	NM_000399	Hs.1395	early growth response 2 (Krox-20 (Drosop	26.2
123619	AA802984		gban07c02.s1 NCL CGAP_P2 Homo sapiens	26.1
124006	AI147155	Hs.279727	ESTs; homologue of PEM-3 (Ciona savignyi)	23.1
116301	AW968706	Hs.293332	ESTs	22.6
121231	AA814948	Hs.98343	ESTs, Weakly similar to ALUC_HUMAN IIII	22.3
106533	AL134708	Hs.145998	ESTs	22.3
109166	AA218581	Hs.73625	RAB6 interacting, kinesin-like (retikines	21.3
131313	R96290	Hs.75874	ribosomal protein L44	20.8
116790	AW181357		microtubule-associated protein tau	18.7
105316	AI671245	Hs.24835	hypothetical protein FLJ14594	18.2
102123	NM_001809	Hs.1654	centromere protein A (17kD)	17.8
126218	AL049801	Hs.13649	Novel human gene mapping to chromosome 13	17.8
119791	AA554907	Hs.58291	ESTs	16.7
113003	AW282315	Hs.7215	ESTs	16.3
102836	U94320	Hs.158330	neuropeptide Y receptor Y5	16.3
126799	AW753865	Hs.74376	oligodendrocyte related ER localized protei	16.3
105298	BE887730	Hs.28369	hypothetical protein FLJ20287	15.5
107160	AA314490	Hs.27669	KIAA1563 protein	14.8
115313	AA808001	Hs.184411	albumin	14.6
123308	C14187	Hs.103538	ESTs	14.2

	126077	M7B772	Hs.210836	ESTs	14.0
	100698	AA884407	Hs.211595	protein tyrosine phosphatase, non-recept	13.9
	108821	NM_006594	Hs.28298	adaptor-related protein complex 4, beta	13.9
5	110288	H40665	Hs.31564	ESTs	13.8
	106498	AJ221919		hypothetical protein FLJ10582	13.8
	112134	R41823	Hs.7413	ESTs;calyntenin-2	13.7
	115265	AA334274	Hs.18368	DKFZP564B0769 protein	13.4
	126639	AW582962	Hs.102897	CGL-47 protein	13.2
10	125598	AF078847	Hs.191356	general transcription factor IIH, polype	12.8
	105200	AA328102	Hs.24641	cytoskeleton associated protein 2	12.3
	119458	AA248897	Hs.48784	ESTs	12.2
	135155	AI207958	Hs.166556	Homo sapiens, Similar to TEA domain fami	12.1
	106614	AA648459	Hs.335951	hypothetical protein AF301222	12.0
15	131941	BE252983	Hs.35086	ubiquitin specific protease 1	12.0
	132988	AF234532	Hs.61638	myosin X	11.7
	132725	NM_006276	Hs.184167	splicing factor, arginine/serine-rich 7	11.7
	111353	W20090	Hs.6616	ESTs	11.4
	123289	AA495904	Hs.103316	ESTs	11.3
20	104968	AI249502	Hs.29669	ESTs	11.1
	123532	AA608733		gb:ae56106.s1 Stratagene lung carcinoma	11.0
	104173	AA084273	Hs.76561	ESTs, Weakly similar to S47072 finger pr	10.7
	125558	AB033064	Hs.236463	KIAA1238 protein	10.7
	127240	AJ005683	Hs.86998	nuclear factor of activated T-cells 5, t	10.6
25	123049	BE047880	Hs.211869	dickekop (Xenopus laevis) homolog 2	10.6
	132315	AF091086	Hs.44563	hypothetical protein	10.5
	134321	BE538082	Hs.8172	ESTs, Moderately similar to A46010 X-link	10.5
	128609	NM_003616	Hs.102456	survival of motor neuron protein Interac	10.4
	131945	NM_002916	Hs.35120	replication factor C (activator 1) 4 (37	10.4
30	110730	N67655	Hs.26411	ESTs	10.3
	119186	A979147	Hs.101265	hypothetical protein FLJ22593	10.3
	115909	AW872527	Hs.59761	ESTs, Weakly similar to DAP1_HUMAN DEATH	10.3
	121916	AW117207	Hs.98523	ESTs	10.2
	131402	Y08890	Hs.113503	karyopherin (Importin) beta 3	10.1
35	101879	AA176374	Hs.243886	nuclear autoantigenic sperm protein (his	10.0
	133161	X91662	Hs.66744	twist (Drosophila) homolog (acrocephalos	10.0
	131307	NM_000025	Hs.2549	adrenergic, beta-3-, receptor	10.0
	113849	AA467211	Hs.8858	bromodomain adjacent to zinc finger doma	9.9
	103446	X98834	Hs.79971	sal (Drosophila)-like 2	9.7
40	105091	AA148859	Hs.179909	hypothetical protein FLJ22895	9.6
	106148	W07288	Hs.118392	ESTs, Weakly similar to LNHUER IgE Fc re	9.6
	127003	AW816515	Hs.173540	ATPase, Class V, type 10D	9.5
	115414	AA662240	Hs.283099	AF15q14 protein	9.4
	117829	BE160952	Hs.247117	ESTs, Moderately similar to ALUF_HUMAN I	9.4
45	126098	M79088		gb:EST01236 Subtracted Hippocampus, Stra	9.3
	121910	AI204600	Hs.96978	hypothetical protein MGC10784	9.2
	130625	AF176012	Hs.280720	J domain containing protein 1	9.2
	129756	R42216	Hs.7769	Homo sapiens clone 24538 mRNA sequence	9.1
	100335	AW247629	Hs.6793	platelet-activating factor acetylhydrola	9.0
50	111109	A940675	Hs.20914	hypothetical protein FLJ23056	9.0
	120217	AA882257	Hs.66035	ESTs	9.0
	112891	T03927	Hs.293147	ESTs, Moderately similar to A46010 X-link	8.9
	131601	NM_007115	Hs.29352	tumor necrosis factor, alpha-induced pro	8.8
	126262	AK065153	Hs.143764	ESTs, Weakly similar to unknown ji.sapie	8.8
55	113903	AJ368034	Hs.36679	ESTs, Weakly similar to A46010 X-linked	8.7
	105253	AW997484	Hs.5003	KIAA0456 protein	8.6
	102581	AJ077228	Hs.77266	enhancer of zeste (Drosophila) homolog 2	8.6
	105172	AA187554	Hs.300496	mitochondrial solute carrier	8.6
	100380	D82343	Hs.74376	neuroblastoma (nerve tissue) protein	8.6
60	129229	AF013758	Hs.109643	polyadenylate binding protein-interactin	8.5
	102725	AB026187	Hs.159158	protocadherin 11	8.5
	130298	A1347487	Hs.132761	class II cytokine receptor	8.4
	132294	AB023191	Hs.44131	KIAA0974 protein	8.2
	118644	AA443241		ribosomal protein L44	8.2
65	106576	AW970602	Hs.106421	ESTs	8.2
	133142	AW952412	Hs.65874	ESTs, Weakly similar to A40348 Elav/Sex-	8.1
	119498	AJ918906	Hs.55080	ESTs	8.1
	100248	NM_015156	Hs.78398	KIAA0071 protein	8.1
	114837	BE244830	Hs.166895	ESTs	8.0
70	107088	AJ823593	Hs.27688	ESTs	8.0
	123960	AW082862	Hs.287733	hypothetical protein FLJ23189	7.9
	105280	AA894638	Hs.14600	ESTs	7.9
	115147	AA745781	Hs.38399	hypothetical protein MGC2454	7.9
	134570	U66615	Hs.172280	SWI/SNF related, matrix associated, act	7.9
75	133063	AJ654133	Hs.30212	thyroid receptor interacting protein 15	7.8
	105730	AW377314	Hs.6364	DKFZP564I062 protein	7.8
	126426	AA125984		gb:zn27h06.r1 Stratagene neuroepithelium	7.8
	107254	Z45998	Hs.22543	Homo sapiens mRNA; cDNA DKFZp76111912 (f	7.8
	134367	AA339449	Hs.82285	phosphatidylglycerol kinase formyltransfer	7.8
	115082	AF262297	Hs.91546	cytochrome P450 retinoid metabolizing pr	7.7
80	125400	AL110151	Hs.128797	DKFZP566D0824 protein	7.7
	129413	AW377610	Hs.11123	DKFZP564G092 protein	7.7
	116766	AJ608657	Hs.95097	ESTs	7.7
	129075	BE250182	Hs.83765	dihydrofolate reductase	7.6

5	105143	AI368836	Hs.24808	ESTs, Weakly similar to I38022 hypothet	7.6
	132438	AW363587	Hs.82916	chaperonin containing TCP1, subunit 6A (7.6
	118036	AA71882	Hs.196008	Homo sapiens cDNA FLJ11723 fls, clone HE	7.6
	131170	NM_014253		odx (odd Oz/ten-m, Drosophila) homolog 1	7.5
	104548	R39398	Hs.91559	ESTs	7.5
10	131495	AA812434		SMC2 (structural maintenance of chromoso	7.5
	132543	BE588452	Hs.344037	protein regulator of cytokinesis 1	7.4
	124040	U23752	Hs.32964	SRY (sex determining region Y)-box 11	7.4
	127695	AA714731	Hs.291457	ESTs, Weakly similar to heterogeneous ri	7.3
	132559	AF119848	Hs.270863	hypothetical protein PRO1550	7.3
15	101050	AU077324	Hs.1832	neuropeptide Y	7.2
	111823	R35252	Hs.130558	ESTs, Weakly similar to 2109260A B cell	7.2
	116401	AW893840	Hs.59698	ESTs	7.1
	105127	AA045648	Hs.301957	nrdix (nucleoside diphosphate linked moi	7.1
	128478	AA708205	Hs.100343	ESTs	7.1
20	110458	H52348	Hs.36636	ESTs	7.1
	118846	AW299598	Hs.50895	homeo box C4	7.1
	120934	AA226198		gbnc26a07.s1 NCL CGAP_Prl Homo sapiens	7.1
	128132	AA225632		gbnc08a07.r1 NCL CGAP_Prl Homo sapiens	7.0
	127431	AW771958	Hs.175437	ESTs, Moderately similar to PC4259 fami	7.0
25	106157	W37943	Hs.34892	KIAA1323 protein	6.9
	117852	AW877787	Hs.136102	KIAA0853 protein	6.9
	106213	NA5018	Hs.8769	hypothetical protein DKFZp781J17121	6.9
	118013	AI674128	Hs.94031	ESTs	6.9
	120147	AB171116		hemoglobin, beta	6.8
30	118257	N34905	Hs.44853	Homo sapiens cDNA: FLJ22669 fls, clone H	6.8
	132581	AK000631	Hs.52256	hypothetical protein FLJ20624	6.8
	120325	AA195551		AP-2 beta transcription factor	6.8
	133276	AW978439	Hs.69504	ESTs	6.8
	127742	AW293496	Hs.180138	ESTs	6.7
35	127664	AA806164	Hs.116502	ESTs	6.7
	108778	AF133123	Hs.90847	general transcription factor IIC, polyp	6.6
	121553	AA412468	Hs.48820	TATA box binding protein (TBP)-associate	6.6
	107059	BE614410	Hs.23044	RAD51 (S. cerevisiae) homolog (E coli Re	6.6
	133658	AA319146	Hs.75426	secretogranin II (chromogranin C)	6.6
40	115197	R18858		ESTs	6.5
	112268	W39609	Hs.22003	solute carrier family 6 (neurotransmitte	6.5
	103346	X87613	Hs.5464	thyroid hormone receptor coactivating pr	6.4
	125967	AA205976		gbzq48a10.r1 Stragene hNT neuron (937	6.4
	118499	N67274	Hs.50141	EST	6.4
45	105301	AW352357	Hs.7457	MAGE1 protein	6.3
	113617	AB89372	Hs.17207	Homo sapiens cDNA FLJ11922 fls, clone HE	6.3
	127968	AA830201	Hs.124347	ESTs	6.3
	134719	AA852985	Hs.89232	chromobox homolog 5 (Drosophila HP1 alph	6.3
	110748	AW581992	Hs.301434	KIAA1387 protein	6.3
50	115844	AI373062	Hs.332938	hypothetical protein MGC5370	6.3
	121886	AA934883	Hs.96467	ESTs, Highly similar to AF257737 1 clla	6.2
	102398	U42359		gb:Human N33 protein form 1 (N33) gene,	6.2
	130882	AA497044	Hs.20887	hypothetical protein FLJ10392	6.2
	132256	AI078645	Hs.431	murine leukemia viral (bmi-1) oncogene h	6.2
55	106383	AA447453	Hs.27860	Homo sapiens mRNA; cDNA DKFZp585M0723 (f	6.2
	135186	U73328	Hs.172648	dlatf-less homeobox 4	6.2
	105510	Z42047	Hs.283978	Homo sapiens PRO2751 mRNA, complete cds	6.2
	109261	BE466639	Hs.61779	Homo sapiens cDNA FLJ13591 fls, clone PL	6.1
	114357	R41877	Hs.6107	Homo sapiens cDNA FLJ14839 fls, clone OV	6.1
60	128501	AL133572	Hs.195009	protein containing CXXC domain 2	6.1
	109747	AI223001	Hs.22969	ESTs, Weakly similar to Z141_HUMAN ZINC	6.1
	128361	AW172570	Hs.14600	ESTs	6.1
	115773	AW445044	Hs.38207	Human DNA sequence from clone RP4-53015	6.0
	104689	AA420450	Hs.292911	Plakophilin	6.0
65	113575	AW138168	Hs.15671	ESTs, Weakly similar to KBF3_HUMAN NUCLE	6.0
	121850	AW394055	Hs.98427	ESTs, Weakly similar to I38022 hypothet	5.9
	119298	NM_001241	Hs.155478	cyclin T2	5.9
	109841	H01052		gb:yg32h01.s1 Soares placenta Nb2hP Homo	5.9
	115822	AI088601	Hs.208414	Homo sapiens mRNA; cDNA DKFZp564D0472 (f	5.8
70	122969	AW821262	Hs.104338	hypothetical protein	5.8
	109872	R65841	Hs.28853	ESTs	5.8
	114208	AL049468	Hs.7859	ESTs	5.8
	113494	T91451	Hs.86538	ESTs	5.8
	127684	AA668631	Hs.159971	KIAA0379 protein	5.8
75	129300	W94187	Hs.110165	ribosomal protein L26 homolog	5.8
	127489	AA650250	Hs.272076	ESTs	5.8
	133479	W01656	Hs.238797	ESTs, Moderately similar to I38022 hypot	5.8
	105909	AA195191		hypothetical protein FLJ20729	5.8
	101255	BE385864	Hs.149894	mitochondrial translational initiation f	5.8
80	134676	W28051	Hs.87819	Homo sapiens, clone MGC:2492, mRNA, comp	5.7
	130895	AA641767	Hs.21015	hypothetical protein DKFZp564L0864 simil	5.7
	126395	AI488004	Hs.278958	hypothetical protein FLJ12929	5.7
	130723	BE247676	Hs.18442	E-1 enzyme	5.7
	107230	AI034467	Hs.34650	ESTs	5.7
	102745	AW763865	Hs.74376	olfactomedin related ER localized protei	5.6
	108699	AA121514	Hs.70832	ESTs	5.6
	128080	F12310		gb:HSC38D041 normalized infant brain cDN	5.6

	117357	N24829		gb:yx98h12.e1 Soares melanocyte 2NbHM Ho	5.6
	120827	AA382625	Hs.132967	Human EST clone 122887 mariner transposo	5.6
	123494	AW179019	Hs.112110	mitochondrial ribosomal protein L42	5.5
5	100439	AA013051	Hs.91417	topoisomerase (DNA) II binding protein	5.5
	126165	AI741816	Hs.125897	ESTs	5.5
	125934	AA193325	Hs.32646	hypothetical protein FLJ21901	5.5
	124370	AI243499	Hs.170652	ESTs	5.5
	106135	AL117474	Hs.41181	Homo sapiens mRNA; cDNA DKFZp727C191 (fr	5.5
10	106668	RA9390	Hs.254129	KIAA1678	5.4
	132967	AA316181	Hs.61635	six transmembrane epithelial antigen of	5.4
	109606	Z43371	Hs.7012	ESTs	5.4
	115816	BE042915	Hs.22572	Homo sapiens cDNA FLJ13675 fis, clone PL	5.4
	125186	AA610620	Hs.181165	major histocompatibility complex, class	5.4
15	131185	BE280074	Hs.23960	cyclin B1	5.4
	111227	T08701	Hs.12268	ESTs	5.4
	106516	AK001269	Hs.30738	hypothetical protein FLJ10407	5.4
	103409	NM_004454	Hs.43697	ets variant gene 5 (ets-related molecule	5.4
	116008	T79153	Hs.48589	zinc finger protein 228	5.3
20	106394	Z42993	Hs.25320	Homo sapiens clone 25142 mRNA sequence	5.3
	115121	AI634549	Hs.325422	ESTs	5.3
	125464	N71807		gb:yz2Bd09.r1 Soares multiple sclerosis	5.3
	115596	AW298597	Hs.61884	Homo sapiens, clone IMAGE:4288026, mRNA,	5.3
	119040	RD2394	Hs.269436	ESTs, Moderately similar to PC4259 ferri	5.3
25	128040	AW500486	Hs.180610	splicing factor proline/glutamine rich (5.3
	110151	H18835	Hs.31608	hypothetical protein FLJ20041	5.3
	105539	AB040684	Hs.109694	KIAA1451 protein	5.2
	130567	AA383092	Hs.1608	replication protein A3 (14kD)	5.2
	111077	NA1367	Hs.173002	ESTs, Weakly similar to I38022 hypotheti	5.2
30	120830	AI568170	Hs.96886	ESTs	5.2
	106516	AL137311	Hs.234074	Homo sapiens mRNA; cDNA DKFZp761G02121 (5.2
	103318	X83301	Hs.324728	SMA5	5.2
	116129	AF169011	Hs.49183	putative ribonuclease III	5.2
	131253	R71802	Hs.24853	ESTs	5.2
35	116680	AW902648	Hs.273829	ESTs	5.2
	123949	AA621665	Hs.208957	EST	5.2
	105511	AB037829	Hs.3882	regulator of nonsense transcripts 2; DKF	5.2
	125847	AW181885	Hs.269745	ESTs	5.1
	108301	AA069728	Hs.184582	ribosomal protein L24	5.1
40	110799	AJ089660	Hs.323401	dpy-30-like protein	5.1
	104899	AA054726	Hs.285574	ESTs	5.1
	125972	AI927475	Hs.35406	ESTs, Highly similar to unnamed protein	5.1
	107869	AW976988	Hs.58595	ESTs, Weakly similar to I38022 hypotheti	5.1
	121309	AA293834	Hs.97312	ESTs	5.1
45	125321	T86652	Hs.178294	ESTs	5.1
	102827	AL021918	Hs.158174	zinc finger protein 184 (Kruppel-like)	5.1
	104446	AF084555	Hs.7351	cyclic AMP phosphoprotein, 19 kD	5.0
	126020	H79883	Hs.114243	ESTs	5.0
	118814	H50834	Hs.77899	gb:yp88a10.s1 Soares fetal liver spleen	5.0
50	130622	AI582291	Hs.16846	ESTs, Weakly similar to C4H10D1 debrisocu	5.0
	110818	AL157503	Hs.27552	Homo sapiens mRNA; cDNA DKFZp586N2424 (f	4.9
	127765	AA071146	Hs.129074	ESTs, Moderately similar to MEG1 MOUSE M	4.9
	108768	AF181721	Hs.61345	RU2S	4.9
	120484	AA253170	Hs.98473	EST	4.9
55	114618	AW163257	Hs.106469	suppressor of var1 (Saccharisae) 3-like	4.9
	129012	R81936		ribosomal protein L44	4.9
	124973	AI476066	Hs.102243	ESTs, Weakly similar to I78885 sarineth	4.9
	124648	AA248086	Hs.125034	hypothetical protein FLJ13340	4.9
	126904	AA948033	Hs.130853	ESTs	4.9
60	131526	AI005169	Hs.28274	Homo sapiens cDNA: FLJ22049 fs, clone H	4.9
	130637	AA356764	Hs.17109	Integral membrane protein 2A	4.8
	125769	AA083456		gb:zn05g08.r1 Stratagene hNT neuron (937	4.8
	128086	H75681		gb:yr77g01.r1 Soares fetal liver spleen	4.8
	100168	AL037228	Hs.82043	D123 gene product	4.8
65	130262	D63218	Hs.153684	fizzled-related protein	4.8
	109260	AW878515	Hs.131915	KIAA0863 protein	4.8
	103120	BE410731	Hs.74050	follicular lymphoma variant translocatio	4.8
	111099	R15337	Hs.21958	Homo sapiens mRNA; cDNA DKFZp547D086 (fr	4.8
	126142	H88261	Hs.40568	ESTs	4.8
70	126802	AW805510	Hs.97056	hypothetical protein FLJ21834	4.8
	105848	AW964064	Hs.24951	ESTs	4.7
	127987	AI022103	Hs.124511	ESTs	4.7
	129708	AA443241		ribosomal protein L44	4.7
	128588	N30435	Hs.11556	Homo sapiens cDNA FLJ12566 fis, clone NT	4.7
75	126629	AI056739	Hs.107260	hypothetical protein DKFZp586I0623	4.7
	111348	AA034922	Hs.9585	ESTs	4.7
	100448	AF294887	Hs.57652	cadherin, EGF LAG seven-pass G-type rece	4.7
	127542	AA703684	Hs.179833	ESTs, Moderately similar to ALU5_HUMAN A	4.7
	132452	AW973521	Hs.247324	mitochondrial ribosomal protein S14	4.7
80	123778	AW362149	Hs.102314	ESTs	4.7
	128521	AI475110	Hs.203933	ESTs	4.7
	110343	AW136703	Hs.17268	ESTs	4.6
	102963	X02404	Hs.274534	calthorin-related polypeptide, beta	4.6
	127207	AA377165	Hs.44833	ESTs	4.6

5	113974	AW959756	Hs.34145	ESTs, Weakly similar to B49647 GTP-bind	4.6
	133098	AW629223	Hs.64794	zinc finger protein 183 (RING finger, C3	4.6
	109920	H05840	Hs.111323	ESTs	4.6
	103487	AA743603	Hs.172108	nucleoporin 88kD	4.6
	125353	AB033043	Hs.148377	hypothetical protein DKFZp761L0424	4.6
10	100893	BE245294	Hs.180789	S164 protein	4.6
	135047	AL134187	Hs.93597	cyclin-dependent kinase 5, regulatory su	4.6
	111148	AB020690	Hs.7782	paraneoplastic antigen MA2	4.6
	107681	BE379594	Hs.49136	ESTs, Moderately similar to ALU7_HUMAN A	4.6
	108480	AL133092	Hs.68055	hypothetical protein DKFZp434I0428	4.5
15	132742	AA025480	Hs.292812	ESTs, Weakly similar to T33458 hypotheti	4.5
	104912	AAB13192	Hs.200596	KIAA0547 gene product	4.5
	110223	H19836	Hs.31697	ESTs	4.5
	113047	AI571940	Hs.7549	ESTs	4.5
	101031	J05070	Hs.151738	matrix metalloproteinase 9 (gelatinase B	4.5
20	113002	BE243513	Hs.7212	hypothetical protein PP1044	4.5
	105304	AW134924	Hs.190325	ESTs	4.5
	112386	AA831785	Hs.171914	Homo sapiens cDNA FLJ14209 fis, clone NT	4.5
	106489	AA452054	Hs.118339	ESTs	4.5
	122792	AW188651	Hs.99519	hypothetical protein FLJ14007	4.5
25	112651	AA585802	Hs.33410	ESTs, Weakly similar to T17279 hypotheti	4.5
	111346	AW970976	Hs.293653	ESTs	4.5
	123596	AA421130	Hs.112640	EST	4.5
	125447	AI582222	Hs.128686	ESTs	4.5
	106178	AL049935	Hs.301763	KIAA0554 protein	4.4
30	102250	AI249361	Hs.74122	caspase 4, apoptosis-related cysteine pr	4.4
	105868	AA378780	Hs.334642	tubulin alpha 1	4.4
	127490	AI031650		ESTs	4.4
	127315	AF116622		gb: Homo sapiens clone FLB4217 mRNA, seque	4.4
	110193	AI004874	Hs.310764	Homo sapiens mRNA; cDNA DKFZp434M082 (fr	4.4
35	105012	AF098158	Hs.9329	chromosome 20 open reading frame 1	4.4
	129445	W52452	Hs.29797	ribosomal protein L10	4.4
	114721	D61939	Hs.103822	ESTs	4.4
	120922	AA481003	Hs.97128	ESTs	4.3
	115167	AA748209	Hs.43728	hypothetical protein	4.3
40	102407	AW602154	Hs.82143	E74-like factor 2 (ets domain transcript	4.3
	106111	AW875398	Hs.6451	PR00659 protein	4.3
	123829	AF251237	Hs.112208	XAGE-1 protein	4.3
	103616	NM_002847	Hs.32971	phosphoinositide-3-kinase, class 3	4.3
	100269	NM_001949	Hs.1189	E2F transcription factor 3	4.3
45	112728	R91913	Hs.272104	ESTs, Moderately similar to ALU1_HUMAN A	4.3
	136098	AW274526	Hs.277721	membrane component, chromosome 17, surfa	4.3
	106034	AW952005	Hs.14928	hypothetical protein FLJ12903	4.3
	133571	BE515037	Hs.177566	melanoma antigen, family D, 1	4.3
	106246	AL036917	Hs.288821	KIAA1638 protein	4.3
50	125724	AL360190	Hs.318501	Homo sapiens mRNA full length insert cDN	4.3
	132206	AA425204	Hs.334721	hypothetical protein FLJ13391	4.3
	130227	BE397151	Hs.153003	serine/threonine kinase 16	4.3
	129550	AF109298	Hs.118258	prostate cancer associated protein 1	4.3
	130382	NM_003450	Hs.155204	zinc finger protein 174	4.3
55	108073	AL157441	Hs.17634	downstream neighbor of SON	4.2
	105403	AI473827	Hs.31793	ESTs	4.2
	118138	AA374756	Hs.93560	Homo sapiens mRNA for KIAA1771 protein,	4.2
	134126	NM_003747	Hs.131814	ankyrase, TRF1-interacting ankyrin-rela	4.2
	118041	AA252457	Hs.88543	ESTs, Moderately similar to T00256 hypot	4.2
60	106012	AI240685		ESTs	4.2
	116732	AW152225	Hs.165909	ESTs, Weakly similar to I38022 hypotheti	4.2
	130632	AW838005	Hs.20082	zinc finger protein 3 (A8-51)	4.2
	125960	AI754693	Hs.145968	ESTs	4.2
	133916	AL039185	Hs.77558	thyroid hormone receptor interactor 7	4.2
65	106232	AB037828	Hs.15370	KIAA1407 protein	4.2
	129228	U40714	Hs.239307	tyrosyl-IRNA synthetase	4.2
	109929	AA773187	Hs.294027	ESTs	4.2
	123729	AL039779	Hs.278672	membrane component, chromosome 11, surfa	4.2
	101288	L36845	Hs.73964	EphA4	4.2
70	132389	AA310393	Hs.190044	ESTs	4.2
	124320	H95749	Hs.102342	EST	4.2
	103023	AW500470	Hs.117950	multifunctional polypeptide similar to 6	4.1
	116133	AW448597	Hs.913652	EST, Weakly similar to I38022 hypotheti	4.1
	126001	AA443323	Hs.107812	BPOZ protein	4.1
75	119271	AI061118	Hs.85328	Fanconi anemia, complementation group F	4.1
	114767	AI858865	Hs.154443	minichromosome maintenance deficient (S,	4.1
	126107	H75477	Hs.93361	ESTs	4.1
	115333	BE241812	Hs.87860	protein tyrosine phosphatase, non-recept	4.1
	100571	L14561	Hs.78546	ATPase, Ca++ transporting, plasma membra	4.1
80	134104	L35253	Hs.79107	mitogen-activated protein kinase 14	4.1
	120150	BE005771	Hs.153746	hypothetical protein FLJ22490	4.1
	134470	X54942	Hs.83758	CDC28 protein kinase 2	4.1
	129348	AI537162	Hs.263988	ESTs	4.1
	106882	AA149537	Hs.26994	hypothetical protein FLJ20477	4.1
	126199	AW068276	Hs.125829	ESTs	4.1
	112727	T91029	Hs.15059	ESTs	4.1
	118872	AK038201	Hs.283316	ESTs	4.1

5	131263	AU077002	Hs.24950	regulator of G-protein signalling 5	4.0
	134417	NM_006416	Hs.82921	solute carrier family 35 (CMP-sialic aci	4.0
	113609	T93263	Hs.16875	ESTs, Weakly similar to S23650 retroviri	4.0
	127153	AI732303	Hs.186518	hypothetical protein MGC2599 similar to	4.0
	124105	H11484	Hs.79133	ESTs	4.0
10	100031			AFFX control - DepX-M	4.0
	106997	AF039023	Hs.167495	RAM binding protein 6	4.0
	128659	AW630087	Hs.103315	trinucleotide repeat containing 1	4.0
	133928	AW403084	Hs.7766	ubiquitin-conjugating enzyme E2E 1 (homo	4.0
	126985	AI470523	Hs.139336	ATP-binding cassette, sub-family C (CFTR	4.0
15	103100	NM_005574	Hs.184585	LIM domain only 2 (rhombotin-like 1)	4.0
	119005	AL038511	Hs.125316	ESTs, Weakly similar to S33990 finger pr	4.0
	116751	N74210	Hs.50454	ESTs	4.0
	128797	NM_002975	Hs.105927	stem cell growth factor; lymphocyte secr	4.0
	111387	AI244489	Hs.285724	ESTs	4.0
20	116676	N45312	Hs.48506	ESTs	4.0
	107348	AW973753	Hs.182426	ribosomal protein S2	4.0
	120528	AI923511	Hs.104413	ESTs	4.0
	115652	BE093589	Hs.38178	hypothetical protein FLJ23468	4.0
	102935	BE561850	Hs.80506	small nuclear ribonucleoprotein polypept	4.0
25	115399	AF151534	Hs.92023	core histone macroH2A2.2	4.0
	133615	M62843	Hs.75236	ELAV (embryonic lethal, abnormal vision,	4.0
	118129	N57493		gbcy54c08.s1 Soares_multiple_sclerosis_	4.0
	126622	W31912	Hs.21168	gbzcd76d03.s1 Pancreatic Islet Homo sapi	4.0
	131965	W79283	Hs.35962	ESTs	3.9
30	102507	U52154	Hs.193044	potassium inwardly-rectifying channel, s	3.9
	126029	AA704253	Hs.169359	ESTs	3.9
	107168	W57578	Hs.237955	RAB7, member RAS oncogene family	3.9
	105908	AI133161	Hs.286131	CGI-101 protein	3.9
	134087	U51166	Hs.173824	thymine-DNA glycosylase	3.9
35	133195	AI434760	Hs.279949	KIAA1007 protein	3.9
	112996	BE276112	Hs.7165	zinc finger protein 259	3.9
	129428	AA256906	Hs.111364	ESTs, Weakly similar to ubiquitous TPR m	3.9
	118967	A668670	Hs.216756	ESTs	3.9
	127335	AA830210	Hs.214263	ESTs, Moderately similar to ALU1_HUMAN A	3.9
40	106636	AW958037	Hs.286	ribosomal protein L4	3.9
	133529	W45623	Hs.74571	ADP-ribosylation factor 1	3.9
	102266	U29725	Hs.3080	mitogen-activated protein kinase 7	3.9
	125905	AI678638	Hs.6456	chaperonin containing TCP1, subunit 2 (b	3.9
	103080	AJ077231	Hs.82932	cyclin D1 (PRAD1; parathyroid adenomas	3.9
45	131971	BE567109	Hs.154938	hypothetical protein MDS025	3.9
	129703	BE388665	Hs.179969	Homo sapiens, clone IMAGE:3457003, mRNA	3.9
	128895	AW467000	Hs.105965	ESTs	3.9
	110924	AW058463	Hs.12940	zinc-fingers and homeoboxes 1	3.9
	112921	R91095	Hs.4276	KIAA1701 protein	3.9
50	120820	AA347417	Hs.96869	EST	3.8
	106459	AA789081	Hs.4029	glioma-amplified sequence-41	3.8
	114253	BE149868	Hs.14831	Homo sapiens, Similar to zinc finger pro	3.8
	106476	AL117352	Hs.77196	Human DNA sequence from clone RP5-876810	3.8
	122682	AA884531	Hs.159293	ESTs	3.8
55	130580	N32388	Hs.334370	uncharacterized hypothalamus protein HBE	3.8
	130174	M29551	Hs.151531	protein phosphatase 3 (formerly 2B), cat	3.8
	115577	AA393167	Hs.41294	ESTs	3.8
	129785	H19006	Hs.184780	ESTs	3.8
	126127	N95428		gbzbd80d09.s1 Soares_senescent_fibroblas	3.8
60	109793	F13088	Hs.8040	heparan sulfate (glucosamine) 3-O-sulfot	3.8
	103175	X69089	Hs.79227	myomesin (M-protein) 2 (165kD)	3.8
	100154	H80720	Hs.81892	KIAA0101 gene product	3.8
	106140	AB006624	Hs.14912	KIAA0286 protein	3.8
	129052	BE275031	Hs.158210	hypothetical protein MGC2555	3.8
65	103319	X83492	Hs.82359	tumor necrosis factor receptor superfam	3.8
	106319	W22335	Hs.7392	hypothetical protein MGC3199	3.8
	102391	AA256674	Hs.77494	deoxyguanosine kinase	3.8
	127282	AA828125		gbzcd71a09.s1 NCL_CGAP_Ov2 Homo sapiens	3.7
	126872	AW450979		gb:UL-H-BI3-sla-a-12-O-UL.s1 NCL_CGAP_Su	3.7
70	107315	AA316241	Hs.90691	nucleophosmin/nucleoplasm 3	3.7
	113119	T47910		gb:yb18b11.s1 Stratagene fetal spleen (9	3.7
	126962	R12014	Hs.20976	ESTs	3.7
	116203	AW137166	Hs.87305	ESTs	3.7
	123377	AW988183	Hs.271297	ESTs	3.7
75	122798	AW366286	Hs.145696	splicing factor (CC1.3)	3.7
	107780	AA018927	Hs.269213	ESTs	3.7
	132733	AB020631	Hs.123854	PCF11p homolog	3.7
	120649	AA687322	Hs.192843	leucine zipper protein FKSG14	3.7
	131163	AA099524	Hs.23754	ESTs	3.7
80	125708	AW962593	Hs.135280	ESTs	3.7
	117417	AI241733	Hs.43871	ESTs	3.7
	106272	AW959731	Hs.323099	ESTs	3.7
	110834	AW273860	Hs.5759	ESTs	3.7
	123663	AL039482	Hs.142517	Homo sapiens mRNA; cDNA DKFZp434P0810 (f	3.7
	124250	AA350256		EST, Weakly similar to 2109250A B cell g	3.7
	127038	AA233014	Hs.105965	ESTs	3.7
	107711	W98141	Hs.220687	ESTs	3.7

	130850	AB040922	Hs.20237	DKFZP566C134 protein	3.7
	119126	R45175	Hs.117183	ESTs	3.7
	125466	R08234	Hs.180461	ESTs	3.6
5	105150	AA631977	Hs.155995	KIAA0643 protein	3.6
	103163	AU077018	Hs.3235	keratin 4	3.6
	104495	AW975687	Hs.292979	ESTs	3.6
	107599	AW664072	Hs.60136	ESTs	3.6
	113577	A1300699	Hs.111334	PRO0470 protein	3.6
10	102681	Y08890	Hs.113503	karyopherin (importin) beta 3	3.6
	109411	R98881	Hs.109655	sex comb on middle (Drosophila)-like 1	3.6
	127563	AB035898	Hs.150587	kinesin-like protein 2	3.6
	131112	H15302	Hs.168950	Homo sapiens mRNA; cDNA DKFZp566A1046 (f	3.6
	141118	F01598	Hs.176930	ESTs	3.6
15	103937	AA934063	Hs.13836	ESTs, Weakly similar to L38022 hypotheti	3.6
	125174	W61835	Hs.231082	EST	3.6
	104799	AA029703		gb:ze95h08.s1 Soares_fetal_heart_NbHH-119W	3.6
	128952	AL043463	Hs.6755	RaP2 interacting protein 8	3.6
	135191	X18868	Hs.333497	cytochrome P450, subfamily 1D (debrisoq	3.6
20	124367	A1683183	Hs.99348	distal-less homeo box 5	3.6
	113560	T91015		ESTs	3.6
	119232	A1655226	Hs.117659	ESTs, Weakly similar to T46481 hypotheti	3.6
	113998	W87536	Hs.36473	ESTs, Weakly similar to JC5238 galactosy	3.6
	115173	BE612940	Hs.88262	ESTs	3.6
25	126600	AA699949	Hs.191385	ESTs	3.6
	127256	A1738610	Hs.267967	ESTs, Moderately similar to ALU8_HUMAN A	3.6
	123419	T66087	Hs.112482	Homo sapiens unknown mRNA sequence	3.6
	102025	U04045	Hs.78934	mutS (E. coli) homolog 2 (colon cancer,	3.6
	100661	BE623001	Hs.132748	Homo sapiens ribosomal protein L39 mRNA,	3.6
30	132339	D80030	Hs.45127	chondroitin sulfate proteoglycan 5 (neur	3.6
	116691	AW190215	Hs.62348	hypothetical protein FLJ11753	3.6
	134853	BE268326	Hs.90280	5-aminimidazole-4-carboxamide ribonucle	3.6
	134075	NM_012201	Hs.78979	Golgi apparatus protein 1	3.6
	128468	T23626	Hs.150580	putative translation initiation factor	3.6
35	127229	AA316181	Hs.61635	six transmembrane epithelial antigen of	3.6
	108451	AA079195		gb:zr9Zn12.s1 Stratagene ovarian cancer	3.5
	133421	AF134160	Hs.7327	claudin 1	3.5
	135332	AW393883	Hs.98968	hypothetical protein FLJ23058	3.5
	132620	AA257992	Hs.50861	Janus kinase 1 (a protein tyrosine kinas	3.5
40	125562	A1494372	Hs.98968	hypothetical protein FLJ23058	3.5
	126996	BE181065	Hs.167531	methylcrotonoyl-Coenzyme A carboxylase 2	3.5
	125558	R59305		gb:zh1Sc10.r1 Soares Infant brain 1NB H	3.5
	117265	AA451966		RA89-like protein	3.5
	130215	BE301883	Hs.152707	glioblastoma amplified sequence	3.5
45	109482	A1002236	Hs.11482	splicing factor, arginine/serine-rich 11	3.5
	133726	A1803188	Hs.252716	oxysterol-binding protein-related protei	3.5
	132317	BE262438	Hs.44592	beta-1,4 mannosyltransferase	3.5
	117613	AW028607	Hs.161102	ESTs	3.5
	100944	L07518		mucin 6, gastric	3.5
50	105226	R58968	Hs.26608	hypothetical protein MGC15880	3.5
	125032	T74884		gb:yc68d02.s1 Stratagene liver (937224)	3.5
	123720	AA609734	Hs.112755	EST	3.5
	128846	AA730767	Hs.285753	SCG10-like protein	3.5
	118443	AW982198	Hs.339808	LBP protein 32	3.5
55	128770	AB015982	Hs.143460	protein kinase C, nu	3.5
	106918	AA076049	Hs.274415	Homo sapiens cDNA FLJ10229 fs, clone HE	3.5
	131244	A1638429	Hs.24763	RAN binding protein 1	3.5
	128765	AF073310	Hs.143648	Insulin receptor substrate 2	3.5
	111223	AA652773	Hs.334838	KIAA1886 protein	3.5
60	104867	A1920802	Hs.19058	ESTs, Moderately similar to 585657 alpha	3.5
	105395	A1580880	Hs.288149	putative methyltransferase	3.5
	133582	BE391579	Hs.75087	Fas-activated serine/threonine kinase	3.5
	128527	AA504683	Hs.101047	transcription factor 3 (E2A immunoglobul	3.5
	105367	AA504747	Hs.136102	KIAA0853 protein	3.5
65	103392	X94683		gb:H.sapiens db/actbp gene exon 1 & 2.	3.5
	101086	AA382524	Hs.250959	histatin 1	3.5
	133423	T84084	Hs.196008	Homo sapiens cDNA FLJ11723 fs, clone HE	3.5
	117714	N45226	Hs.46495	EST	3.5
	110986	AL133117	Hs.81376	Homo sapiens mRNA; cDNA DKFZp596L1121 (f	3.5
70	114098	AF060219	Hs.27007	chromosome condensation 1-like	3.4
	117147	AW901347	Hs.38582	hypothetical protein FLJ23342	3.4
	133347	BE257758	Hs.71475	acid cluster protein 33	3.4
	132456	AB011084	Hs.48924	KIAA0512 gene product; ALEX2	3.4
	133765	M62194	Hs.75929	cadherin 11, type 2, OB-cadherin (osteob	3.4
	109734	A1927212	Hs.3734	ESTs	3.4
75	132788	BE083422	Hs.58851	hypothetical protein MGC2688	3.4
	106685	AU078617	Hs.16251	cleavage and polyadenylation specific fa	3.4
	105593	AA279341	Hs.174151	aldehyde oxidase 1	3.4
	131361	M92642	Hs.26208	collagen, type XVI, alpha 1	3.4
	108687	BE544475	Hs.54347	ESTs	3.4
80	113115	AF141426	Hs.8705	ESTs	3.4
	107234	AA972447	Hs.288833	Homo sapiens mRNA; cDNA DKFZp434K087 (fr	3.4
	123110	AA488258	Hs.193510	EST	3.4
	131019	W28614		chortonic somatomammotropin hormone 1 (p	3.4

5	129079	AK000157	Hs.108502	hypothetical protein FLJ20150	3.4
	111122	N63753	Hs.16492	DKFZP564G2022 protein	3.4
	103934	BE278111	Hs.134200	DKFZP564C186 protein	3.4
	128671	AI885045	Hs.211586	phosphoinositide-3-kinase, regulatory su	3.4
	123258	AA490929	Hs.105274	ESTs, Weakly similar to RMS1_HUMAN REGUL	3.4
10	128826	Z40313	Hs.106330	Homo sapiens clone IMAGE23371, mRNA seq	3.4
	120149	AA227609	Hs.94834	ESTs	3.4
	128817	BE395776	Hs.168640	apoptosis, progressive (mouse) homolog	3.4
	110679	AA004798	Hs.108311	ESTs, Weakly similar to T00351 hypotheti	3.4
	122385	AA813546	Hs.99034	GTP-binding protein Rho7	3.4
15	134455	BE378152	Hs.83530	hypothetical protein	3.4
	115506	AB037766	Hs.45207	hypothetical protein KIAA1335	3.4
	134267	AI174596	Hs.196209	RAE1 (RNA export 1, S.pombe) homolog	3.4
	106691	AA443164	Hs.23259	hypothetical protein FLJ13433	3.4
	105169	BE246284	Hs.180789	S164 protein	3.4
20	120120	BE547267	Hs.59791	hypothetical protein MGC13183	3.4
	126638	AA849257	Hs.86998	ESTs	3.4
	128531	H03721	Hs.63236	ribosomal protein S15a	3.3
	106650	AL049951	Hs.22370	Homo sapiens mRNA; cDNA DKFZp564O0122 (f	3.3
	108859	AL121500		ESTs	3.3
25	112276	R53442	Hs.26038	ESTs, Weakly similar to I38022 hypotheti	3.3
	125593	H23989	Hs.169743	Homo sapiens clone 25121 neuronal affact	3.3
	113474	R50752	Hs.23856	hypothetical protein MGC5297	3.3
	132994	AA112748	Hs.278905	clone HQ0310 PRO3310p1	3.3
	124691	R05835	Hs.110153	ESTs	3.3
30	112511	AW970420		dynactin 2 (p50)	3.3
	132985	AL045579	Hs.62113	KIAA0717 protein	3.3
	125743	H17151	Hs.7416	gbym37a05.r1 Scores Infant brain 1N1B H	3.3
	133363	AI868286	Hs.71962	ESTs, Weakly similar to B36298 prolina-r	3.3
	107908	AF087999		ESTs	3.3
35	105312	BE613348	Hs.211579	melanoma cell adhesion molecule	3.3
	110256	H83947	Hs.237955	RAB7, member RAS oncogene family	3.3
	132073	AA285052	Hs.38516	Homo sapiens, clone MGC15887, mRNA, com	3.3
	107090	AW809208	Hs.183297	DKFZP566F2124 protein	3.3
	105463	AA825974	Hs.32646	hypothetical protein FLJ21901	3.3
40	109592	AI198059	Hs.26370	ESTs	3.3
	113649	N94768	Hs.16400	ESTs, Weakly similar to KIAA1435 protein	3.3
	103898	AA248884		gb:k3517.seq.F Human fetal heart, Lambda	3.3
	116439	AA251594	Hs.43913	PIBF1 gene product	3.3
	129535	AA397972	Hs.112603	chimerin (chimaerin) 1	3.3
45	113283	T66813	Hs.12947	EST	3.3
	128992	H04150	Hs.107708	ESTs	3.3
	133180	N54868	Hs.66309	hypothetical protein MGC11061	3.3
	134076	AF086215	Hs.78980	gb:homo sapiens full length insert cDNA	3.3
	128301	U90552	Hs.284283	butyrophilin, subfamily 3, member A1	3.3
50	127728	AW404061		protein kinase C, beta 1	3.3
	126516	R95872	Hs.117572	chemokine binding protein 2	3.3
	127506	T61039	Hs.76057	ribosomal protein L10a	3.3
	104769	AA025887	Hs.293943	hypothetical protein MGC11266	3.3
	126666	AA648986	Hs.151999	ESTs	3.3
55	130453	U80735	Hs.173854	PAX transcription activation domain inte	3.3
	107131	AW981605	Hs.21145	hypothetical protein RG083M05.2	3.3
	130422	AW160614	Hs.180034	cleavage stimulation factor, 3' pre-RNA,	3.3
	121292	AA401807		gb:cv6511.s1 Scores_totat_fetus_Nb2HFB_	3.3
	123284	AA488986	Hs.293796	ESTs	3.3
60	130734	AW137091	Hs.18624	KIAA1052 protein	3.3
	105400	AF198620	Hs.10283	RNA binding motif protein 8A	3.3
	106014	AA121123	Hs.269267	ESTs, Weakly similar to AF161361 1 HSPC0	3.3
	114988	AA251089		gb:zstd405.s1 NCL_GCAP_GCB1 Homo sapiens	3.3
	132867	AF226667	Hs.58553	CTP synthase II	3.3
65	124169	BE079334	Hs.271630	ESTs	3.3
	114652	AI521936	Hs.107149	novel protein similar to archaeal, yeast	3.3
	113876	AI799751	Hs.5635	ESTs	3.3
	111520	AI985359	Hs.301134	ESTs	3.3
	121748	BE536911	Hs.234545	hypothetical protein NUF2R	3.3
70	106834	AL044182	Hs.28070	KIAA0753 gene product	3.3
	128869	AA788242	Hs.80618	hypothetical protein	3.3
	129519	AA208534	Hs.264243	tetraspan NET-6 protein	3.3
	126770	AI282320	Hs.81361	heterogeneous nuclear ribonucleoprotein	3.3
	116734	AW900992	Hs.93798	DKFZP586D2223 protein	3.3
75	100253	D38024	Hs.157425	double homeobox, 2	3.3
	130999	AA326683	Hs.21992	likely ortholog of mouse variant polyade	3.3
	114092	H81213	Hs.14825	ESTs, Weakly similar to KIAA1503 protein	3.3
	129284	AA318224	Hs.288141	ESTs	3.3
	119127	AA708036	Hs.12248	ESTs	3.3
80	123910	AA621262	Hs.179923	ESTs, Weakly similar to S65557 alpha-1C-	3.3
	132664	AI740461	Hs.54542	ESTs	3.3
	116397	BE139479	Hs.161492	ESTs	3.3
	107003	AW138437	Hs.24790	KIAA1573 protein	3.3
	126735	M69113	Hs.226795	glutathione S-transferase pi	3.2
	130847	AI672483	Hs.20220	lipase protein	3.2
	101186	AA020956	Hs.179881	core-binding factor, beta subunit	3.2
	113628	T94318	Hs.17359	ESTs, Moderately similar to RL44_HUMAN 6	3.2

	121782	AW452957	Hs.63348	Homo sapiens, clone MGC:15203, mRNA, com	3.2
	119863	AA081218	Hs.58608	Homo sapiens cDNA FLJ14206 fis, clone NT	3.2
	106103	BE620779	Hs.12094	mitochondrial ribosomal protein L30	3.2
5	123808	AA620552		gb:ae5Bg11.s1 Stratagene lung carcinoma	3.2
	133761	AF041430	Hs.75922	brain protein 13	3.2
	110661	AA379597	Hs.5199	HSPC150 protein similar to ubiquitin-con	3.2
	115239	BE251328	Hs.73291	hypothetical protein FLJ10881	3.2
	117457	N29882	Hs.44071	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.2
10	128862	BE250742	Hs.106673	eukaryotic translation initiation factor	3.2
	129673	D38552	Hs.1191	KIAA0073 protein	3.2
	105154	AA307279	Hs.35947	methyl-CpG binding domain protein 4	3.2
	126722	N66148	Hs.11125	HSPC033 protein	3.2
	109966	H09103	Hs.30897	EST	3.2
15	129315	NM_014563	Hs.174038	spondyloepiphyseal dysplasia, late	3.2
	109617	A1631874	Hs.155140	casein kinase 2, alpha 1 polypeptide	3.2
	105252	AB039570	Hs.9728	ALEX1 protein	3.2
	101754	S70114	Hs.239489	TIA1 cytotoxic granule-associated RNA-bi	3.2
	110384	H45282	Hs.268798	ESTs	3.2
20	134118	BE336680	Hs.182877	KIAA0116 protein	3.2
	134869	AL157518	Hs.90421	PRO2463 protein	3.2
	100780	BE561958	Hs.293441	immunoglobulin heavy constant mu	3.2
	125728	AW954565	Hs.57987	B-cell CLL/lymphoma 11B (zinc finger pro	3.2
	129794	AF161399		hypothetical protein FLJ13433	3.2
25	129056	AJ769958	Hs.108336	ESTs, Weakly similar to ALUE_HUMAN III	3.2
	107129	AC004770	Hs.4756	flap structure-specific endonuclease 1	3.2
	103038	AA926960		CDC28 protein kinase 1	3.2
	130653	AF082649	Hs.252587	pituitary tumor-transforming 1	3.2
	125394	BE178502	Hs.173772	ESTs, Weakly similar to I76885 serine/th	3.2
30	132305	AJ808090	Hs.44344	hypothetical protein FLJ20534	3.2
	131136	AB033089	Hs.23413	KIAA1273 protein	3.2
	102983	BE387202	Hs.118638	non-metastatic cells 1, protein (NM23A)	3.2
	117639	AA377165	Hs.44833	ESTs	3.2
	127076	AJ422951	Hs.146162	ESTs	3.2
35	126153	H85692	Hs.40730	ESTs	3.2
	132676	N92589	Hs.281038	ESTs, Weakly similar to I38022 hypotheti	3.2
	104946	AW242407	Hs.73848	cardioembryonic antigen-related cell ad	3.2
	122110	A1123000	Hs.301240	melanocortin 1 receptor (alpha melanocyt	3.2
	127705	AJ003322		gb:AJ003322 Selected chromosome 21 cDNA	3.2
40	109442	AW296134	Hs.86999	ESTs, Weakly similar to S65857 alpha-1C-	3.2
	100474	NM_000699	Hs.300280	amylase, alpha 2A; pancreatic	3.2
	115536	AK001468	Hs.82180	anillin (Drosophila Scars homolog), act	3.2
	119651	AW663858	Hs.333513	small inducible cytokine subfamily E, me	3.2
	127211	AA305520	Hs.108612	hypothetical protein FLJ22004	3.2
45	134984	AJ803516	Hs.272891	hippocalcin-like protein 4	3.1
	105551	AW005822	Hs.25292	ribonuclease H1, large subunit	3.1
	119750	AJ538880	Hs.94612	ESTs	3.1
	125590	R23858	Hs.143375	Homo sapiens, clone IMAGE:3840937, mRNA,	3.1
	104590	AW373052		nuclear receptor subfamily 1, group 1, m	3.1
50	110724	AW016783	Hs.30799	Homo sapiens cDNA FLJ13471 fis, clone PL	3.1
	118429	AF191018	Hs.275923	putative nucleotide binding protein, est	3.1
	133915	AA815092	Hs.77554	Homo sapiens cDNA FLJ14967 fis, clone TH	3.1
	123721	AW403911	Hs.266175	phosphoprotein associated with GEMs	3.1
	128538	R44214	Hs.101189	ESTs	3.1
55	129179	AW959025	Hs.109154	ESTs	3.1
	108793	AA129395	Hs.71139	ESTs	3.1
	108807	AJ652236	Hs.49376	hypothetical protein FLJ20844	3.1
	133461	NM_000782	Hs.334345	cytochrome P450, subfamily 11A (phenobar	3.1
	132571	AW674699	Hs.5169	suppressor of G2 state of SKP1, S. cere	3.1
60	134937	AJ251449	Hs.171939	ESTs	3.1
	125766	BE174587	Hs.289721	growth arrest specific transcript 5	3.1
	112369	AW966243	Hs.4243	hypothetical protein FLJ12850	3.1
	127002	AL353940	Hs.24979	hypothetical protein DKFZp761P1010	3.1
	128179	AW293689	Hs.127116	ESTs	3.1
65	117121	H95044	Hs.321386	EST	3.1
	128556	AF255303	Hs.112227	membrane-associated nucleic acid binding	3.1
	128403	AJ908008	Hs.295382	Homo sapiens cDNA FLJ14459 fis, clone HE	3.1
	127930	AA809672	Hs.123304	ESTs	3.1
	114250	AJ914699	Hs.13297	ESTs	3.1
70	108828	AK001693	Hs.273344	DKFZP564O0463 protein	3.1
	105225	AA211777		gb:u57d02.s1 Stratagene muscle 937209 H	3.1
	117997	N52090	Hs.47420	EST	3.1
	104558	R58878	Hs.88959	hypothetical protein MGC4816	3.1
	124777	R41033	Hs.140237	ESTs, Weakly similar to ALU1_HUMAN ALU S	3.1
75	106035	N35568	Hs.5245	hypothetical protein FLJ20643	3.1
	127521	AW297206	Hs.164018	ESTs	3.1
	120215	AF109219	Hs.108787	phosphatidylinositol glycan, class N	3.1
	119403	AL117554	Hs.119908	nuclear protein NOP5/NOP58	3.1
	105024	AA126311	Hs.9879	ESTs	3.1
80	123485	AJ308876	Hs.103849	hypothetical protein DKFZp761D112	3.1
	109416	BE268388	Hs.86945	ESTs, Weakly similar to A46010 X-linked	3.1
	132490	NM_001290	Hs.4980	LIM domain binding 2	3.1
	115348	AA281562	Hs.766	ESTs	3.1
	117297	AW779829		gb:hm88a05.x1 NCI_CGAP_Kit11 Homo sapien	3.1

5	112501	AA972447	Hs.288833	Homo sapiens mRNA; cDNA DKFZp434K087 (fr	3.1
	107532	AAA43473	Hs.173684	Homo sapiens mRNA; cDNA DKFZp762G207 (fr	3.1
	130753	AA205223	Hs.189	phosphodiesterase 4C, cAMP-specific (dun	3.1
	132425	N87549	Hs.125287	zinc finger protein ZNF140-like protein	3.1
	115188	AK000219	Hs.88367	hypothetical protein FLJ120212	3.1
	129707	AI9572317	Hs.12082	Homo sapiens mRNA; cDNA DKFZp566L203 (fr	3.1
	106474	BE383668	Hs.42484	hypothetical protein FLJ10618	3.1
	106472	AI207162	Hs.3815	stathmin-like protein RB3	3.0
10	102687	NM_007019	Hs.93002	ubiquitin carrier protein E2-C	3.0
	117602	N35020	Hs.44685	C3HC4-like zinc finger protein	3.0
	105522	W19789	Hs.336535	Homo sapiens, clone IMAGE:4179482, mRNA	3.0
	133650	D84294	Hs.118174	tetratricopeptide repeat domain 3	3.0
	134624	AF035119	Hs.8700	deleted in liver cancer 1	3.0
15	112435	NM_013255	Hs.288791	muskelin 1, intracellular mediator conta	3.0
	134654	AK001741	Hs.8739	hypothetical protein FLJ10879	3.0
	106651	AA460421	Hs.30875	ESTs	3.0
	109597	AA989362	Hs.293780	ESTs	3.0
	132342	AW162758	Hs.341729	ESTs, Weakly similar to ALU5_HUMAN ALU S	3.0
20	106057	BE614474	Hs.289074	F-box only protein 22	3.0
	106378	AA824288	Hs.21331	hypothetical protein FLJ10036	3.0
	126560	AA011597	Hs.177398	ESTs	3.0
	115467	AI366784	Hs.48820	TATA box binding protein (TBP)-associate	3.0
	128004	AI879099	Hs.102397	GIOT-3 for gonadotropin inducible transc	3.0
25	125219	AI804331	Hs.99423	ATP-dependent RNA helicase	3.0
	126598	AI221147	Hs.145088	ESTs, Weakly similar to T15936 hypothe	3.0
	133966	BE280478	Hs.182895	hypothetical protein MGC3243	3.0
	119165	R61715	Hs.310558	ESTs, Moderately similar to ALU1_HUMAN A	3.0
	131580	AA460352	Hs.26866	KIAA1171 protein	3.0
30	100237	D30715		Human PAP (pancreatitis-associated prote	3.0
	105515	T24968	Hs.23038	HSPC071 protein	3.0
	123073	AA485061	Hs.105652	ESTs	3.0
	111375	H56499	Hs.252692	ESTs, Weakly similar to I38022 hypothe	3.0
	130724	AK001507	Hs.44143	Homo sapiens clone FLB6914 PRO1821 mRNA,	3.0
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	118922	AW206193		hypothetical protein DKFZp76182423	3.0
	131902	AA180145	Hs.34348	Homo sapiens mRNA; cDNA DKFZp434P0235 (f	3.0
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	122219	AA438002	Hs.183161	ESTs	3.0
40	132195	BE018717	Hs.42124	ESTs	3.0
	102298	AA382169	Hs.54483	N-myc (and STAT) interactor	3.0
	103286	D38616	Hs.54941	phosphorylase kinase, alpha 2 (liver)	3.0
	130168	AK001389	Hs.15144	hypothetical protein DKFZp5640043	3.0
	126897	AI377150	Hs.150914	ESTs	3.0
45	128902	AA036637	Hs.107052	ESTs	3.0
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	126595	NM_003478	Hs.101289	cullin 5	3.0
60	123470	AW303285		Human DNA sequence from clone RP11-110H4	3.0
	109252	BE440157	Hs.85944	ESTs	3.0
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	102126	AW950870	Hs.78961	protein phosphatase 1, regulatory (inhib	3.0
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	105968	H09232	Hs.26484	HIRA-interacting protein 3	3.0
	125770	AA143045	Hs.81685	v-kit Hardy-Zuckerman 4 feline sarcoma v	2.1

TABLE 71B

Pkey: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

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114988	genbank_AA251089	AA251089
123423	genbank_AA588484	AA588484

Table 72A shows the Seq ID No, Pkey, ExAccn, UnigenelD, and Unigenes Title for all of the sequences in Table 73.

80	Pkey:	Unique Eas probaset Identifier number
	ExAccn:	Exemplar Accession number, Genbank accession number
	UnigenelD:	Unigenes number
	Unigenes Title:	Unigenes gene title

Seq ID No: Seq ID number correlation for those sequences in Table 73

Pkey*	ExAcon	UnigeneID	Unigene Title	Seq ID No
5	103080	AU077231	Hs.82632 cyclin D1 (PRAD1; parathyroid adenomas	Seq ID No B1 & B2
	410102	AW248508	Hs.279727 ESTs; homologue of PEM-3 [Clona savignyi	Seq ID No B3 & B4
	101104	AW862258	Hs.169266 neuropeptide Y receptor Y1	Seq ID No B5 & B6
	447761	AF061573	Hs.18492 protocadherin 8	Seq ID No B7 & B8
10	428183	AW969726	Hs.58381 ESTs, Weakly similar to serine protease	Seq ID No B9 & B10
	439221	AA737106	Hs.32250 ESTs, Moderately similar to I7885 serin	Seq ID No B11 & B12
	121619	AA526339	Hs.178062 ESTs, Weakly similar to phosphatidyleri	Seq ID No B13, B14, & B15
	104659	AW969769	Hs.105201 ESTs	Seq ID No B16
	105782	H09748	Hs.57987 B-cell CLL/lymphoma 11B (zinc finger pro	Seq ID No B17 & B18
15	129977	NM_000399	Hs.1395 early growth response 2 (Krox-20 (Drosop	Seq ID No B19 & B20
	100299	D49493	Hs.2171 growth differentiation factor 10	Seq ID No B21 & B22
	116301	AW969706	Hs.293332 ESTs	Seq ID No B23 & B24
	106533	AL134708	Hs.145998 ESTs	Seq ID No B25-B27
	131313	R96290	Hs.75874 ribosomal protein L44	Seq ID No B28 & B29
20	105316	AI671245	Hs.24835 hypothetical protein FLJ14594	Seq ID No B30 & B31
	113003	AW292315	Hs.7215 ESTs	Seq ID No B32
	102838	U94320	Hs.158330 neuropeptide Y receptor Y5	Seq ID No B33 & B34
	102745	AW753865	Hs.74376 olfactomedin related ER localized protei	Seq ID No B35-B40
	123308	C14187	Hs.157208 ESTs	Seq ID No B41 & B42
25	120147	AJ917115	hemoglobin, beta	Seq ID No B43
	123049	BE047680	Hs.211869 dkkkopt (Xenopus laevis) homolog 2	Seq ID No B44 & B45
	119082	AF252297	Hs.91546 cytochrome P450 reductase metabolizing pr	Seq ID No B46 & B47
	105301	AW352357	Hs.7457 MAGE1 protein	Seq ID No B48 & B49
	128478	AA708205	Hs.100343 ESTs	Seq ID No B50-B53
30	106111	AW875398	Hs.6451 PRO0859 protein	Seq ID No B54 & B55
	131307	NM_000025	Hs.2549 adrenergic, beta-3-, receptor	Seq ID No B56 & B57
	120830	AI568170	Hs.96886 ESTs	Seq ID No B58 & B59
	127664	AA806164	Hs.116502 ESTs	Seq ID No B60
	102725	AB026187	Hs.159156 protocadherin 11	Seq ID No B61 & B62
35	132520	AA257992	Hs.50651 Janus kinase 1 (a protein tyrosine kinas	Seq ID No B63 & B64
	130637	AA356764	Hs.17109 integral membrane protein 2A	Seq ID No B65 & B68
	117802	N35020	Hs.44695 C3HC4-like zinc finger protein	Seq ID No B67 & B68
	128797	NM_002975	Hs.105827 stem cell growth factor; lymphocyte secr	Seq ID No B69 & B70
	129703	BE388865	Hs.179999 Homo sapiens, clone IMAGE:3457003, mRNA	Seq ID No B71 & B72
40	125770	AA143045	Hs.81866 v-kit Hardy-Zuckerman 4 feline sarcoma v	Seq ID No B73 & B74
	414761	AI077228	Hs.77256 enhancer of zeste (Drosophila) homolog 2	Seq ID No B75 & B76
	420462	AF050147	Hs.97532 chondromodulin 1 precursor	Seq ID No B77 & B78
	410268	AA316181	Hs.61835 six transmembrane epithelial antigen of	Seq ID No B79 & B80
	104681	U29590	Hs.37744 Homo sapiens beta-1 adrenergic receptor	Seq ID No B81 & B82
45	416836	D54745	Hs.30247 cholecystokinin	Seq ID No B83 & B84

Table 72B

Play: Unique Eos probeset identifier number
 CAT number: Gene cluster number
 Accession: Genbank accession numbers

	Pkey	CAT Number	Accession
55	131307	3138_1	NM_000025 X72881 X70811 M29932 X70812 S53291 AW015148 AW581776 AI276134
	131313	93372_1	R06290 H02411 C18327 AA357588 AA367657 H89632 C17954 AA568860 AI752083 AA599451 H04280 AI128118 AW193364 N94503
			AA029995 T40538 AA368746 AI189909 BE047384 AA747591 R22855 AI032539 AI151343 AA148534 H63941 T49595 AA694405 H74226
			AI200363 R79731 AA702947 AI400076 AI088494 C17938 AA599478 H02962 R77665 C17370 R66818 H73711 R58545 D79189 AW265710
			R77684 T52101 AW953745 AW953739 D79107 AA029105 AW953738 AA456487 R67000 AA156823 AA368336 H63662
	116301	62669_2	AW969706 AA456258 AA491881 BE501639 D62113 AW969710 AI591236 AI379869 AW969697 AA040063 AI807206 AW663917 AA454645
			AA489238 BE241958 AA743491
60	103080	17092_1	AU077231 AA852219 M74092 X69798 M64349 NM_001758 AA228806 M73554 BE409154 AA160096 BE384352 AA160620 BE382880
			BE261734 AA113821 BE407745 AA156380 BE390287 BE390020 AA100854 AA127152 AW794066 AW367101 AW367093 U47703 AI347077
			W05266 AI824103 AI489061 AA642944 AI042553 AA906539 W60380 AI571777 AI135581 AA112340 W75469 AA582929 AI085348 AI278890
			AA126942 AI023701 AI873252 AA156319 AI180622 W60289 AI274886 R81309 AA100601 AA227161 AI566929 AA160603 AI074344 AI344581
			AI150778 AA852218 AA158286 N20142 AA622148 AA854225 AA576367 AW182124 T89175 AI758455 AA780573 N71757 R81200 AI669636
			AI674613 AA642544 AW503909 AA128851 W39350 N40420 AA113072 BE168116 AI620504 AI298125 BE075272 N40078 BE075109 BE060779
			AI918938 BE168117 BE087369 AW955539 BE080949 BE080727 BE075271 BE075108 BE080955 BE089655 BE081115 AW750304 H86084
			AI146884 BE075154 AW992247 AI188525 AI752230 AW283140 W03329 N26056 AA948080 AA113073 H98284 AA227101 AA631077
			AA148042 AI740837 BE087278 AA149570 W44495 BE089351 AA376044 N25775 H27771 AA064705 BE091204 R89337 N32676 N27141
70			BE164704 H88049 W67603 AA425549 W31090 AA807411 BE173280 BE000178 T08020 W23852 AA082709 BE167894 AA076515 R97329
			BE541980 N42086 AA102307 AA113772 BE276181 H20622 W44436 W67604 W45412 AW771113 AI700678 AA602628 AA133137 BE274186
			BE396090 BE013371 BE612645 W46650 W95203 W92651 AI087288 R76299 AW604781 N55320 AI912334 AA403248 AW189156 H24970
			AW298822 AW080962 AI073747 W24123 AA577586 H21715 H27925 H26436 AI288304 AA148043 AA204678 BE047090 W49531 AA908347
			AA599485 AI276505 AI953979 AA563710 H25674 H51747 AA425389 AA516104 AI095335 T77237 AA151696 T32084 AI689037 AI624162
			W49709 AW514883 AA100676 AI366087 AAC69474 AA525859 AW771076 AA029402 AA994114 AI351505 AW770816 AI333694 AI289794
			AI346589 AA487700 AI081104 AA613344 AI377520 AI284911 AI311390 AA622062 AI055890 AI660881 AI368117 AA403090 AI272818
			AI073353 W46300 AA062689 AI755078 AI753397 AI633564 AI273471 AI339890 AA699584 AA983722 AI079958 AI752231 AA076431 AA113245
			AI168564 AA918965 AI066484 AI123599 AI921510 W94588 AA535600 AA064665 AA705388 AA064623 AA962503 AI924928 AW131205
			AW275281 AI280632 T29597 W48728 W954336 W39317 W94768 AI084717 W46567 AI245545 AW302501 N72201 AW510563 AW079132
			AA207054 AI143740 AW440672 AA632154 AI290286 AI350704 AI271377 AA025369 AI864756 T77451 H97348 AA852165 AI932951 N98526
			AA487486 R92970 AA934071 AI080448 AA063257 C05788 N99089 RA2969 AA887085 AA862686 AA533833 AA682304 H51748 BE539444
			AI382164 AI814595 BE537043 AI168307 BE408935 AA453506 R89428 AA936527 AA936890 AW369618 AW264602 R18074 AI474189
			AW372354 AI094358 R37210 AA948510 AA226909 BE172527 AI086852 BE406324 AW292848 AI768962 BE540703 BE409478 AA931692

132520	45737_1	AA257992 AA317029 AA362097 D17042 H48100 AW638107 AW838105 AW838110 AW838231 AW610241 AW838442 AA045061 AW384991 BE00088 AA131806 BE180577 AW838269 AL039831 AJ754380 C06051 AA131737 AW838239 AJ767465 AJ60134 AA610312 AW838190 AA379252 AW838282 AA484027 AJ423413 AJ685064 BE328307 AJ241857 AW838281 AW838284 AJ671267 AJ814928 AA283367 AJ476306 AJ270180 AA622362 AJ076497 AJ635919 AJ444994 AJ194028 AJ669159 AJ926131 AA448853 AJ350143 AW079289 AW467807 AA480442 AA522835 BE180570 AW380087 AW389109 AJ081015 AJ690818 AJ589485 AJ698510 AA642019 AA714366 AJ680430 AA985527 AJ740475 C21398 AA257993 AJ302393 AJ689018 AW770194 AW753750 AJ079164 BE550338 AA559851 T18108 AJ684022 AJ932827 AA045095 AA045082 AJ954225 AA768569 AA709308 AW958363 N35020
5	117602 10565_4 102725 11582_1 102745 13186_1	AB026187 NM_014522 U79247 F13304 AA224524 F10902 R39431 AW753865 F07644 F11280 F06355 F08136 U79289 F07459 F08750 F12419 F12842 F06488 F06585 F13403 F05921 F05512 F11683 F05416 F12841 F12810 F05418 F12850 R24561 F06276 H11803 H10237 H11542 H22894 R59563 H19351 H18722 F11237 F08507 H23129 R61595 F07796 F06201 F12289 F07107 T78113 F08734 F13344 F05760 F11784 F08780 F05836 R20568 F07739 F11497 R17410 H17414 R20440 T66090 R25292 T66236 T78766 T79908 R25286 R80071 C14761 AW905192 AA331914 AW965291 H08000 F05212 F08313 F05825 H06399 H15135 H11378 R66424 R61541 AA235405 AJ205041 R59564 H23124 H18638 R37359 AJ571275 RA1780 T86174 T88159 R54102 W07657 H10784 R52337 R42890 H14354 R40952 T17391 H12068 R56797 R51000 R80011 R37817 R39434 H22826 T16403 H09128 R49114 H15161 H11729 R39160 H10468 H24454 H11432 R54433 H08768 H24042 H09511 H17281 H15292 R37849 AJ991985 R52815 R42850 T17390 T16438 T17388 T16285 R48963 R50782 R44247 R46729 R59558 R40696 R43575 R44420 T17403 R37764 R46637 R51039 R40513 T23785 F10433 T16360 H10181 R43688 T23543 H08591 R44351 R37575 R49506 F04379 F04058 F05067 F02010 F09158 F10036 F08900 F02559 F09914 F09434 F05034 H17415 F02644 H10650 F10451 H14589 F10444 T16440 R44517 R48643 F03988 F10443 F02170 F09343 F10414 F04794 F11122 F04997 F03894 AW005932 F02767 F10941 F01777 R45260 F03386 R45261 T65009 F10990 F08942 F01673 H23263 F04533 F02082 F01669 F03889 H09568 R40763 H06400 R50958 N80570 AJ082296 AJ188226 T23763 AA814486 AW015623 AJ886272 H08514 AA515969 F10049 AJ984267 AJ886279 AA568516 F02071 AJ783943 AJ804884 F01468 AA730438 AF035031 F03889 R41440 R59465 R14437 T89036 R43560 H10821 R52850 R56722 R14559 T09299 H10467 R25829 F13548 R56796 R51151 D82657 T32952 T66257 H05669 F12430 T74326 H08499 R34430 R13083 H23364 R21134 T77098 AW957157 H24150 H11403 R52336 F12830 T77173 T74281 T77663 T74736 H10649 H12087 R20092 T74736 R54530 T77552 R56529 H17280 T75171 H14894 T74975 H15281 R18574 R54157 R13446 H16221 R35120 R35031 R21277 R19632 R36820 R50899 R13923 R36771 R26485 R33061 R20100 H24426 H09184 H16958 R19263 H15156 H09510 R36032 R19891 H14402 H14885 T17068
10		AF252297 N27888 F13415 R34552 R14377 AA323962 AW611514 AW814097 AW195487 AJ028040 AJ097663 AA012834 AW969885 AA968198 RA9069 AW873673 R37774 F08840 AA484668 AW873684 AA170805 AA170825 AA565275 AA565280 AA012833 U94320 NM_006174 U66275
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20		AJ817116 AA633686 AJ580389 Z39483 AW292315 AJ090408 AW517041 AJ928695 AJ092060 AA718741 N98235 T23629 AW969789 AA484137 AJ291362 N64753 AL133784 AA007153 BE046923 D59990 C15166 D59991 D60194 AA648108 N76160 D61027 D60630 U26880 AF272890 AA708168 AA010748 R23839 H59572 R23833 AJ625747 AA011176 AW685324 H02674 H59573 AA757831 H12502 R66851 AA702310 AA748431 AA749352 C01127 AJ003679 T96352
25		AW352357 AA862419 T80568 AA332510 AW149659 AA341609 AA809550 AJ183690 AA730875 T31719 AW965361 AA779709 T05481 AA564806 AH142536 AJ553857 D53384 D53747 D54101 D55112 AW071935 AJ082447 AJ290911 AW188872 AA199743 AJ091646 AJ246702 AZ71662 AW117296 AJ032138 AJ741469 AJ538705 AA233541 AJ862685 AW138288 AJ689541 AA599916 AJ174443 AJ432176 AJ131328 AW136277 AA852418 AA243035 T03902 C15651 D52660 H08108 AA844525 AA20648 AJ262445 AW068986 AW497637 AA779042 AA298564 BE262936
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35	120147 386807_2 113003 420161_1 104659 82594_1 104691 41308_1	AA806184 AA878584 AW978234 AW023951 AA651859 AJ699785 AA913686 AW974569 AJ681287 AW876398 AJ064661 NM_014138 AF090943 BE071887 BE547232 BE622589 AJ345700 AA284315 AA147700 AW376340 BE220170 BE348475 AA025037 AA057284 AA025038 T16193 AW130196 AW594516 AJ899991 AJ139091 AW875747 AA330435 AJ24977 AJ670778 AJ051887 AA912574 AW130213 AJ828335 AJ570587 AJ332760 AJ313115 AA904653 AA477920 AA147645 AJ916912 AW768839 AA715098 AA292723 AA732421 T33122 AJ631560 AJ698686 AJ185386 RA3829 AA421638 AA961400 C00503 AA604025 AA554028 AA553885 BE172244 R24040
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75	100299 2801_1 129977 2039_1	AA278541 R76523 AA665187 H85083 F24755 R77729 AA135137 BE250395 R76239 AW794625 AW794404 H61957 AA308197 AW996031 AA345524 N52726 AA354360 AA179785 N57375 R16447 AA160645 W21481
80	123308 322009_1 101104 26442_2 130637 7040_1	D49493 NM_004962 D49492 AA948479 AA993843 AA017558 AA992567 AA912897 AJ185383 AA018264 N93253 AA297544 T19187 R53287 AA069337 AA297489 N62906 AW023929 AA018253 AA017615 W25110 R52085 R52633 W16549 H88918 H89134 AA089338 NM_000399 AA018140 AF139463 JD4076 AW390694 AW361756 AL079830 AJ190587 AJ731059 AA742743 AJ1835915 AA878209 AJ262612 AJ284201 AA446300 AA715016 AA448027 AJ274101 AA593330 AA593338 AW015388 AJ881724 AJ347884 AL045275 AA970069 AA018188 AW014396 AW769445 AJ588869 AW336296 AJ801548 AJ367702 AJ884410
		C14187 AA498211 D80456 AA484051 D80455 AA528446 AW882258 L07615 AA355764 NM_004867 AF038953 W16828 R50284 AJ929589 R01594 AA010474 W37917 N64212 N78175 R57511 AA329322 W77834
		AA169869 AA285240 AA366670 T93146 AA325779 AA357064 AA328151 AA306939 AA306801 N31280 AA306202 AA312530 BE242703 AA364371 N42259 AL021786 H50985 H38038 AJ655965 AJ586732 AJ953982 AW972835 AJ077300 AJ940482 AJ709066 AA648335 W72197 N32815 AA768073 AW338181 AW001742 AJ181996 AJ015666 N58011 AA677584 AJ183750 AW105514 W37875 AW331679 AA775257

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		AA773947 AA469192 AI199289 AI127085 H89232 N30719 AK028165 AW029469 AI709314 AA780834 AA778057 H89125 AI654762 T93061
		N59622 AI366625 AA719982 AI248242 AA233925 AW262512 AW438666 AA010378 AA484010 AW438790 N22875 AA483718 AI185407
		AA736720 AA684587 AA648672 AA503406 AA508123 AA503140 H46638 N75812 AA730938 D60548 AA483039 AA507705 AA480448
		AI768654 AA658955 AA730803 AA330312 AW021127 BE172031 AW961052 AA339070 AA648172 BE172692 AA174175 AA492012 AA491590
		AW116733 AA484130 AA730783 AA730510 D62577 D62828 AI469294 AI801343 N53447 AA740226 AI831983 AA516146 D79799 AI758212
		AA484040 H38039 AI038772 AI039410 AA528387 AA730576 AA527231 AA748111 D62946 U36439 AA721708 H22130 AA559229 H51620
		AA283355 AA730970 R01595 N72450 AA469123 AA579359 AA480477 AA283306 AA347822 AA328013
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	410258	11897_1
	414761	14860_1
		AW248508 AI278454 AI369343 AW291235 AI343946 AI347189 AA970152 AI279668 AI971894 AA664359 AI191039 AA084598 AA081641
		AA316181 BE439545 AC005053 AF186249 AW386101 AC004969 AA730199 AA032221 AI666139 AI167942 AA809228 AI184070 AI394674
		AW969977 AA032279 AW079284 AA513174 AA888312 AI453179 AA483363 AA528432 AA578511
		AU077228 U61145 AL044256 AA206185 AL044975 NM_004456 X95653 AW890905 AA332806 AW965453 BE289226 U52865 BE275009
		AA428252 AA769212 AA312778 AA810901 AA461315 AI959286 AI953668 AW295248 AI291422 AA704747 Z44716 BE541235 AW608806
		AA588563 AW403768 AW408386 AA053521 T87571 AA581163 BE183241 T97906 R89149 AI808196 BE618521 AI970278 AI652680 AW130143
		AI970272 AW187254 BE550449 AI628403 AA010143 AW005107 AA251815 AA805836 N53459 AA055309 AA643678 AI345816 AI345618
		AI635728 AI871286 AI018437 AI262614 H75287 AI033155 AI203388 AA205802 AI475265 AW594186 AI696069 AI333312 AW264710 AA876764
		AA864892 AA173153 AI292066 T79837 W93985 AA506427 AA815135 AI376342 AA010144 AI310421 AI223350 AA970576 N33926 T88364
		AI050913 N55088 AA101673 AA626665 AA251840 N88857 AI890053 H05930 AI474199 AI436166 AA628810 N64452 AI205538 AA055310
		BE244495 AI365179 T99536 AI203088 Z40549 AW139858 AA599527 R91847 AA483681 AW068982 H51748 AA091201 H13030 AA459732
		T99430 AI051764 R45991
	416836	16233_1
		D54745 AU077189 NM_000729 R71188 H87563 R80701 AW956319 AA376289 R82442 H46452 R22481 R64323 AW043690 L00354 AW005571
		H19813 AI745597 AI769202 AI205982 AW205841 R64324 AI201975 H46993 C18067 R71189 N29729 AI799838 AI091209 H87455 R82443
		AW970995 AW072136 N40841 H13148 AI219052 N30191 T28007 AI817428 AA503602
	420462	18379_1
		AF060147 NM_007015 AB006000 AB005989 BE218114 AI703147 AI985891 BE222034 BE549774 BE327618 AI651459 BE549987 AI657194
		BE222414 BE046984 AW470357 AW339338 C02526 AW590220 AI298082 AW286998 AI333135 AI867818 AA730514 BE348513 AA405500
		AW136179 AA327834 BE327350 BE327366
	428183	287965_1
	439221	46993_1
		AW969728 AA424028 AI266636 AI271571 AA423988 AI286634 AA702780 AA452037 AI424856 AA742931 AA483361
		AA737106 N35765 N35779 AF086045 N30152 AW374028 AI478237 AA923582 AI382236 AA846668 AI627389 AI371709 H98083 H95983
		H26576 H95984 AA745021 AA639180 H26575
	447761	7355_1
		AF061573 NM_002590 AA780138 AW135620 AI197684 AA483348 R05468 AW969724 H29216

Table 73: Sequences

Seq ID NO: B1 DNA sequence

Nucleic Acid Accession #: NM_053056.1

Coding sequence: 210..1097

5	1	11	21	31	41	51	
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10	TCGGCGCAGT	AGCAGCGAGC	AGCAGAGTCC	GCACGCTCCG	CGCAGGGGCA	GAAGAGCGCG	120
	AGGGAGCGCG	GGGCAGCAGA	AGCGAGAGCC	GAGCGCGGAC	CCAGCCAGGA	CCCACAGCCC	180
	TCGCCAGCTG	CCACGGAAGA	GCCTCAGCCA	TGGAACACCA	GCTCCTGTGC	TGCGAAGTGG	240
	AAACCATCCG	CCGCGCGTAC	CCCGATGCCA	ACCTCCTCAA	CGACCGGGTG	CTGCGGGCCA	300
	TGCTGAAGGC	GGAGGAGACC	TGCGCGCCCT	CGGTGTCTTA	CTTCAAAATG	GTGCABAAGG	360
15	AGGTCTGCCC	GTCCATGCGG	AAGATCGTCG	CCACCTGGAT	GCTGGAGGTC	TGCGAGGAAC	420
	AGAAGTGGCA	GGAGGAGGTC	TTCCCGCTGG	CCATGAACCTA	CTTGGACCGC	TTCTGTGCGC	480
	TGGAGCCCGT	GAATAAGAGC	CGCTTGACGC	TGCTGGGGGC	CACCTGCATG	TTCTGTGGCT	540
	CTAAGATGAA	GGAGACCTTC	CCCTGACGG	CGAGAGAGCT	GTGCATCTAC	ACCGACACTC	600
	CCATCCGCGC	CGAGGAGCTG	CTGCAATGAG	AGCTGCTCCT	GGTGAACAAG	CTCAAGTGGG	660
20	ACCTGGCGCG	AATGACCCCG	CACGATTTCG	TTGAACACTT	CCTCTCCAAA	ATGCCAGAGG	720
	CGGAGGAGAA	CAACACAGATC	ATCCGCAAA	ACGCGCAGAC	CTTCGTTGCC	CTCTGTGCCA	780
	CAGATGTGAA	GTTCAATTTCC	AATCCGCGCT	CCATGGTGGC	AGCGGGGAGC	GTGGTGGCCG	840
	CAGTGCAGGG	CCGTAACCTG	AGGAGCCCGA	ACAATCTCCT	GTCTTACTAC	CGCCTCACAC	900
	GCTTCTCTTC	CRGGTGTATC	AAGTGTGACC	CAGACTGCGT	CGGGGCTGTC	CAGGAGCAGA	960
25	TGGAAGCCCT	GCTGGAGTCA	AGCCTGCGCC	AGGCCACGCA	GAACATGGAC	CCCAGGCGCG	1020
	CGGAGGAGAA	GGAGGAGGAG	GAGGAGGAGG	TGGAACCTGG	TTGCACACCC	ACCGACGTGC	1080
	GGGACCTGGA	CATCTGAGGG	CGCCAGGCAG	GCGGGCGCCA	CGCCACCCCG	CAGCGAGGGC	1140
	GGAGCCGGCC	CCAGGTGCTC	CCCTGACAGT	CCCTCCTCTC	CGAGCAATTT	TGATACCAGA	1200
	AGGGAAGACT	TGATTTCTCT	TGTTGTGGT	TGTTTCTTCC	TTTGTCTCTT	CCCCCTTCCA	1260
30	TCCTGACTTT	AAGCAAAAGA	AAAAGATTAC	CCAAAACCTG	TCTTTAAAGG	AGAGAGAGAG	1320
	AAAAAAAGAA	TAGTATTTCG	ATAACCTGGA	GCGGTGGGGG	AGGAGGGTTG	TGCTACAGAT	1380
	GATAGAGGAT	TTTATACCCC	AATATCAAC	TCGTTTATAT	ATTAATGTAC	TTGTTTCTCT	1440
	GTGTGAAGAA	TAGGCATTAA	CACAAAGGAG	GCCTCTCGGG	AGAGGATTAG	GTTCATCTCT	1500
	TTACGTGTTT	AAAAAAAGC	ATAAAACAT	TTTAAACACA	TAGAAAAAIT	CAGCAAAACCA	1560
35	TTTTTAAAGT	AGAGAGGGGT	TTTAGGTAGA	AAAACATATT	CTTGTCTTTT	TCCTGATAAA	1620
	GCACAGCTGT	AGTGGGGTTC	TAGGCATCTC	TGTACTTTGC	TTGCTCATAT	GCATGTAGTC	1680
	ACTTTATAAG	TCATGTGTAT	TTATTATATT	CCGTAGGTAG	ATGTGTAAAC	TCTTCACTTT	1740
	ATTTCATGGT	GAAGTCACCT	CTTGGTTACA	GTAGCGTAGC	GTGGCCGTGT	GCATGTCTCT	1800
	TGCGCCGTGG	ACCACCACTC	CAACAAACCA	TCCAGTGACA	AACCATCCAG	TGGAGGTTTG	1860
40	TCGGGCAACA	GCCAGCGTAG	CAGGGTCGGG	AAAGGCCACC	TGTCCCACTC	CTACGATACG	1920
	CTACTATAAA	GAGAGAGCGA	AATAGTGACA	TAAATATATC	TATTTTATAT	CTCTTCTTAT	1980
	TTTGTAGTGG	ACCTGTTTAT	GAGATGCTGG	TTTCTTACCC	AACGGGCCCT	CAGCCAGCTC	2040
	ACGTCCAGGT	TCAACCCACA	GCTACTTGCT	TTGTGTTCTT	CTTCATATTC	TAAACCAATT	2100
	CCATTTCCAA	GCACCTTCAG	TCCAATAGGT	GTAGGAAATA	GCGCTGTTTT	TGTTGTGTGT	2160
45	GCAGGCGAGG	CAGTTTCTTA	ATGGAATGGT	TTGGAATGAT	CCATGTACTT	GTTTGCGAAG	2220
	AGGACTTTGA	GGCAGGTGTG	GGCCACTGTG	GTGGCAGTGG	AGGTGGGGTG	TTTGGGAGGC	2280
	TGCGTGCCAG	TCAGAGAGAA	AAAGGTTTGC	ATTCTCACAT	TGCCAGGATG	ATAAGTTCCT	2340
	TTCCCTTTCT	TTAAAGAAAT	TGAAGTTTAG	GAATCCCTTG	GTGCCAACCT	GTTGTTGAAA	2400
	GTAGGGACTT	CAGAGGTTTA	CCTAGAGAAC	AGGTGGTTTT	TAAGGGTTAT	CTTAGATGTT	2460
50	TCACACCGGA	AGGTTTTTAA	ACACTAAAT	ATATAATTTA	TAGTTAAGGC	TAAAAAGTAT	2520
	ATTATATGCA	GAGAGATGTC	ATAAGGCCAG	TATGATTTAT	AAATGCAATC	TCCCCCTGAT	2580
	TTAAACACAC	AGATACACAC	ACACACACAC	ACACACACAC	AAACCTCTCT	CCTTTGATGT	2640
	TACGATTTTA	ATACAGTTTA	TTTTTAAGCA	TAGATCCCTT	TATAGGTGAG	AAAAAAACAA	2700
	TCGGAAGAAA	AAAAACACCA	CAAGAGCAAT	GATTCAGCCT	GTGTTGGCGT	TCCCAGAGTC	2760
55	ATCTGATTTG	ACAGGCAATG	GTGCAAGGAA	AATTAGGGTA	CTCAACCTAA	GTTCGGTTCC	2820
	GATGAATTC	TATCCCTCTG	CCCTTCTCTT	AAAAAACTTA	GTGACAAAAT	AGACAATTGG	2880
	CACATCTTGG	CTATGTAATT	CTTGTAAATT	TTAATTAGGA	AGTTTGGAGG	GGAGGTGGCA	2940
	AGAGTGTGGA	GGCTGACGTG	TGAGGAGGGA	CAGGCGGGAG	GAGGTGTGAG	GAGGAGGCTC	3000
	CCGAGGGGAA	GGGGCGGTGC	CCACACCGGG	GACAGGCGGC	AGCTCCATTT	TCTTATTGCG	3060
60	CTGCTACCGT	TGACTTCCAG	GCAAGGTTTG	GAATATTTCA	CATCGCTCTT	GTGTATCTCT	3120
	TTCACTTTGT	TTGCTGCTAT	TGGAGGATCA	GTTTITTTGT	TTACAATGTC	ATATATCTGC	3180
	ATGTACTAGT	TTTAGTTTTC	TCCTAGAACCA	TTGTATTACA	GATGCCCTTT	TTGTAGTTTT	3240
	TTTTTTTTTT	ATGTGATCAA	TTTTGACTTA	ATGTGATTAC	TGCCTTATTC	CAAAAAGGTT	3300
	GCTGTTTTCAC	AAATACCTCAT	GCTTCACTTA	GCCATGGTGG	ACCCAGCGGG	CAGGTCTCTC	3360
65	CTGCTTTTGC	GGGCAGACAC	GCGGGGCGGA	TCCACACACG	GCTGGGGGGG	GCGGGCCCGG	3420
	AGGCGCGGTG	CGTGAGAAC	GCGCGGTGT	CCCGAGAGAC	CAGGCTGTGT	CCCTCTTCTC	3480
	TTCCCTGCGC	CTGTGATGCT	GGGCACTTCA	TCTGATCGGG	GGCGTAGCAT	CATAGTAGTT	3540
	TTTACAGCTG	TGTTATCTTT	TGCGTGTAGC	TATGGAAGTT	GCATAATTAT	TATTATTATT	3600
	ATTATAACAA	GTGTGCTCTA	CGTGCCACCA	GCGCGTTGTA	CCGTGTAGAC	TCTCATTCGG	3660
70	GATGATTTGA	ATAGCTTCTG	GAATTTGTTT	AAGTTTGGGG	TATGTTTAAT	CTGTTATGTA	3720
	CTAGTGTCTT	GTGTTGTTAT	GTGTTGTTAA	TTACACCATTA	ATGCTAATTT	AAAGAGACTC	3780
	CAATCTCAA	TGAAGCCAGC	TCACAGTGCT	GTGTGCCCCG	GTCACTTAGC	AAGCTGCCGA	3840
	ACCAAAAGAA	TTTGACACCC	GCTGCGGGCC	CAGTGTGTTG	GGGCGCTGCC	CTGGCAGGGT	3900
	CATCCTGTGC	TCGGAGGCCA	TCTCGGGCAC	AGGCCACACC	GCGCCACACC	CTCCAGAACCA	3960
75	CGGCTCAGCG	TTTCTCTAAC	CATCCTGGCT	GCGCGGTCTG	TCTGAACACC	GCGGGGGGCT	4020
	TGAGGGAGCG	TTTGTCTGTC	GTGATGGGGC	AAGGGCACAA	GTCTGTGATG	TTGTGTGTAT	4080
	CGAGAGGCCA	AGAGCTGTGT	GCAAGTGCAC	GGGGCACAGC	GGAGTCTGTC	CTGTGACGCG	4140
	CAAGTCTGAG	GGTCTGGGCG	GCGGCGGGCT	GGGTCTGTGC	ATTTCTGTTT	GCACCGGGCC	4200
80	GCTTCCCGAG	ACCAACATGT	AACCGCATG	TTTCCAGCAG	AAGACAAAAA	GACAAACATG	4260
	AAAGTCTAGA	AATAAACTG	GTAARACCCC	AAAAAATAAA	AAAAAA		

Seq ID NO: B2 Protein sequence

Protein Accession #: NP_444284.1

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797

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	2	ATWMLVCEEE	QKCEBEEVPL	AMNYLDRFLS	LEPVKESRLQ	LLGATCMFVA	SKMKETIPLT	120
	3	AEKLCIYTDN	SIRPESLLQM	EZLLVNLKIK	NLAAMTPHDF	IEHFLSRMPE	AEENKQIIRK	180
	4	BAQTFVALCA	TDVKFISNPP	SNVAAGSVVA	AVQGLNLRSP	NNFLSTYRLI	RFLSRVVKCD	240
	5	PDCLNACQEQ	IEALLESSLR	QAQQNMDPKA	AEKEEEEEEE	VDLACTPTDV	RDVDI	
Seq ID NO: B3 DNA sequence								
Nucleic Acid Accession #: XM_044166								
Coding sequence: 1..1576								
15	1	CTTTTGTTTC	GCCATGCCCTA	GTCTAGTGTGT	ATCTGSAATA	ATGGAAAGAA	ATGGGGGCTT	60
	2	TGGAGAACTA	GGATGTTTCG	GGGAAGOGC	TAAGGACCGA	GGGCTGCTGG	AAGACTAGCG	120
	3	CGCCCTTCAG	CTGGCTCTCG	ATCAACTCTG	CCTCTGCGGT	TTGGGGGAGC	CCCCCGCCCC	180
	4	CAGGGCGGGC	GAGGACGGGG	GAGGTGGGGG	GGGCGGGCGC	CCGCGCGAGC	CGACAGCCCC	240
	5	CCCGCAGCCG	CGCGCGCGCG	CGCGCGCGCG	GGCGCGCGCG	CGCGCGCGCG	CGACGGCCCC	300
20	6	CGCAGCGCAG	ACGCCCCCAGC	CCCCCACCGC	CCCCAAAGGG	CGCAGCGAGC	CCAAGCTCTG	360
	7	CGCTCTCTAC	AAAGAGGGCG	AGCTGCGCCT	GAAGGGCAGC	AGCAACACCA	CGGAGTGTGT	420
	8	TCCCGTGCOC	ACCTTCGAGC	ACGTGGCGGA	GATCGTGGGC	AGGCAAGGCT	GCAAGATTAA	480
	9	GGCTTGAGG	GCCAGAGCCA	ACACCTACAT	CAAGACACCG	GTGAGGGGGC	AGGAACCACT	540
	10	GTTCAATGGT	ACAGGGCGAC	GGGAGGACGT	GGCCACAGCC	CGGCGGGAAA	TGATCTCAGC	600
25	11	AGCGGAGCAC	TTCTCCATGA	TCCGTGCTCT	CCCAACAACG	TCAGGCGCGC	CCTTGTGTGT	660
	12	GGCTCTCTGT	CTGCCCCGGC	AGGTGACCAT	CCGTGTGCGG	GTGCGCTACC	GGTGTGTGGG	720
	13	GCTGTGTGGT	GGCCCCAAGG	GGGCAACCAT	CAAGCGCATC	CAGCAGCAAA	CCAACACATA	780
	14	CATTATCA	CCAGGCGGTG	ACCGCGACCC	CGTGTTCGAG	ATCAGCGGTG	CCCCAGGCAA	840
	15	CGTGGAGCGT	GGCGCGGAGG	AGATCGAGAC	GCACATCGCG	GTGCGCACTG	GCAAGATCCT	900
30	16	CGAGTACAAC	AATGAAAAGC	ACTTCTCTGG	GGGAGGCCCC	GAGCAGCAAA	TGATAGCCG	960
	17	CTACTCCGAC	GCTCGGGGGG	TGCACGAGCC	CGGCTGCAAG	CCCCCTCTCA	CCTTCCGGCA	1020
	18	GAACAGCCTG	GGCTGCATCG	CGCAGTGCAG	AGTGGACTCT	GGCTTTGAGG	CCCAACGCTT	1080
	19	GGGTGAGCAG	GGCGGGGACT	TTGGCTACGG	CGGCTACCTC	TTCCGGGCTT	ATGGCGTGGG	1140
	20	CAAGCAGGAT	GTGTACTACG	CGGTGGCGGA	GACTAGCCCC	CGGCTGTGGG	CGGCGCAGGA	1200
35	21	GAAGCCCAAG	CCCACTCCCG	TGCTCTTCTC	CTCTGCTCTC	TCTCTCTCTC	CCTCTCTCTC	1260
	22	CAAGGCCCGC	GCTGGGCCCC	GGGGCGCACA	CCGCTCCCTT	GGCACTTCCG	CGGACCCCGA	1320
	23	GCTGGCCGGA	CTCCCCAGGC	GGCCCCCGGG	AGAGCCGCTC	CAGGGCTTCT	CTAAACTTGG	1380
	24	TGGGGCGCGC	CTGCGGAGCC	CCGCGCGCGG	GGGGGATTGC	ATGGTCTGCT	TTGAGAGCGA	1440
	25	AGTGACTGCC	GGCTTGTGTG	CCTGCGGACA	CAACCTGTTC	TGATGAGAGT	GTGAGTACG	1500
40	26	CATCTCGGAG	AGGACGGACC	CAGAGTGTCC	CGTCTGCCAC	ATCACAGCCA	CGCAAGCCAT	1560
	27	CGAATATATC	TGCTAAGCCC	CGTGCCCCAT	GGCTCCGGGG	CCCACTCCAC	TGGGCCCCACC	1620
	28	CTGGACCTGT	TTTCTCACTA	AGGCTTTTGG	AAAGCGGTGA	TTTGGGGGGC	AAGGTGTCTT	1680
	29	GAGATACCTG	CTGCTGGGGG	AAGGGGGGAG	GGAGGCACTG	GTGGCTGGAG	GGTGCGCCAC	1740
	30	TTTCAGAGCC	CTGTGTCAAC	CTGTCTCTGA	AAGATTGGGA	GGGGGCCAGA	CTGAAATTTT	1800
45	31	TACTAGAGTT	ACACCTCTGA	TACCTCAACA	CACCTTAAAT	CTGGAAGCA	GCTAAGAGAA	1860
	32	ACTTTTGTGT	TGCCAGAGGT	GGCCACTAAG	GCACTCTGAC	GGCTCTGACC	CACCTCCCCC	1920
	33	GCTGTGTGTC	ACTCCACCCC	TTCTTCCGAG	GAGGGGGTGG	GTAAAGGGGA	GAGGGAGAAAT	1980
	34	TACCACCTGT	ATCGAGAGGT	GCTCTTTGCA	ATCCCTAAGC	CCTCTGGTCC	TGACCTCCGA	2040
	35	CCTCCAGCTG	CTGTCTGTGT	CCTTGTCTTT	GTCTTCTCTC	CCCTCCCTCT	GGCCCTGCCC	2100
50	36	CTACAGCCCG	AGCTTTGGGG	ACACCATCTT	TCTGGGGAGA	AGTAGGGGGA	GGAATATTGT	2160
	37	GATGGTCCCT	CCATTCCTCT	TCAGGCATCT	GGAGGCCCTC	TCCCCCACTC	CTCCAAAGAA	2220
	38	ACATCTCAAA	TTATTTGATG	AATGTATCCC	CATTCTCAGT	GAATATGTGA	GGAGGGGACT	2280
	39	ATACTCGGGG	TAAAGGCTCA	AAACCCACCC	TTCATCACTA	TGGGCATTAT	ATTTAGGGAG	2340
	40	TAGTCTCTGG	CTGGGATTTT	CTGGTGTGGS	AAGTGGGGGC	GCCAGAGTAG	TGTGTCTGCT	2400
55	41	NITTAAGAGA	CGAGGAAGAG	GGGTGAGGCA	GGAGGAGAGA	CTGGTGGAGG	GAAGAGCTGC	2460
	42	TCTTCCCATG	CAGTGCOCGA	CTCCCTGCAC	CCCTCTCAAC	CTGACCTGAA	CTTTTATTGA	2520
	43	ATCCTTATTA	CTGTGAATCC	TTATTAGCTT	GAATCTCTCA	TGCAATCAT	GGAGTCTGTG	2580
	44	TCCACCTGTA	TGTGGTTGAG	GAGAAGCCAG	GTCTTCAAGG	AGGGGTGAGC	CTGGGGCAAA	2640
	45	GCAGGACCTG	GGGGAGGTGG	GCAGCAGGGC	CTATCTGAG	AATCAGATAT	TGTTACAGGC	2700
60	46	CTTGACCCCC	CTTGTCTGCT	TCCCTCTGTC	TCATTGGGGG	CTGCCACAG	CTCTCCACCC	2760
	47	TCCGTGTTCC	GCTGGCCCGG	CCAGAGAGGG	ATGGAGGGAT	GGGAGTCCCA	GGAGATCTTT	2820
	48	GTAATATAGT	GGGTGGGACT	GTCTGTAGTG	ATCACCCGAG	CACCTTAAAG	TCCAGAGTCC	2880
	49	CATTCTCTCT	GGATGGAGCA	GGTGGAGGTG	CAGAGGGGAT	TTCTCTCTCT	CCTCTCTCTC	2940
	50	GTGAGAAATT	AACACCTCTC	CACAGCCTTC	CCCTCCAGAA	CACCAGCCAG	GGAGGGGTGG	3000
65	51	GGAGGAGGAT	CACAGCCAGG	AAACCTGCCC	TGTGACGACT	TCCCTCTCTC	CCGCTCTATG	3060
	52	GAGCCATCCT	GAGATGTCTG	TACAATAGAA	ACCAAAACCA	ATGGGCACCC	TGGTGTGCGG	3120
	53	GGGGGAGGAT	GGGGAGGGGG	GTGGGAGAGG	GGGATGTCTG	TCTGTCTCTC	CCCTCCCCCT	3180
	54	CTCCACTCTT	TACCCACAAA	GGCAGAGAGC	TGTTACACTA	GGGGGCTCAG	CAAAATCAAT	3240
	55	CCACCCCTTA	CCATTTAGAG	CAAACTTAGA	AACAACACCA	AAACAGCAAT	AGTGAGAGAC	3300
70	56	AAAATAGAGG	AGAGAAAGAG	AGCATGAGAG	GGAGCGAGAC	AGGCGACCAA	CACAGAGGAG	3360
	57	AGAAACACAA	AATAGCAAAA	AAAAAATAAA	AAAGCAGTTC	TTTATAATTT	AATATTCTAT	3420
	58	TTTATAAAG	GGCTTTATTA	CCATATAAAT	GTAGCAAGAA	ACCTGGGCTA	ATATGAA	
Seq ID NO: B4 Protein sequence								
Protein Accession #: XP_044166.2								
75	1	FCFAMPSLVV	SGIMERNGGF	GELGCFGGSA	KDRGLLEDER	ALQLALDQLC	LLGLGEPAP	60
	2	RAGEDGGGGG	GGAPAGFTAP	PPAPFPFPFA	APPAAPTTPA	AAQTPQPTA	PKGASDAKLC	120
	3	ALYKEAEELR	KSSSNITTECV	PVPTSEHVAE	IVGQGGCKIK	ALRAKNTYXI	KTPVRGEEFV	180
	4	FMVTRREEDV	ATARRBIIISA	AEHFSMIRAS	RNKGGAAPGV	APALPGQVTI	EVRVPYRVVG	240
	5	LVVPGKATI	KRIQQQTNTY	IITPSRDRDP	VFEITGAPGN	VERAREEIEI	HLAVRTGKIL	300
80	6	EYNNENDFLA	GFPDALIDSR	YSDANRVHQP	GCKPLSTFRQ	NBLGICIGECG	VDSGFAPRL	360
	7	GRQGGDFGYG	GILFPGYGVG	KQDVYGVVAE	TSPPLWAGQE	NATFTSVLFS	SASSSSSSSA	420

KARAGPPGAH RSPATSAGPE LAGLPRRPPG BPLQSPSKLG GGGLRSPGGG RDCMVCPESE 480
VTAALVPCGH NLFCECAVR ICERTDPECP VCHITATQAI RIFS

5 Seq ID NO: B5 DNA sequence
Nucleic Acid Accession #: NM_000909.1
Coding sequence: 209..1363

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   GTTCAGTTCA AGGGAATGAA GAATTCAGAA TAATTTTGGT AAATGGATT CAATATCGGG 120
   AATAAGAATA AGCTGAACAG TTGACCTGCT TTGAAGAAAC ATACTGTCCA TTGTCTAAA 180
   ATATCTTATA ACAACCAAC CAATCAAAAT GAATTCACAA TTATTTTCCC AGGTTGAAAA 240
   TCATTCAGTC CACTCTAATT TCTCAGAGAA GAATGCCAG CTTCTGGCTT TTGAAAAATGA 300
15 TGATGTGTCAT CTGCCCTTGG CCATGATATT TACCTTAGCT CTGTCTTATG GAGCTGTGAT 360
   CATTCTTGGT GTCTCTGGA ACCTGGCCTT GATCATATC ATCTTGAAAC AAAAGGAGAT 420
   GAGAAATGTT ACCAACATCC TGATGTGAA CCTTTCCTTC TCAGACTTGC TTGTTGCCAT 480
   CATGTGTCTC CCTTTTACAT TTGTCTACAC ATTAATGGAC CACTGGGTCT TTGGTGAGGC 540
   GATGTGTAAG TTGAATCCCT TTGTGCAATG TGTTCATC ACTGTGTCCA TTTCTCTCT 600
20 GGTTCCTCAT GCTGTGGAAC GACATCAGCT GATATCAAC CCTCGAGGGT GGAGACCAA 660
   TAATAGACAT GTATTGTAG GTATTGCTGT GATTGGGTC CTGTCTGTGG CTCTCTCTT 720
   GCCTTCTCTG ATCTACCAAG TAATGACTGA TGAGCGGTC CAAAATGTAA CACTTGATGC 780
   GTACAAAGAC AAATACCTGT GCTTTGATCA ATTTCCATCG GACTCTCATA GGTGTCTTA 840
   TACCACTCTC CTCTGGTGC TGCAGTATT TTGTCCACTT TGTTTTATAT TAATTGCTA 900
25 CTTCAAGATA TATATAGGCC TAAAGAGGAG AAACAACATG ATGACACA GAAGAGACAA 960
   TAAGTACAGG TCCAGTGAAC CAAAAGAAAT CAATATCATG CTGCTCTCCA TTGTGGTAGC 1020
   ATTTGCAATC TGTGTGCTCC CTCTTACCAT CTTTAACACT GTTTTGTATT GGAATCATCA 1080
   GATCATTTCT ACCTGCAACC ACAATCTGTT ATTCTGCTCT TGCCACTCA CAGCAATGAT 1140
   ATCCACTTGT GTCAACCCCA TATTTTATGG GTTCTGAAC AAAAACTTCC AGAGAGACTT 1200
30 GCAGTTCTTC TTCAACTTTT GTGATTTCGG GTCTCGGGAT GATGATTATG AAACAATAGC 1260
   CATGTCCACG ATGCACACAG ATGTTTCCAA AACCTCTTTG AAGCAAGCAA GCCCAGTGGC 1320
   ATTTAAAAAA ATCAACACAA ATGATGATAA TGAAAAAATC TGAAACTACT TATAGCCTAT 1380
   GGTCCCGGAT GACATCTGTT TAAAAACAAG CACAACCTGC AACATACTTT GATTACCTGT 1440
   TCTCCCAAGG AATGGGGTGG AAATCATTTG AAAATGACTA AGATTTTCTT GTCTGTCTTT 1500
35 TTACTGCTTT TGTGTAGATT GTCATATTA CATTTGGAAC AAAAGGTGAG GGCCTTGGGG 1560
   TCTTCTGGA ATAGTTTGA CCAGACATCT TTGAAGTCTT TTTGTCAAT TTATGCATAT 1620
   AATATAAAGA CTTTITACT GTACTTATG GAATGAAATT TCTTAAAGT ATTAAGATGC 1680
   GCTGACTTCA GAAGTACCTG CCATCCAAAT CGGTCAATAG ATTGGGTCTT CTGTATTAGA 1740
   TTAGATTAGA TTGATTGTC AACAGATTGG GCCATCCTTA CTTTATGATA GGCATCATTT 1800
40 TAGTGTGTTA CAATAGTAAC AGTATGCAA AGCAGCATTC AGGAGCCGAA AGATAGTCTT 1860
   GAAGTCATTG AAGAGTGGTT TTAGGTTTCT GTTTTGTGTT GGTTTTGTGTT TGTTTTTTTT 1920
   TTTTTCACCC TTAAGGGAGG CTTTCATTTC CTCCGACTG ATTGTCACTT AAATCAAAAT 1980
   TTAAAAATGA ATAAAGAGAC ATACTTCTCA GCTGCAAATA TTATGGAGAA TTGGGCACCC 2040
45 ACAGGAATGA AGAGAGAAAG ACCTCCCAAC ACTTCAAAAC CATTTTGGTA CCGACAAAC 2100
   AGAGCATTTT AGAGTAATTA ATTTAATAAA GTAAATTAGT ATTGTGCAA ATAGCTAAAT 2160
   TATAITATT TGAATTGATG GTCAAGAGAT TTTCCATTTT TTTTACAGAC TGTTCAGTGT 2220
   TTGTCAAGCT TCTGGTCTAA TATGTACTCG AAAGACTTTC CGCTTACAT TTGTAGAAC 2280
   ACAAAATACG TTTTCCATAC AGCAGTGCTT ATATAGTGAC TGATTTTAACT TTTCATGTCT 2340
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   AGGGAAAAAT ACACAAAAC TGCAGATACT TCAATATAGC CATTTTAACT TGTATAACT 2460
   GTGTGACTTG TGGGCTCTTA TAAATAATGC ACTGTAAAGA TTACTGAATA GTTGTGTCT 2520
   GTTAATGTGC CTAATTTTCA GTATCTTGTG ATCATGATG AGCCTCAGAA TCATTGGAG 2580
   AAACATATAT TTAAGAAACA AGACATACTT CAATGTATTA TACAGATAAA GTATTACATG 2640
55 TGTTTGATT TAAAGGCGG GACATTTTAT TAAATCAAT ATTGTTTTG CTTTTCGTA 2700
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Seq ID NO: B6 Protein sequence
Protein Accession #: NP_000900.1

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   LIIILKQKE MRNVINILIV NLSFSDLLVA IMCLEPTFVY TLMDSWVFGS AMCKLNPFVQ 120
   CVSITVSIFS LVLLAVEREQ LIINERGWRE MNRHAYVGLA VINVLAVASS LEPLIYQVMT 180
65 DEFFQNVITLD AYKDKYVCFD QPFSDSHRLS YTTLLLVLOY FGPLCFIPIC YFKIYIRLKR 240
   RNMMDKMDK NKYRSSRTKR INIMLLSIVV AFVAVCWLELT IFNTVFDMNH QLIATCNHML 300
   LFLLCHELTAM ISTCVNPIFY GPLNKNFQRD LQFFNFCDP RSRDDDYETI AMSTMTDVS 360
   KTSLEQASPV AFKKNINND NEKI

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70 Seq ID NO: B7 DNA sequence
Nucleic Acid Accession #: NM_002590.2
Coding sequence: 204..3416

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   CTGSAGGCTC GGAGCTGCTA CCCGCAGACT TCTCCCGCAC AGGGCTCGCA AAGAGCGTGA 120
   TTCGAGAGAC CTGAGACTGA CGCCCGACCT GGAACCTAGA GAGAGCTTCC TTAGCCTTTC 180
   GGATCGCACT TGAAGCTGGA GGCAATGAGT CTGTGAGGCG TTGGGGCAGC CCTTGCCTTT 240
80 TCCCCTTCCA GCTCTTCAAC CTCTGCTGGG TGCTCTCAGT GGCCCAAGAC AAAACAGTCC 300
   GATACAGCAG CTTGAGGAG GATGCCCCG GCAOGGTCAAT CGGAGCCCTG GCCGAGSACC 360
   TGCAATATGA AGTATCGGGT GACACAAGCT TCCGCTGAT GAAGCAATTC AACAGCTCTC 420
   TGCTCCGGGT GCGGGAAGGC GAGGGGAGC TGACGTCGG GAGCGCGCGC CTGACCGCG 480
   AGCGGCTGTG TGGCAGGCC CCGCAGTGCG TGCTGGCCTT CGATGTGTGC AGCTTCTCGC 540

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5 AGGAGCAGTT CCGGCTGGTG CACGTGGAGG TAGAGGTGAG GACGTCACAC GACCACGGCG 600
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 GCATCCCTCT GGAGGTGCGG GTGGACGAGG ACGTGGGCGC CAACGGGGCTG CAGACCGTGC 720
 GCGTGGCCGA GCGGCRACAG CCGTTTCGCG TGGAGCTGCA GACGCGAGCG GACGCGCTC 780
 AGTGCAGAGA CCGTGGTCTG CTGCGAGGAG TGGACGCGCA GAGCCAGGCC GCCTACAGCC 840
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 20 ACAGCGCGCT CTTCAGCGCG CCGGTCTATG AGGTGTGGGT GCGCGAGAAC AACCGCGCAG 1740
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 35 CCGTCAACCG CCGCAAGAG GAGGTGCGCA AAGGCGGCGC CCGCGCGGA GAGCGCGCG 2580
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 GCGTCTGAGG CCGTCTGAG AAGTACTGCG ACAGAGCTA TGACAGGACA GCGCTCTG 3300
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 50 ATGCTCTCTC TCCTCACACA TATACAGGTC ACTCGAGAA GCGCTTAAAT TATGAGCG 3480
 TTCTAGTGT GTATATATAA ATATGCAAGA TGTGCTTAC AATGAAGTGG TTGGAAGCTA 3540
 TTCTCAATCA CCGTCTGAG GTTGTGTAAT TGCAACAA AATGAGTGA ATGTAATTT 3600
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 TATGCTATT CTGAGTGT TTAACCTGTA CATGCTGTA TGAATGTT GTATATAAT 3720
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 AAAAAACCTA GTGTTTGA AATTGCTCT TGCGAGTAT AACTGTGATA TCCTGACTCT 3900
 GTGCTAGATT TCAAGTTCAA TGTATTAA TTACATTGG TTTTCCGTA ACCGTGTCAT 3960
 60 TTATAGCAC AGTAATAAA GATTGTCTAT GTGTTTGA AAAAAA AAAAAA 4020
 AAAAAA AAAAAA AAAAAA AAAAAA AAAAAA

Seq ID NO: B8 Protein sequence
 Protein Accession #: NP_002581.2

65 1 11 21 31 41 51
 MSFVERNGSP CLFPLQLFSL CMLVSAQSK TVRYSTYED APGTVIGTLA EDLHMKVSGD 60
 TSFRLMKQFN SLLLRVREGD GQLTVGDAGL DRERLCQAP QCVLAFDVVS FSQEQFRLVH 120
 VEVEVRDVM HAPFPFRAQI PVEVSEGA AV GTRIPLEVPV DEDVGANGLO TVRLAEFHPSP 180
 FKVELQTRAD GAQCADLVLL QELDRESQAA YSLELVAQDG GRPPRBATAA LSVRLDAND 240
 70 HSPAFPQCAV AEVELAEDAP VGSLLLDLDA ADPDEGNMGD VVFARGATE PEARRLRFD 300
 PRSGRLTAG PVDYERQDTY ELDVRAQDRG PGPRAACTKV IVRLRVNDN APDIAITPLA 360
 APGAPATFPF AAAAAAALG GADASEPAGA GTPEAGATSL VPEGAARESL VALVSTSDRD 420
 SGANQVACA LYGHEKFRLO PAYAGSYLVV TAASLDRETI AEYNLTIVAE DRGAPPLRTV 480
 RPYTVRVGDE NDNAPLETLP VYEVSVRENN PPGAYLATVA ARDRDLGRNG QVTYRLLEAE 540
 75 VGRAGGAVST YVSVDPATGA IYALRSFDYE TLRQLDVRIQ ASDGGSPOLS SSALVQVRVL 600
 DQNDHAPVLV HPAPANGSLE VAVPGRTAKD TVVARVQARD ADEGANGELA FELQQQEPRE 660
 AFAIGERTGE TLLTGDLSEQ PPGRVFRALL VISDGGREPL TTTATVFFV TAGGGGPPAA 720
 PASAGSPERS RPPGSLGLVS GSVLQNDTFL IVIIVLAGSC TLLALALIAI ATTCKNRKKE 780
 80 VRKGALREE RPPGAGGAGS APGSPREAAAR GAGPRPMFMD VLTFFPGTGA PFGSPAADAP 840
 PPVAAAEVFP GSEGGSATGE SACHFEGQOR LGGAHAEPYG ASFGFGKEPA PPVAVNKGHS 900
 FWTISGREAE KFSGKDSGKG DSDFNDSDD SDGALKKDL INHMQSLWA CTAECKILGH 960
 SDRCNSPSCS GNAHFPSPRP PQMSTFCKS TSLPRDLPRR DNYXQALPK TVGLQSVYEK 1020
 VLHRYDRTV TLLSPRPFR LFDLQEIGVF LYQSPFGRYL SPKKGANENV

Seq ID NO: B9 DNA sequence
Nucleic Acid Accession #: AL121939.12
Coding sequence: 185..1426

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5      1      11      21      31      41      51
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GCTCAGGCTG GCTGAGAGGC TCCAGGCTGC AGCGTCCCGG CCGGCTCCTC GGGGAGCTCT 120
GATCTCAGCT GACAGTGCCC TCGGGGACCA AACAGCCTG GCAGGACAAA ATTAGAAGAT 180
10     CAAAATGGAA AATATGCTGC TTTGGTTGAT ATTTTTCACC CTTGGGTGGA CCCTCATGTA 240
TGATCTGAAA ATGGAATGGG ATTTTATGTG GCACTTGAGA AAGGTACCCC GGATTTGTCAG 300
TGAAAGGACT TTCCATCTCA CCAGCCCCGC ATTTGAGGCA GATGCTAAGA TGATGGTAAA 360
TACAGTGTGT GGCATCGAAT GCCAGAAAGA ACTCCCAACT CCCAGCCTTT CTGAATTGGA 420
GGATTATCTT TCCTATGAGA CTGTCTTTGA GAATGGCACC CGAACCTTAA CCAGGGTGAA 480
15     AGTTCAAGAT TTGGTTCTTG AGCGGACTCA AATATCACC ACAGAGGGAG TATCTGTTAG 540
GAGAAAGAGA CAGGTGTATG GCACCGACAG CAGGTTGAGC ATCTTGGACA AAAGGTTCTT 600
AAACAATTTC CTTTTCAGCA CAGCTGTGAA GCTTTCCAGG GGCTGTAGTG GCATCTCAT 660
TTCCCTCAG CATGTCTTAA CTGTGCCCCA CTGTGTTTAT GATGGAAGG ACTATGTCAA 720
AGGAGTAAA AAGCTAAGGG TAGGGTGTGT GAAGATGAGG AATAAAGTG GAGGCAAGAA 780
20     ACTTCAGAGT TCGGTTCTTG GCAGGAGAGA AGCTAGTGGT GGTGACCAAA GAGAGGGTAC 840
CAGAGAGCAT CTGCAGGAGA GAGCGAAGGG TGGGAGAAAG AGAAAAAAT CTGGCCGGGG 900
TCAGAGGATT CGGTAAGGGA GCGCTTCCCT TCAGTGGACC CCGGTCAAGA ATACCCACAT 960
TCCGAAGGGC TGGGCAAGAG GAGGCATGGG GGAAGCTACC TTGACTATG ACTATGCTCT 1020
CTGGAAGCTG AAGCTGTCTC ACAAAGAGAA ATACATGGAA CTGGAATCA GCCCAACGAT 1080
25     CAGAAAGATG TCTAGAGAGA TGTATCCACT CTCAGGATTT GATAACGATA GGGCTGATCA 1140
GTGGGTCTAT CGGTTTIGCA GTGTGTCTGA CGAATCCAAT GATCTCCTTT ACCCAATATG 1200
CGATGCTGAG TCGGGCTCCA CCGGTTCCGG GGTCTATCTG CGTCTGAAAG ATCCAGACAA 1260
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CGGGGTTCAG AAGGACTACA ACGTTGCTGT TCGCATCACT CCCCTAAAA ACGCCAGAT 1380
30     TTGCTCTGG ATTCAAGGGA ACGATGCCAA TTGTGCTTAC GGCTAACAGA GACCTGAAGC 1440
AGGGCGGTGT ATCATCTAAA TCACAGAGAA AACAGCTCT GCTTACCGTA GTGAGATCAC 1500
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GGAGATTTTC GTCCATTAAA AAAATGTATA GGTGCAGATA TTGAACATAG GTGGGCACCT 1620
35     CAATGCCAAG TATATACTCT TCTTTACATG GTGATGAGTT TCATTGTATG AAAAATTTTG 1680
TTGCCCTCTT AAAAATTAGA CACACTTTAA ACCTTCAAGC AGGTATTATA AATAACATGT 1740
GACTCCTTAA TGGACTTATT CTCAGGGTCC TACTCTAAGA AGAATCTAAT AGGATGCTCG 1800
TTGTGATTA AATGTGAAT YGCATAGATA AAGGTAGATG GTAAAGCAAT TAGTATCAGA 1860
ATAGAGACAG AAGGTTACAA CACAGTTTGT ACTACTCTGA GATGGAYCCA TTCAGCTCAT 1920
40     GCGCTCAATG TTTATATTGT GTTATCTGTT GGGTCTGGGA CATTTAGTTT AGTTTTTTTG 1980
AAGAATTACA AATCAGAGAA AARGCAGAC ATTATAAACA AAACATATAA CTGTTTACT 2040
GCTTTAAGAA ATAAATTTA CAATGTGTAT TATTTAAAAA TGGGAGAAAT AGTTTGTCT 2100
ATGAATATA CCTAGTTTAG AAATAGGGA GCTGAGACAT TTAAAGATCT CAAGTTTTTA 2160
TTTAATTAAT ACTCAAMTA TGGACTTTTC ATGTATGCAT AGGGAAGACA CTTCACAAAT 2220
45     TATGAATGAT CATGTGTTGA AAGCCACATT ATTTATGCT ATACATTCTA TGTATGAGT 2280
GCTACATTTT TAGGACAAAG AATCTGTAA TCTTTTTCAG GAAAGAGTCT TTTTCTCTT 2340
GACAAATCC AGCTTTTGTG TGAGGACTAT AGGGTGAATT CTCTGATTAG TAATTTTGA 2400
TATGTCCTTT CTAAAGATG AATAAATT ATGAATATGA CTTAAAAAAA AAARWOGAGC 2460
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Seq ID NO: B10 Protein sequence
Protein Accession #: CAC35071.1

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55     1      11      21      31      41      51
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VQIGEQKEL PPSISELED YLSYETVEFN GTRLTARVKV QDLVLEPTQN ITTKGVSVRR 120
KRQVYGTDSR FSLIDKRLPT NPPFSTAVKL STGCSGLIS PQHVLTAAC VHDGKDYVKG 180
30     SKLLRVGLLK MRNKSQKKR RQSKRSRREA SGGDQREZTR EHLRERAKGG RRRKKSGRGQ 240
RIAEGRPSFQ WTRVKNTHIP KGWARGGMD ATLDDYDALL ELKRAHKKKY MELGISPTIK 300
KMPGGMHFS GFDNDRADQL VYRFSVSDE SLDLYQYCD ARSGSTGSGV YLRKLDKPKK 360
NWRKKIIVYV SGEQWVDVHG VQKYNVAVR ITPLKYAQIC LMIHGNDAAC AYK

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Seq ID NO: 11 DNA sequence
Nucleic Acid Accession #: NM_002035.1
Coding sequence: 108..1106

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CCAGCGCCCT CGCCCTGCCC GGGGCGCATG TGGTGGTTAC AGGAGGTTCC AGTGGCATCG 240
75     GGAAGTGCA TGTATGAG TGCTATAAAC AAGGAGCTTT TATAACTCTG GTTGCAAGAA 300
ATGAGGATAA GCTGCTGCAG GCAAGAGAA AATTTGAAT GCACTCTATT AATGACAAAC 360
AGGTGGTGCT TTGCATATCA GTTGTATGAT CTCAGGACTA TAACCAAGTA GAGATGTCA 420
TAAACACAGC ACAGGAGAAA CTGGGTCCAG TGGACATGCT GGTAAATTTG GCAGGAATGG 480
CAGTGTGAGG AAAATTGTA GATCTTGAAG TTAGTACCTT TGAAGGTTA ATGAGCATCA 540
80     ATTACCTGGG CAGCGTGTAC CCCAGCAGG CCGTATCAC CACCATGAAG GAGCGCGGCG 600
TGGGCAAGAT CGTGTGTTG TOCTCCAGG CAGGACAGTT GCGATTAATC GGTTCACAG 660
CCTACTCAGC ATCCAGTTT GGCATAGGG GATTGGCAGA AGCTTTGAG ATGGAGGTGA 720
AGCATATAA TGTCTACATC ACAGTTGCTT ACCCACCAGA CACAGACACA CCTGGCTTTG 780
CGAAGAAAA CAGACAAAG CCTTTGGAGA CTCGACTTAT TTCAGAGACC ACATCTGTGT 840
GCAACCCAGA ACAGGTGGCC AAACAAATTG TTAAGATGCA CATAACAGGA AATTTCAACA 900

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GTTCCCTTGG CTCAGATGGG TACATGCTCT CGGCCCTGAC CTGTGGGATG GCTCCAGTAA 960
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 CTGAAATGCG AGACAAAACCT GCCTAATCTT CTTACCCCTT GGAAGAAGAC TGTTTCCAAA 1140
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 TGTTTTCGAA TACGTTCAGT TGGACCATGG CTCTTCAGGA ATGTGGCTGC AAGCAAGGGG 1260
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 TTTGTGCTCA GGACTCCTC TGCTGCTGCT GGAACCTCAT GGCTTCTCTC TCTCTTTGAT 1740
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 CCAGTAGGAA AAGCAATGCT TCTTGTCTT TAGACTCAAA TGCTTAGGGA ACGTTTCATT 1860
 TCTCAATCAT GGGGAAGGCG AGCCTCCTTA AATGTTTTCT GAAGAGCGGT AAAATCTAGA 1920
 AGCTTAAGAA TTTACAGTTC CTTCAATAAC CATGATGACC TGAAGTTCAC CTATCCCAT 1980
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 TTTTGTAAA AAAAAAATAA AAGGAAAAAA AAGACCAGCT AAAATTTTCG ACTTGACTTT 2100
 TTAACCTAAC TCATGAATTA ATTAAGCAA ATGAAAAAAT TAAAAAGTGT GACTTTTTCT 2160
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 AAAAAAGACA AGGCTGATTT TGAAGAGAGT TGCCTTTGAA ATAAATGAT CA

Seq ID NO: B12 Protein sequence
 Protein Accession #: NP_002026.1

1 11 21 31 41 51
 MLLLAALFLV AFVLLLYMVS FLISPKPLAL PRAHVVTGG SSGIGKCIAT ECKKQGAFIT 60
 LVARNEDKLL QAKKEIMES INDKQVVLCT SVDVSQDYNQ VENVIKQAE KLGFDVLMVN 120
 CAGMAVSGKF EDLEVSTFER LMSINVLGSV YPSRAVITM KERRVGRIVF VSSQAGQLGL 180
 PGFTAYSASK FAIRGLAERL QMEVKPYNVY ITVAYPPDID TPGFAEENRT KPLETRLISE 240
 TTSVCKPEQV ARQIVKDAIQ QWENSSLGSD GYMLBALTCG MAPVTSITEG LQQVVTWGLF 300
 RTIALFYLGS FDSIVRRCM QREKSENADK TA

Seq ID NO: B13 DNA sequence
 Nucleic Acid Accession #: CAT Cluster

1 11 21 31 41 51
 CTGGGATGC ATTATATATT GCATTATATT TGCCGGTAAA ACTCGGTAA TTTTAAAAAT 60
 CGGCAAAATA TTGGTGCTTT TCCGAAAATT TGATCCCGGG CTCCTTATA GGATAATTGG 120
 TTTGGATTGG TTAAGTCCAA TTATTAAATG CTGGGTTTC AAATTCOCAG CTGGAAGGAC 180
 CACCCATTTA AAAACTTCAG AAGGCAGGAT CCTGCTCAAT TTATAAGGCT TTGGAATAAT 240
 CCAGSCATGG GTTTGACATA TTTCCAGAGC TCAATCTGCA AGTGTTCAC ATGCACATAC 300
 AAGATCCAGA GTCTCATGTT AAAATCACTT ACATACCCAG AAAGACCACC ACITTCGAGG 360
 TATAATATTG TACTTAAAGA CAGAGAGGAA GTGTTTCTTA ATCCAAACAC ATGTACACCA 420
 AAGAACACAT AAGATGCCCT CTTCATCAA ATGCACCTGC TTGTGAATTA ATGGACTTGT 480
 AAATGAAACA ATGCAATCAG TCTTTTATAA TGCACTGTTC AATTTGAGAT TCAAGTATTT 540
 CTATTTCTTG GAAAAAATTT TAAGAATCAA AAATARAAG AATAAAAGT GCATACAGTT 600
 AAACATTCCA AAAAAAATAA AA

Seq ID NO: B14 DNA sequence
 Nucleic Acid Accession #: XM_086767.1
 Coding sequence: 276..611

1 11 21 31 41 51
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 CAAAGATTAC AAGACTAGCT TATGTGTGGA CTGTGACTGT TTTAAGGAAA AATCATGTCC 120
 TCGGCTGGGT TATCAAGCCA AGCTATTTAA AGGTGTTTAA AAAGAAAGGA TGGAAAGGAG 180
 ACCCTCTGGT ACCACTGTGT TTTGGATAC AAGTGGTACA TATCCATTCT GTAGCCTATT 240
 ATTTTGTCT CAGTATAATT GTTCCAGATA AAACATGAT GATGCTCTG TTTTCATTTA 300
 AATTATTAAA TCAGCTTGGG ATGATTTAAG AGCCAAGGCT TTATGAAAAG AACAAACCAT 360
 TTTATAAAT TCAAGAAGTC AAGATTCTTG CTCATTTTAA TAATGACTTT GTAAATATTT 420
 CAGCATGGG TTTGACATAT TTCCAGAGCT CAAATCTGCA GTGTTCACA TGCACATACA 480
 AGATCCAGG ACCTCATGTT AAATCACTTA CATACCCAGA AAGACCACCA CTTTGCAGGT 540
 ATAATATTGT ACTTAAGAC AGAGAGGAAG TGTTCCTTAA TCCAAACACA TGTACACCA 600
 AGAACACATA AGATGCCCTC TTCCATCAA TGCACTTGCT TGTGAATTA TGGACTTGT 660
 AATGAACAAA TGCATACAGT CTTTATAAT GCACGTGTTA ATTTGAGATT CAAGTATTT 720
 TATTTCTTGG AAAAAATTTT AAGAATCAA AATAAAGAAA ATAAAAATG CATACAGTTA 780
 AACATTCC

Seq ID NO: B15 Protein sequence
 Protein Accession #: XP_086767.1

1 11 21 31 41 51
 MMDGSEFSLK LNLQGMIEEP RLYEKNKPFY KLQEVKILAQ FYNDFVNISB IGLTYFQSEN 60
 LQCTCTTKYI QRLMLKSLTY PERPPLCRYN IVLKDRREVF LNPNTCTPEN T

Seq ID NO: B16 DNA sequence

Nucleic Acid Accession #: CAT cluster

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	AAGTGCTATT	AGCCCAAGCT	TCCTACATTC	ATTAAAGAG	TGACTATCAA	AAACAGCAAC	180
	ATGCACAAATG	GTACATATGC	ACAAATGGA	ATTATATCAA	CAATATACA	AAATACCCAA	240
10	AATAAAATAT	TTACAGGITT	AAAAATATAA	ACATTGATTC	CTCTATCCCA	TAAACCAT	300
	GGAGTGGAGA	AAGGAGGAAA	GACCCATITG	CTATTTAGAA	TCCTTTTAA	AACAAGTTT	360
	TAAACATAG	AATTAGTTCT	AGGAGACAAT	TTTTGATGTT	TTTCAGGGGT	TAAACATTT	420
	ATTATAAAA	TAACATCTAT	AAACCTACTA	ACAATTTTCC	TCCTGTGCAC	AAAAATAATA	480
	CTGCCAAAC	CTGTCTCTCA	AGACATGCCT	GACITTCAGG	AAAGCTAATT	ATGGAATGG	540
15	AGTTTCTCT	TTGGGTATC	TTTGTTACTA	TTTTCAATA	ACCAGCAACT	CCCTATATA	600
	CCTGAGATA	CTTTATATAA	ATAACGTGGG	CGAAACCTGA	AGTTCACAAT	GAGCCTGCTA	660
	GGTAGCTGGT	GTCAAGTAGA	AATGATAGGA	ATTGACTTTG	CCAACCAACT	CAAAAGCATT	720
	TTCCCTGATA	TCCTTCCATG	ACCTACCACT	ATCAGATCCT	CCATATTCAA	TAAGATTAT	780
	CCTGGAAGCA	ATGAAAATGT	TAAATATTAC	TTTGCTAGAG	TTTCTCTCC	TTTATTTAGA	840
20	AATAAATGTG	TAGTGGGGAC	CAGTGGTTGT	AATGTAGATA	CTTGAGAAGT	TTCATTGATT	900
	CCTTCAGACC	CATGCCG					

Seq ID NO: B17 DNA sequence

Nucleic Acid Accession #: NM_022898.1

Coding sequence: 268..2739

25	1	11	21	31	41	51	
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	GAAAGAGCAA	AATAAAGAG	AAGAAGAGGA	GGAAGAGAGG	GAAAGAGAGG	AAGGGAATAA	120
30	AAACACCAAC	CCGGGAGAG	GAGGAGGTGC	GGCGGCGCG	CGCGGCGCG	CAGCGCGCG	180
	AGCGGCGCG	CGCGGCGCG	GACCCCTCC	CCCGGCTCC	CCCATCAGTG	CAGCTCTCC	240
	GGCGATGCCA	GATAGATGC	CGGGGCAATG	TCCCGCCCA	AACAGGCAAA	CCCGAGCAC	300
	TTGTCCCAAG	GGGAGCTCAT	CACCCAGAG	GCTGACCATG	TGGAGGCCG	CATCTCGAA	360
	GAAGACGAG	GTCTGGAGAT	AGAGAGCCCA	AGTGGCTTGG	GGCTGATGGT	GGGTGGCCCC	420
35	GACCTGACC	TGCTCACTTG	TGGCCAGTGT	CAATGAACT	TCCCTTGGG	GGACATCCTG	480
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	CGGTGGAGA	TGGGATGCCA	AGTCAACCC	GACGAAGATG	ACCACCTGCT	CTCACCCACG	660
40	AAAGGCATCT	GTCCCAAGCA	GGAGAACATT	GCAGGTAAAG	ATGAGCCCTC	CAGCTACATT	720
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	ACGCAACGCT	TCCGCATCTA	CCTGGAGCCC	GGGCGGCGCA	GCAGCTCGCT	CAGCGCGCG	840
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45	CCGCGCTTC	CGGAGGCGCG	CTGCGGCGG	ACGCGGCTC	TCTTCAGTCC	CGCGGCGCG	1020
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	AGTGCTTGG	ACCGAGTCT	CGCGCTGAAC	CCCATGGCCA	TGAGCTGCGC	CGCGCTGAG	1140
	TTCTCGCGC	GCTCGCGCA	GCTGGCGGG	AACAGCTCCA	CGCGCGCGC	CGTGTCCCG	1200
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	GTGGATGTAC	AGCGGATAAC	AATCTTTCAA	GTGCTAGCAC	TTTGTTCAG	AATCGGAATG	3420

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Seq ID NO: B18 Protein sequence
 Protein Accession #: NP_075049.1

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Seq ID NO: B19 DNA sequence

Nucleic Acid Accession #: NM_000399.2

Coding sequence: 339..1769

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Seq ID NO: B20 Protein sequence

Protein Accession #: NP_000390.2

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Seq ID NO: B21 DNA sequence

Nucleic Acid Accession #: NM_004962.2

Coding sequence: 457..1893

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30	TGTGAGTTCC	TGAGCTCTAA	GATCGTTCTG	CCATCCAAAC	ATGCCACCAT	CCAGAGCATT	1740
	GTACGGGCTG	TCGGGATCAT	CCCTGGCATC	CCAGAGCCCT	GCTGTGTTCC	CGATAAGATG	1800
	AACTCCCTTG	GGGTCTCTTT	CCTGGATGAG	AATCGGAATG	TGGTTCGTAA	GGTGTACCCC	1860
	AACTCATCTG	TGGACACATG	TGCTGCGCGG	TGAGACCACT	CCAGGTGGGA	AAGAAGCCAC	1920
	GCCACGACGA	GCTGCTCTCT	CGGAGCCTTC	TGCAACACAG	ACTTGTGGTG	CAGCTGCAGA	1980
35	CACAGAGCAC	AGCTCATGGG	CAACATCACT	GGGCCCCAGA	GAGAGCTGTC	CGCCAGTSCA	2040
	TCATTAGGGG	GCTTTTCATT	GCTAGTGACT	AGCCCTTAA	ATGCCAGCCT	GAGTACCTGA	2100
	AGGAATCTGG	GAAATAGCCC	TGGCCTGAAA	GTGGCCCATC	ATTGATACCC	ACTGTTCTGA	2160
	AGGCTTGAAA	ACAAACATA	TCCACACAT	TGGCTTGATG	TGATCATCAT	CTCATAACTG	2220
	AGCAGAAGA	CTATGCAAT	CTTAGGGGCG	TGCTCTCTG	CACACGAAA	GAACTCTGTT	2280
40	TAAATGCTCA	GTTCAAGACA	CTTTGGGCCA	CATAGTGATT	TTGGAAAAA	GGATAATCGT	2340
	GGTGTAATAG	AGTGTTCCTT	TTCAAAGTCC	ACTGCAGAGC	TTTTATCCAT	ATGGTATGCA	2400
	CATGTAGCCA	ATATTGGTTT	CTTTTCTTCA	ATATATATAT	TTTTATTTAA	AACAACAAAA	2460
	AGGGAGGGCG	TTGACACATG	TCCCCACAGA	GATAGTCATG	CTGAGTGGGG	GTGTTTAAAA	2520
	CATGCATATT	GAAATTAACAC	ATATAGTAAC	GTGGGAATAC	TAAAAAATAA	CCAAGATTTT	2580
45	ATATTTTGT	AAATTAACAT	TCTATAGTCT	TAGATGTGTT	ATGTTATGTT	TTTTATGGA	2640
	AAGCTAATAA	ATTAAAGGTA	CAGTGGTATC	TTGA			

Seq ID NO: B22 Protein sequence
Protein Accession #: NP_004953.1

50	1	11	21	31	41	51	
	MAHVPAETSP	GPFGQLLLLL	LPLFLJLLRD	VAGSHRAPAN	SALPAAADGL	QGDRLQHRP	60
	GDAAATLGPS	AQDMVAVEMH	RLYKYSRQG	ARPGGNTVR	SFRARLEVD	QKAVYFFNLT	120
55	SWQDSEMIT	ATHFHYSEPP	RNPRALEVL	KPRAKNASGR	PLPLGPFTRQ	HLFRSLSQN	180
	TATQGLLRGA	MALAPFPRLG	WQAKDISPIV	KAARRDGELL	LSAQLDSEER	DPGVPRPSPY	240
	APYILVYAND	LAISEPNSVA	VTQLRYPFPF	AGDPEPRAP	NNSADPRVRR	AAQATGFLQD	300
	NELEPLDERP	FRABAGHFEK	EQLNPSPPRA	LKPRFGRKDR	RKKQGEVFMA	ASQVLDYDEK	360
	TMQKARKQON	DEPRVCSRRY	LKVPFADIGW	NEWIISPKSF	DAYYCAGACE	FEMPKIVRPS	420
60	NHATIQSIVR	AVGIIRGIPE	PCCVPDMNNS	LGVLFLDENR	NVVLKVYPMN	SVDTCACR	

Seq ID NO: B23 DNA sequence
Nucleic Acid Accession #: AK026322.1

65	1	11	21	31	41	51	
	ATTCTTTAAA	TACTTAAACA	TGGTTATAAC	AGCTGTGTTT	TAAGCTCCTT	GTCTGTTAAT	60
	TCCATCATCT	GTCAATTTTG	CATCTGTTT	TATTGACTAA	CTTCTTCCT	CATCATGGTC	120
	ACATATCCTT	GCTCTTCCCG	ATATTAGTA	AAGTTAGTT	GGATGCTGGA	TTGTTTAAAT	180
70	TTAGCATTTT	GCTTTCACCT	CTTTTCACCT	TGCTTTTAAA	AGTATTGGAC	TTGTTTGA	240
	TAGTGAAT	ACTTGCAGAT	CAGCTTGATC	ATCTGAGAC	TTGTTTAA	CTTTTGTGCA	300
	AAAGGCTATG	CTACTTCAAG	TATAATAAAA	CCTAGTTTAA	GTGTTATCCT	ATAACTAAGG	360
	CATGTGTACA	ATTGGAATGT	CTCCAACCTT	GTGTGACTC	TGAAAAATGT	TCAGCTCCCA	420
	ATTTCGAGT	AAATTTTCTT	GTTCAGCCTT	CGACTCTCAT	CCTACTCAAG	TGTGGCTCTG	480
75	TATCCACAAA	CAGCTTGGGA	GATCTCATGA	AGATTTCIGA	AACITTTGCT	CTGCAGGATA	540
	CCTTCCTTTG	TGGTTATGTT	CCCTGAAAAC	TCCAGCCTCC	GTGCTTTCAA	TTCACTGAAA	600
	CTACTACTCT	GCTTGGATTG	CCCTCTTATA	CAATGGTCTA	CCAAGTGACT	GCAACAGAAA	660
	ATCTAAGGGA	ATTTCAGGAG	TCACCTCAAT	TATTTTCTCT	TTTTTCAGGG	ATTATAGTAG	720
80	TACTATACCA	CCTGTGAGCC	AATGTGTGAG	AATGGTGGTT	TCATACATTT	TCTCCAAATC	780
	TTCTTGTGTA	CAGGAGCCTC	CATTACTTTT	CAACAGATAA	TGCAGTTGCA	GTTGCTCTTC	840
	CTTTTCTTCA	TTATGTGTTT	ATCTCTGGCA	GTTTGAGCCA	AGAGAGGGCA	CGGAGAGTAA	900
	CAATGACTAG	AGAGCACTTC	TGTTGAGGCT	CATTCAATGA	CCCTACCCC	AGTGCTTTAT	960
	GAATGTGTGC	TGCAGATGTC	ATACAGCATC	ACAGCTTCTT	CTCTAATTTA	TGAGCCATAA	1020
	TTTTTTT	TGTATTTTAA	TTGTATTACC	TGCTTGGTTC	CAAGAGGATG	ATGAGGAGGA	1080
	CTACTATAGG	ATAAATTTGT	TTTTATAGAG	CAATTTCTCA	TGGGTACCGA	GGGATAGTAC	1140

TCCATTTTCC TCACTGATAT CGGCTTGATC ATCTGAGTCA GTGGGCTCAT TGTGGAAACA 1200
 TATGGAATCC TTATGCTTT TTCTCAGGCT GCCTCTGTTA CATGAAATAA AGCCAGAGTT 1260
 GATTGTGAAA AAAAAAAAAA AAAA

5 Seq ID NO: B24 DNA sequence
 Nucleic Acid Accession #: cat cluster

	1	11	21	31	41	51	
10	TGTATACATT	CCTTTCAAAT	AAAGACCTTG	AGAAAAACAGC	AGAGCCCAAGT	GAAGATCACC	60
	TAAAGAACTT	TGTGGCTAAAT	TTATACTTCA	TGTAGTAGCA	GTGGGTACTG	GGCAGGGTCT	120
	CTTTCCCACT	CTGATGATTT	GTGCTCTTAT	TTTTCTTAGA	TTTACCTCAT	CTAGGGCATA	180
	TTCTTTTCCC	TCTTCTCTTT	TACCTTCTCT	GGTCTGTATC	CCTCTGTACT	CAGTTCCCTT	240
15	AAATTATGGG	ACTACAAACT	AATATACTAG	AAAAGCATAC	ACTTATTTTA	TTTGAATGCA	300
	GAAATGCTAT	CTATCAGTAT	ATATACATAA	GAATGTATAT	TACAGTATAT	CTATATATAC	360
	TAAACACTGT	AACCTTCAGT	ATTCCCCAGT	TAGCCTACCT	AACCTCTCTG	TGGGTATGTG	420
	TAATTCCTAT	TAGACTACTA	GAGAAAAACC	AACCTGGCAGT	TTGCTAAGCA	TATCTACTGG	480
	TGTTTCTTCT	GGGCTCTTCT	TTGGCTAATT	GATGTAAATTA	TACTGGCTCT	AAAGATTTC	540
20	TGCCCCATAA	GTAAATAGTA	TAGCCACATT	CTGAACATAT	CAAAAGTACA	AACCTAGGAG	600
	GAGTGTATGT	ACAAAATATG	AAAATTTTAT	GAAAATGAAC	ATGTTTTTAT	GATGTTATTT	660
	CTAGTTCATA	AGAATGTGAT	GACTGCTTTG	CTTCATTTAT	GTACGTCTCC	ATTATATTCT	720
	TGCTGTCTAT	TAGACTACTA	TTTATATCAG	ATTAGGATAA	ACTAAGCCAT	TTTATGTATT	780
	TTATTTTAAA	CCTTATTTTG	GCAAGATAAT	TCCTTAGAAT	TGGAAAAGCT	GTACCTTGA	840
25	AATTACCAAT	TATTTACAAA	ACATAGAAAT	GTATTTGTAGC	TACAAAGACA	ACCAAGCATT	900
	TTCTGTGTTT	TAATGATATG	CTAAAAAAGT	ACATTTAGTT	TATTTTACTC	AGTTTGTAAA	960
	TGATTTTFTT	ACTGGCTCTA	TTGCCCTTAA	ATACTAAGA	GATTAATGAT	TCTTTGTATA	1020
	ATTTCCTTTT	TCTTTGTCTT	TTTFTTTACA	TTTGCAGAG	TTATATCTAT	AGTTTGTATA	1080
	ACATTTCTTT	ATGTATTTCT	GATAACTGAA	AACAACATAA	GGTGTGGGCT	ATTAGAAAAT	1140
30	AATTTGTAGC	AGTAAAGATA	CTGATGTAAT	ATGTATGTTG	GACTGAAGTA	TTTCTTTATA	1200
	AACATCTCTT	TTGATTTTAA	GCAAAAATGA	TGTTAAAGCA	TGTTTTTACA	TCAGTAAAGT	1260
	CATTGTCCGA	CCTTCTGAAA	ATGAAAGGTT	TTTACCTAGA	TACTGTAAAT	TACAACCTCT	1320
	TAACAATCAT	ATTGTCTATT	GTGTTTCTCT	GCAAAACAAA	ATGTTTATGG	GCCTTCATGA	1380
	GGCTTAAGAT	TGTAGCCAAA	AATGGACTGA	GTTCAGGACC	CTTCAAGCAG	TAGGCATTCA	1440
35	GTTCACAGAG	AGTTGGTACT	TTGTAACCCA	GACTTACAGT	TTAAAAATAT	CAAGTTAGCT	1500
	GATGTTTCTT	TATAATAAAA	ATACTATTTT	GCCTTAGAGT	TGTATTACAA	ATATTTGTGC	1560
	TTAACATTAG	AAATAGCTGT	TTTAAATGTT	AGTTAACATA	TTAATTTTCT	CAGAAAAAAA	1620
	GCATGGTTTA	TTTTTAATAA	TGAAATAGAG	AACATAATAC	GTAATGTTCA	GTATAACAGC	1680
	TGAGTTAAAA	CATCTGCCAG	GATTATACATC	AGTGGCTTTT	TGCCAATGCA	TAGAGGCATT	1740
40	TTTCTCTAAG	TATGATGGCT	AATGATAACT	ATTCCTTTGT	ACACATTTCA	GTCACTCCCA	1800
	TACAAGTAAC	TAGTGGGTGA	TATGTTTCAC	TCCAAAGGGT	GTATTAATTC	TGAATGCTAA	1860
	TCATGAAGAC	TAAAGTTAGG	ACAACACTTC	AAACCAGGAA	GTGGAAGCTG	ATTTA	

Seq ID NO: B25 DNA sequence
 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence: 1..1144

	1	11	21	31	41	51	
50	ATGGAGCGCG	GGATGCACCT	CGGTGCAGCG	GCCTCCGCGG	AGGACGACCT	CTTCTGCAC	60
	AGAGGCTTGA	GCCTCTCCAC	CTCCAGCGCG	TTGGAAGCGG	CTTCCGCTC	CACGCCGCCG	120
	GGCTAGGACC	TGTCCCTGGC	GCCTCCGCGG	CGGGAAGCGC	CGGCGTCTC	CTCCTGCTCG	180
	CCCTCGGCTT	GCCTCGAGCC	GCCTGACCCC	GAGGGGCGAG	GGCTGCTGTT	GCCTCCGCGG	240
	GGAGGAGCGG	GCGGCGGCGG	CGCGGGAAGT	GGCGGCGGCG	GCGGCGGCGG	GGTGGGCTGC	300
55	CCCGGCGTGC	TAGTAGGTTT	AGCGCGGCTT	CGGCGGCGAC	CTAGCCTAAG	CAGCTTGCCT	360
	GCGCGGCGCG	CCCTTTGCTT	CAGTAAAGGC	GAAAGCGCGA	CGCGGGGCTC	GGTGGCGGAG	420
	AGCAGCGCGG	GCGAGCAGAG	CCCGGAGGAC	GACAGCGAGC	GTGCTGCGGA	GCTCTGCTCG	480
	CGGGCGGCGG	TAGCCGACCC	CGGGGCGCTC	CGGGGAGCGG	GAGGTGGTGG	CGCGAAGGCA	540
	GCGAGGCGCT	GCTTCAATGC	CACTCTCCAC	GGCGGCGGCA	GGTCCCTCC	GGGGGGGCTG	600
60	GGCGGCGGCG	GCGCGCGGCG	TAGCAGCAGC	GCTAGCAGTG	GCGCGGCTGG	CGGTAGCGGT	660
	AGCGGCGAGG	GCGGCGAGAG	CAGCAGCAGC	AGCAGCAGCA	GCAAGAAATC	CAAGAGCAAA	720
	AAGGCGCTGC	GGCTTAACAT	CAATGCCCGA	GAGCGCGGCG	GGATGCAGCA	CCTGAACGAC	780
	GCGCTGGACG	AGCTGCGCGC	GGTGAATCCC	TACGCGCACA	GCGCTCGGCT	GCGAAAGCTC	840
	TCCAGAGATG	CCAGCTGCTT	GCTCGGCAAG	AACATACATC	TCAATGAGGC	GAGGCGGCTG	900
65	GAGGAGATGC	GCGGCTTAGT	CGCTTACCTC	AACAGGCGCC	AGGCCATCTC	GGCTGCTCTC	960
	CTGCCCAGCT	GCGCGGCTGC	AGCGGCGAGCA	GCTGCTGCCC	TGCACCCGCG	GCTCGGCGCC	1020
	TACGAGCAGG	CAGCGGCTGA	CCCGTTTACG	GCGGAGCTGC	CCCGGCTGTC	CTCCTGCGCG	1080
	GAGAAAGTGC	CCCTGTTTAA	CAGCGTCTCC	TCCAGGCTCT	GCAACAGAGT	CAGGAGAGAG	1140
	CCTT						

70 Seq ID NO: B26 Protein sequence
 Protein Accession #: FGENESH predicted

	1	11	21	31	41	51	
75	MERGMHLGAA	NAGEDDLFLK	KSLSASTSKR	LEAAFRSTPP	GMGLSLAPPP	RERPASSSSS	60
	PLGCFEPADP	EGAGLLLPFP	GGGGGGGAGS	GGGGGGGAGV	EGLLVGSAGV	GGDPSLSSLP	120
	AGALCLKYU	ESASRGSVAE	SSGGGQSPDD	DSGRCELVL	RAGVADPRAS	PGAGGGGAKA	180
	AECSNAHLH	GGASVPPGGL	GGGGGGGSSS	GGGGGGGSGS	SGSGSSSSSS	SSSSKKSKEQ	240
	KALRLINAR	ERRRMHDLND	ALDELRAVIP	YAESPSVRKL	SKLATLLAK	NYILMQAAL	300
80	ENRRLVAYL	NQGQALSAAS	LPSSAAAAAA	AAALHPALGA	YEQAAGYPPS	AGLPPAASCP	360
	EKCALFNSVS	SSLCTQCTEK	P				

Seq ID NO: B27 DNA sequence
 Nucleic Acid Accession #: cat cluster

	1	11	21	31	41	51	
5	TTTTTTTTT	TTTTTTTTTAA	ATGTTTGATC	AAAAATATTT	AATAAAGATT	CTTCTGACA	60
	TAGATATACACA	TACAAAATGGT	CGTACATAGC	TGTCATATGT	TGATTGAOCT	ATTTTATATTA	120
	TATATCATCTC	TTTACACATC	AGCAACCCGC	CAACAGATCC	ATCACAGCTC	CCAACCTCAC	180
	ATCCAACTCG	ACMAACTGAA	TTTGTATTAT	CTGCAAGGAG	TGGAAATATG	GAGGACTACA	240
	TTTTTAAAAA	AGATTTTTCTT	GAATTTTACA	GGGCGGAAAG	GCAGTCAAC	AGCCATGCHA	300
	AACTAAACCT	GAAGAGCTCAC	TTTGGGTAAA	TGAGCTTCTG	TTCTTCTCTA	GTTTTCTTTC	360
10	TTTTTAAATT	TTAATTTTTTT	AGAAAATAATA	CAAAAGGATT	CACACCATAT	GCARAATCAA	420
	CCAGTCTTTT	AACCTAATAA	ATTCTCCACA	GTTAAATAAA	CATATATGTA	CATATATATT	480
	AAAAGCAATT	AAATTAGACG	TTTTTAAAAA	GCACAGCACCA	GCCCTGAAAA	ATATTTGGCT	540
	AGCATGTTCT	TACGTAATAGC	AACATATTGC	GIGATGTITT	TCOCTTTTGG	AATGTAAGGG	600
15	AGTCCOCTTT	CAAAAAGAGG	ATCAATTCCAT	TCATCAATTA	AGATATACAG	TTTCTCTGTA	660
	TTTTTGGACT	GAGCAATTT	ATTTAAAGCTC	AAITTAATAA	CAGGGATGAC	GCAACTGAAA	720
	ATATCCAGGT	GAACCTTTAT	AAACCTTAAGC	AGGTCGAGTA	CATCAATATT	TCCTCTTACA	780
	CTGTGTGGCA	AATAAACCTT	TAAACACTTG	GCACACAGCA	TAGTAAATCT	ATAAAACAAT	840
	TTTAGAGGCA	TAAAAAAAT	CTGCACATAA	GACCCATGAC	TTTAACACAT	GATAAATACT	900
	GTGTATGTGG	TAGGGTTCAT	GAAGAAATAC	AAATAAATAC	CATGAATTTG	TAATACATCA	960
20	TTTGACGATTA	GAAGTATACA	AGGTGCACAT	ARAATATTTT	AATGCAATT	CTTTCAGCCA	1020
	CAGTCAGTTT	TTTTATATCA	CTCTCGCCAA	AACITTTGAGC	ATTTTTCACG	GATTAAGATT	1080
	CAGAGACAAT	AAAAAAATACA	AGTCTTTTCAT	AGTAACATGT	TTCTCTCTCT	TGCTCTGGG	1140
	TTTTTTTTC	CCCTCACTTA	AGTCAACATT	TCAGGTTTTT	CTCTGCTGCT	AGAAATCAAA	1200
25	TTTTATTTC	AGTGCCCTTT	CTGATTTGTC	TBAATGAATA	TTCCATCTCT	CATGCTACCG	1260
	ATCGCTC						

Seq ID NO: B28 DNA sequence
Nucleic Acid Accession #: NM_002581.2
Coding sequence: 368..5251

	Coding sequence: 368..5251								
	1	12	21	31	41	51			
30	GGGGGAGGGA	ATTGAGCGGA	TCAGTCTTAA	GAGGAGCTTT	TTTTTGGAGC	GAGAAATCAT		60	
	ATAAATAAAA	ATGAAATAAA	ACAGAGGAGA	AGGCAACAGG	CTGTGTAGGG	GAAAAATAGG		120	
35	CAGATAAAGG	AGCGGGGAGA	GAAATTAATT	GCCAAACGAG	AGGAGTTTGG	CTGTATTTTT		180	
	CAAAAGGTGG	GAGAGTGGAG	CACACACCTT	GAGGAGGAAA	GCGAGAAAGA	AAGAAGAAAA		240	
	GCAACTGAAG	GGGGGCTCGG	CCAAAGAGGG	TGAAGAAGCG	AAGAAGATCG	AGGCGCTCGG		300	
	CTGCTCCAAAG	CTGGCAGCTC	CGGGTGGCGG	TGCAGGGGCT	AAGGGGGGGG	CGGGGGGAAC		360	
40	GTGCGGACATG	CGCTCTTGGA	TGTGGGTGCT	GCACCTGGGG	CTGTCTAGAGC	CCGCGCTGGG		420	
	GTGGGGACATG	CGCGAGCGCT	CCGCGCGGCT	CCGAGAGACG	CCGCGGGCGG	CGCGACCCCG		480	
	CGCGCCCGCG	CGCGCCCGCG	CCACCTGTGC	CGAGCGCGCG	CGCGCGCCCG	CGCGGCTTGC		540	
	CGCGCCCGCG	CGCGCGCGCG	GGGTGGCTGT	GCAAGCCGTG	CGGTGTCCCG	GGCGCGCGCG		600	
	GCAGCGGGAG	CGGAGGGGGG	CCACCGAGGA	GCTGAGCCCG	CCGAGCCCGG	CGCTCTATTT		660	
45	CAGCGGGGCG	CGCGAGGACG	TGCGAGTCTT	CGGGGCGGAG	CTCGAGCTGC	CGCGGGAGCG		720	
	GTGTCGCTG	GAAGTTGGCT	TGCGAGCGGG	GGGGGGCGAG	AGGCTCTCGG	CAGTGATCAC		780	
	AGGGCTGTAT	GACAAATGTT	CTTATATCTC	AGGTGACCGA	GAGTGGGTCT	TGGGCATTCA		840	
	ACCATCATGT	GACCAAGACA	ACAAAGACCC	AGCTACTATT	TTCTCTTGA	AGACAGACCG		900	
	AGCCCGGCAA	GTGACCAACA	TCAATGCCCA	CCGCAGCTAC	CTCCGAGGCC	AGTGGGTATA		960	
50	CTCAGTCTCC	ACTTATGATG	GCGCATCTAT	GAAGCTCTAT	ATGATATGTT	CCCAAGTGGC		1020	
	CACCTCTGGG	GAACCAAGTGG	GTGGCTATAT	CAGCCCACTG	AGTCAGAAGT	CGAAAGTGCT		1080	
	CATGTTAGGG	GGCAGTGCCC	TGAATACAAA	CTACCGGGGC	TACATCTGAG	ACTTCTACTT		1140	
	GTGGAAGTGG	CGGAGGACTG	AGCGGGAGAT	ACTGTCTGAC	ATGGAAGACC	ATGCGGCCCA		1200	
	CACCTGCTCT	CTCAGCTTCC	TCTCTCAGGA	GAACTGGGAC	ATGTGGAAGC	ATGCGTGGCT		1260	
55	CCCCATGAAG	GATGGGACGA	GCCCCAAGT	GGAACTCAG	ATGCGCCACG	GCTTTCTGCT		1320	
	GGACAGAGT	GTGAGGCGCT	CTCTGTGGG	ACAGACATTG	TGTGACAACA	CAGAGGTTCAT		1380	
	TGCCAGCTAC	ATACAGCTCT	CAAGTTTCCG	CCAGCCCAAG	GTGGTGGGCT	ACCGCTTGGT		1440	
	CAACCTCTAT	GAAATGATGC	ATAGGAACCT	GACGGTGAGG	CGCGAGCAGG	TGGACTTCCA		1500	
	GCACCATCAG	CTGGGCTGAG	CCCTTCAGCA	ATACAACATC	TCTCTGGGAG	TGGACGTGCT		1560	
60	GGAGGTGAGC	AACCTCTCCC	TTCCGCGCGG	CCCTACTCTG	GCCAACTGAG	ACATCAGCAA		1620	
	GATTTGGGAT	GAGAACTGTG	AGCCCGAGTG	CAACCAACAG	CTGAGCGGCC	ACGACGGCGG		1680	
	GGATTTGGCG	CACCTCTCGC	ACCTCTGCCT	CGTGAAGAGC	CAGCAACAGG	GGGTGTGAGA		1740	
	CATGAGCTGC	AACATGAACT	GTCTCAATTT	TGATGTGGGA	GAGTACCTTG	ACCCGAAATG		1800	
	CACCAATGTC	ACTCAGACTG	GCTTTGAGCG	CGACTCTCCA	CACAGAGCCT	ACTTGGATGT		1860	
65	TAAATGAGCT	AAGAACATTC	TTAAATGAGA	TGGATCAACA	CTACTCAATA	TTTTCTTTGC		1920	
	AAAATCCTCA	GAGGAGGAGT	TGGCAGGAGT	AGCAACTTGG	CCATGGGACA	AGGAGGCCCT		1980	
	GATGCACTTA	GGTGGCAATT	TCTTGAACCC	ATCTTTCTAT	GGCATGCTCT	GGCACACCCA		2040	
	CACCATGATC	CATGAGATTTG	CTTCAGAGCT	GGGCTCTCTT	CACGCTCTTC	GAGGACTCTC		2100	
	AGAAATCCAG	TGCTGCAAGT	ACCCCTGCAT	GGAGACAGAG	CCCTCTCTTG	AGACTGGAGA		2160	
70	CCCTTGCAGT	TATACCAAGG	CAGGCCCTAA	ACACAAGTCC	TGTGTGAGAC	CAGGCGCAGG		2220	
	AAATGACACC	TGTGGCTTTC	ATAGCTTCTT	CAACACTCTT	TACAACAAC	TCATGAGCTA		2280	
	TGCAAGTATG	GAGTGTACGG	ACTCTCTCAC	GCCCAATCAA	GTGGCCAGAA	TGCACTGTTA		2340	
	CTTGGAGCTG	GTCTACCAAG	CTGTGCACGC	CTCAGGAAAG	CCAGCGCTGA	TGTGCCCTGC		2400	
	TGCCCAAGTT	CTGGGCCACA	CAACGGGACT	TGTGACACTG	GAGTGGCTTC	CACTTATAGA		2460	
75	CGCCCATTTT	TTTGAAGAG	AATTTGGATC	AGCATGTCTT	CTTTGGCTTG	AAGGAGAAAT		2520	
	CCTGGTGCAG	TATGCTTCCA	ACGCTTCTCT	CCCAATGCCG	TGCGAGCCAT	CAGGACATCT		2580	
	GAGCCCTCTG	GAGGACGAGG	GTCATCTCTA	TGTTGAACAG	CCCTCTAAGT	CCAGTGTCCG		2640	
	CACCTGAGAG	CCAAATTTAG	CTGTCAACCC	ACACAGGTTT	CTCCAGCCTT	CGCCTGAGCC		2700	
	TCAAGCTCTG	TACCTCGAGC	TGGAGTCTCT	CTACCCCTTG	GTCCCTCAAT	CTCTCAACAT		2760	
80	TTTGGTGAAC	TTTGTCTCCA	GAGCTTGGGA	CTCTATGAGA	GCTGTGAAGT	ACATCAAACT		2820	
	GTTEGCTGTC	AGTGGGAGGA	ACATCTCTCT						

GTACCACTAT TGGGTCATAA CTATTTTCAGG AACTGAAGAG AGTGAGCCAT CACCTGCTGT 3180
 CACATACATC CATGGACGTG GGTACTGTGG CGATGGCATT ATACAAAAG ACCAAGGTGA 3240
 ACAATGCGAC GACATGAATA AGATCAATGG TGATGGCTGC TCCCTTTTCT GCGGACAGA 3300
 AGTCTCCTTC AATTGTATTG ATGAACCCAG CCGGTGCTAT TTCCATGATG GTGATGGGT 3360
 ATGTGAGGAG TTGGAACAAA AAACCCAGCAT TAGGACTGT GGTGTCTACA GCGCCAGGG 3420
 ATTCTGGAT CAGTGGGCAT CCAATGCTTC AGTATCTCAT CAAGACCAGC AATGCCAGG 3480
 CTGGGTATC ATCGGACAGC CAGCAGCATC CCAGGTGTGT CGAACCAAGG TGATAGATCT 3540
 CAGTGAAGGC ATTTCCAGC ATGCTTGTA CCTTGCACC ATCAGCTACC CATATCCCA 3600
 GCTGGCTCAG ACCACTTTTT GGCTCCGGGC GTATTTTCT CAACCAATGG TTGCCGAGC 3660
 TGTGATTGTC CACCTGGTGA CGGATGGGAC ATATTATGGG GACCAAAAGC AGGAGACCAT 3720
 CAGCGTCGAG CTGCTTGATA CCAAGATCA GAGCCACGAT CTAGGCCTCC ATGTCTCTAG 3780
 CTGCGGAAC AATCCCTGA TTATCCCTGT GGTCCATGAC CTCAGCCAGC CTTCTACCA 3840
 CAGCCAGGCG GTACGTGTGA GCTTCAGTTC GCGCCGTGTC GGCATCTCGG GGTGGCCCT 3900
 CCGTTCCTTC GACAACTTTC ACCCGCTCAC CCTGAGCAGC TGCCAGAGAG GCGAGACCTA 3960
 CAGCCTGCTC GAGCAGAGCT GCGTGCATT CGCATGTGAG AAAACTGACT GTCCAGAGCT 4020
 GCGTGTGGAG AATGCTTCTC TCAATTGCTC CAGCAGCAGC CGCTACCAAG GTGCCAGTG 4080
 TACTGTGAGT TGCCGACAG GCTAGCTGCT CCAGATACGG CGGATGATG AGCTGATCAA 4140
 GAGCCAGAGC GGACCCAGCG TCACAGTGAC CTGTACAGAG GGCAAGTGA ATAAGCAGGT 4200
 GGCCTGTGAG CCAGTGCAGT GCAGCATCCC AGATCAACAT CAAGTCTATG CTGCTCTCT 4260
 CTCTGCTGCT GAGGCGACCA CCTTTGGCAG TCAATGTTC TTCCAGTGCC GTCACTCTGC 4320
 ACAATTGAAA GGCACACAA GCCTCCTGAC CTGCATGGAG GATGGGCTGT GGTCTCTCCC 4380
 AGAGGCTGAG TGCCGACAG TGTGCTCTGC TCCACCCCT GTGCCCAAGT CAGACCTCCA 4440
 GACCGCCCGG TGCCGAGAGA ATAAGCACAA GGTGGGCTCC TTCTGCAAT ACAATGCAA 4500
 GCGTGGATAC CATGTGCTG GATCTCTCG GAAGTCAAAG AAACGGGCTC TCAAGACTCA 4560
 GTGATCCAG GATGGCAGCT GCGAGGAGG AGCTGTGTGT CCTGTGACT GTGACCCACC 4620
 TCCACCAAAA TTCCATGGGC TCTACCATG TACTAATGGC TTCCAGTCA ACAGTGTG 4680
 TAGATCAAG TGTGAAGACA GTGATGCTC CCAGGACTT GGGAGCAAT TCATTATTG 4740
 CCGGAAAGAT GGCACCTGGA ACGGCTCCTT CCATGTCTGC CAGGATGTC AAGGCCAGTG 4800
 CTGCTTCCA AAGCAGCTCA ACAGCAACCT CAAACTGCAG TGCCCTGATG GCTATGCCAT 4860
 AGGTCGAGG TGTGGCACTT CGTCTCTGGA CCAACACAGC GAGTCCATCA TCTGCTCAAT 4920
 GAGCGTAGC GTGGCGGACA TCCGCCACTG GCTGAACCCC ACACGGGTAG AGAGAGTTGT 4980
 CTGACTGCT GGTCTCAAGT GGTATCTCA CCTGCTCTG ATTCAGTGT TCAAAGGCTG 5040
 TGAGCCCTTC ATGGGAGACA ATTATTGTGA TGCCATCAAC AACCGAGCTT TTGCAACTA 5100
 TGACGCTGGG GATGTCTGCA CTCTCCAGT GAAGACCAAA AAGGTCAACC CATTCCTAT 5160
 GTCTCTGAC CTACAGGCT ACTGTGCTG TCGGGACCCC CAGGCCAAG AACACAGCG 5220
 GAAAGACTCT CCGGGATACA GCCATGGCTA AGGAAGACA AGAAGTGTG AAGAATTCC 5280
 CAGCGCAGG CAGCAGATCC CTTGTGATT GATTTCAGAG TCAGCTGCTC AACGGAATG 5340
 CCTCTCACA CAGGGATCC TTAGCACCCA ACGGTCTGC CTTAATTTT ACCCAGGAAG 5400
 GACTCACATT GGGCGAATG AACCAAGTTT CGCCATGCTG GATGATGAAA TGGATCCCCA 5460
 TCCAAAGTC TAGATGGAT TGCATATACA GTGTGCAGTC CCAGAGCTTC CTAAATTTCT 5520
 AGCCATTGT CACACAACCA CAGCAAAAA AAA

Seq ID NO: B29 Protein sequence
 Protein Accession #: NP_002572.1

1 11 21 31 41 51
 MRLMSVILHL GLLSAALGCG LAERPRRARR DPRAGRPRP AAGPATCATR GPRPPRLAAA 60
 AAAAGRAWFA VRVRRRRQQR EARGATEEPS PPSRALYFSG RGBQLRVIRA DLELPDRAFT 120
 LQVWLEAEGG QRSFVITGL YDKCSYISRD RGWVVGIIHTI SDQDNKDPRY FFLKTDRLAR 180
 QVTINAHRS YLPGQWVYLA ATYDQGFML YVNGAQVATS GEQVGGIFSP LTQCKKVLML 240
 GGSALNHNRY GYIEFSLWK VARTOREILS DMSTEGAHTA LPQLLLQENW DNVKHAWSPM 300
 KDGSFKKVEF SNAHGLFLLT SLEPFLCQQT LCINTKVIAS YKQLSSFRQP KVVRYRVVNL 360
 YEDDHKNPTV TREQVDFQHH QLAERFKQYN ISWELDVLEV SNSSLRRRLI LANCDISKIG 420
 DENCDPEONH TLTGSDGGDC RHLRHPAFVK KQHNGVCDMD CHYERFNFDD GBCDDPEITN 480
 VTQCTFDPDS PRRYALDVNE LKNILKLDGS THLNIFPAKS SEELAGVAT WPDKEALMI 540
 LGGLVLPSPF YGMPFYHTM IBEIGHSLGL YHVFEGISEI QSCBDPCMET EPSFETGDLG 600
 NDIMPAPKKH GCGDGPQND TCGEHSFENT PYNFMSYAD DDCTDSFTPN QVARMHCYLD 660
 LVYQGWQPSR KPAPVALAPQ VIGHTDSVT LEWFPPIDGH FFERELGSAC HLCLEGRILV 720
 QYASNASSPM PCSPSGHNSP REARGHPDVE QPCKSSVRTW SPNSAVNPHV VPPACPEPQG 780
 CYLELEFLYF LVPESLTIWV TFVSTWDSS GAVNDIKLLA VSGKNISLGP QNVPCDVPLT 840
 IRLNDVGEV YGIQYITLDE HLEIDAAMLT STADTPLCLQ CKPLKYKVVV DPFLQMDVAS 900
 ILHLNRKFVD MDLNLGSSVQ YWVITLSTGE ESEFSPAVTY IHGRGYCGDG IIOKDQGEQC 960
 DDHKNKINGG CSFLCRQEVF FNCIDERSRC YFHDGQVCE EFEQKTSID CGVYTPQGF 1020
 DQNASNAVS HQDQCQPGWV IIGQPAASQV CRTKVIDLSE GISQAWYPC TISYPYSLA 1080
 QTTFWLRATF SQPMVAANVI VHLVTPGTYY GDQKQETISV QLLDTKDQSH DLGLHVLSCR 1140
 NNPLIIPVVH DLSQPFYLSQ AVRVSFSEPL VAISGVALRS FDNFDPVTL SQRGETYSP 1200
 AEQSCVEFAC EKTDCRELAV EASLNCSSS DRYHGAQCTV SCRTGYVLQI RRDDELISQ 1260
 TGPSVTVTCT EGKWNQVAC EPVDCSIDPH HQVYASFSFC PEGTTFGSQC SFQCRHPAQL 1320
 KGNNSLLTCM EDGLNSFPFA LCELMCLAPP FVPNADLQTA RCARENKHKV SPCKYKCKPG 1380
 YEVEGSSRSK KKAFAKTCCT QDGSQWEGAC VPVTCDDPPP KFEGLYQCTN GFQFNSCRI 1440
 KCRDSDASQ LGSNVTLCRK DGTWNGSFHV CQEMQGCSCV PNLNSNLKL QCPDGYAIGS 1500
 ECATSCLDEN SSGIILEMNV TVRDIPHNLN PTRVERVCT AGLKMYEHPA LIRCVKGECP 1560
 PMGDNYCDAI NNRAPCNVDG GDCCSTSTVKI KKVTFPMESC DLQSDCACRD PQAQESBRKD 1620
 LRYSHG

Seq ID NO: B30 DNA sequence
 Nucleic Acid Accession #: NM_032808.1
 Coding sequence: 61..1008

1 11 21 31 41 51
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 ATGTTGCATG AGCTGCTCC GCTGCAGGAG ATCCAGCTGG TGGCGGCGCA GCTGGCCGTG 120

GTGGAGCCCT ATGCGCTCCG CGGCTCAAC TACCTGCGG TGCTCAATGT CTCTGGCAAC 180
 CAGCTGACCA CACTGAGGA ATTAGTCTTC CACTGCGTGG GCAACCTGGA GACACTCATC 240
 CTGGACTCCA ACCCGCTGGC CTGCGACTGT CGGCTCCTGT GGGTGTTCGG GCGCGCGTGG 300
 CGGCTCAACT TCAACCGGCA GCAGCCACAG TGGCCACGCG CGAGTTTGT CCAGGGCAAG 360
 GAGTTCAAG ACTTCCCTGA TGTGCTACTG CCAACTACT TCACCTGCGG CGCGCGCCGC 420
 ATCCGGGACC GCAAGGCCCA GCAGGTGTTT GTGGAAGAGG GGCACACGAT GCAGTTTGTG 480
 TGGCGGGCCG ATGGCGACCC GCGGCCGCC ATCTCTGGC TCTCACCCCG AAAGCACCTG 540
 GTCTCAGCCA ABAGCAATGG GCGGCTCACA GTCTTCCCTG AAGGCAOGCT GGAGGTGCGC 600
 TACGCCAGAG TACAGGACAA CGGCACGTAC CTGTGCTCG CGGCCAACGC GGGCGGCAAC 660
 GACTCCATCG CGCGCCAGCT GCATGTGCGC AGCTACTGCG CGGACTGGCC CCATCAGCCC 720
 AACAGACCTI TGTCTTTCAT CTCCAACAG CGGGCGAGG GAGAGGCCAA CAGCACCCGC 780
 GCCACTGTGC CTCTCCCTCT GCACATCAAG ACCCTCATCA TCGCCACCAC CATGGGCTTC 840
 ATCTCTTTCC TGGGGGTGCT CTTCTTCTGC CTGTGCTGC TGTTTCTCTG GAGCCGGGGC 900
 AAGGGCAACA CAAGACACAA CATGAGATC GAGTATGTGC CCGAAAGTTC GGAAGCAGGC 960
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 CGTCCCTGTC TGGCCCCCGC CAGCCCTCAC CACCTGCGCT CTTTCTACCA GACCTCAGA 1200
 AGCCCGAGAC TGGGGACCCC ACCTACACAG GGGCATGAC AGACTGGAGT TGAAGCCGA 1260
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 TTGGTATTCA ATAAATATGG ATTATTATGA AAATTGAAA TAATAAAAAG AGAAAAAAC 1380
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 TCCAACTCAG TTTCTTGTTC TTCTCTCTCT CTTCTCTCTC TTCTCTCTCC TTTCTCTTCT 1500
 CTTCCCACTG GGGGAGGGAT CACTCAGGAA AACAGGAAAG GAGGTTCAG CCCCAACCAC 1560
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 CCAGGGCTG GAGGTGGGGC CCACCTCAGC CTCTGCTCCC AGCTCTGCTG CTCACTTGCT 1860
 GTGTGGCTTC AAGCAGGTCA CTGGCTCTC TGGGCTCAG TCTCCACATC TGTACAAATG 1920
 GGAACATTAC CCCTGCGCT GCTACCTCA CAGGCTGTT GTGAGGAAT GATGAGATGA 1980
 TGTATGTGAA ACCTTTGTA ACCTGTAAG CGCTGTGCAC ACGTG

Seq ID NO: B31 Protein sequence
 Protein Accession #: NP_116197.1

1 11 21 31 41 51
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 MLHLLRLQEQ IQLVGGQLAV VEPYAFRGLN YLRVLNVSGN QLTTLLELVF HSVGNLLETLI 60
 LDNSPLACDC RILWVFRERW RLFNFRQQPT CATPEFVQGK EFKDFPDVLL PNYFTCRRAR 120
 IEDRKAQGVF VDEGHTQFV CRADGDPFPA ILWLSPRKEL VSAKSNRLT VFPDGTLEVR 180
 YAQVDNCTY LCIAANAGGN DEMPALHVR SYSPDWPHQP NKTFAFISNQ PGEGBANSTN 240
 ATVPFFFDIK TLIATITMGF ISELGVVLF LVLPLLSRG KGNTKHNIRI EYVPRKSDAG 300
 ISSADAPRRF NMKMI

Seq ID NO: B32 DNA sequence
 Nucleic Acid Accession #: CM1 cluster

1 11 21 31 41 51
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 CAGCACATAC AAGAAACATA CAGTGTACCT CAAAAGGGGC CCTTGAAATG TCATCAAAGG 60
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 GTATTGCGTA CGAAGGAAGC CAGGCTGGTC CTGGCAGGAA GTAAATGATA ATCTTTGGGA 180
 AACCAGGACC CTGCTCCCA GCGCAGAGGT GGAGGAGGGC GGTGAGGCTG GGTCTACAG 240
 TGGCACAGCA CTGACAAAGG TAGAGGGAAA TGTAAATAGCA CATCTACGCT GCAGCTGGT 300
 GAAAGTGGCC GGGGTGGTCC TTGGAAACA GTTGGGCTGT TCTTGGCAGG AATTAGTGAC 360
 AGCCTTTCG TCACGGGCG GAGCGCTTG ATTTAAAAA AATAAATAA TAAACGTCT 420
 GGGTATAGAA A

Seq ID NO: B33 DNA sequence
 Nucleic Acid Accession #: NM_006174.1
 Coding sequence: 71..1408

1 11 21 31 41 51
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 AGATGACTTA CAGTATTTTC TGATTGGGCT CTATACATTT GTAAGTCTTC TTGGCTTTAT 240
 GGGGAATCTA CTATTTTAA TGGCTCTCAT GAAAAAGGT AATCAGAGA CTACGGTAAA 300
 CTCTCTCAEA GGCAATCTGG CTTTTCCTGA TATCTTGGTT GTGCTGTTT GCTCACCTTT 360
 CACACTGACG TCTGTCTTGC TGGATCAGTG GAGTTTGGC AAAGTCATGT GCCATATTAT 420
 GCTTTTCTT CAATGTGTGT CAGTTTGGT TTCAACTTTA ATTTAATAT CAATTGCCAT 480
 TGTGAGTAT CATATGATAA AACATCCCAT ATCTAATAAT TTAACAGCAA ACCATGGCTA 540
 CTTCTGATA GCTACTGTCT GGACACTAGG TTTTCCATC TGTCTCCCC TTCCAGTGT 600
 TCACAGTCTT GTGGAATCTC AAGAAACATT TGGTTCAGCA TTGCTGAGCA GCAGGTATTT 660
 ATGTGTAGG TCATGGCCAT CTGATTCATA CAGAAATGCC TTACTATCT CTTTATTGCT 720
 AGTTCAGTAT ATTCTGCCCT TAGTTTGTCT TACTGTAGT CATACAAGTG TCTGCAAGG 780
 TATAAGCTGT GGAATGTCCA ACAAAGAAA CAGACTTGAA GAAATGAGA TGATCAACTT 840
 AACTCTTCAT CCTATCCAAA AGAGTGGGCC TCAGGTGAAA CTCCTGGCA GCCATAATG 900
 GAGTATATCA TTATCAAAA AACACAGAG AAGATATAGC AAGAGACAG CATGTGTGTT 960
 ACCTGTCCA GAAGAGCCTT CTCAGAGAA CCACTCCAGA ATACTCCAG AAAACTTTGG 1020
 CTCGTGAAGA AGTCAGTCTT CTTATCCAG TAAGTTCATA CAGGGGCTCC CCACTGTCTT 1080
 TGAGATAAAA CCTGAGAAA ATTCAATGT TCATGAATG AGAGTAAAC GTTCTGTATC 1140

AAGAATAAAA AAGAGATCTC GAAGTGTTTT CTACAGACTG ACCATACTGA TATTAGTATT 1200
 TCGTGTAGT TGGATGCCAC TACACCTTTT CCATGTGGTA ACTGATTTTA ATGACAATCT 1260
 TATTTCAAAT AGGCATTICA AGTTGGTGTA TTGCATTGTG CATTGTGTGG GCATGATGTC 1320
 CMGTGTCTT AATCCAATTC TATATGGGT TCTTAATAAT GGGATTAAAG CTGATTAGT 1380
 GTCCCTTATA CACTGCTTC ATATGTAATA ATTCTCACTG TTT

Seq ID NO: B34 Protein sequence
 Protein Accession #: NP_006165.1

1 11 21 31 41 51
 MOLELDEYYN KTLATENNTA ATRNSDFEVH DDYKSSVDDL QYFLIGLYTF VSLLGFMGNL 60
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 QCVSVLVSTL ILISIAIVRY HMIRKPISNH LTANEGYFLI ATVNTLGFAT CSPLFVFFSL 180
 VELQETFGSA LLSSRYLCVE SWPSDSYRIA FTISLLLVQY ILPLVCLTVS HTSVCRSISC 240
 GLSNKENRLE ENEMINLTLH PEKKSGPQVK LSGSHKWSYS FIKGHRRRYS KKTACVLPAP 300
 ERPSQENHSR ILLENFGSVR SGLSSSSKEI EGVPTCFEIK PEENSVDVHEL RVKRSVTRIK 360
 KRSRSVFYRL TLLILVFAVS WMLPLHLPVV TDFNDNLISN RHFILVYCIC HLLGMMSCCL 420
 NPILYGLFNN GIRADLVSLI HCLHM

Seq ID NO: B35 DNA sequence
 Nucleic Acid Accession #: NM_014279.1
 Coding sequence: 286..1689

1 11 21 31 41 51
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 GGGACACGAG CAGGCGCGCG CCGCGGAGC CAGCGGAGCC GGGGCGAGAG CCGGAGCGCG 240
 TCCGCGTCCA CGCAGCCGCG GCGCGGCCAG CACCCAGGCG CTTGCATGCC AGGTGCTTGG 300
 AGGTGCGAGC GAGACATGCA CCGCGCCCGG AAGCTCTCTA GCTCTCTCTT CTTCTCTCTG 360
 ATGGGCACTG AACTCACTCA AGTGTGCGCC ACCAACCCCTG AGGAGAGCTG GCAGGTGTAC 420
 AGCTCTGCCC AGGACAGCGA GGCAGGTGT ATCTGCACAG TGGTCCGCC ACACAGAGCC 480
 ATGTGTTTAC GGGATGCCCG CACAAAACAG CTGAGGCAGC TACTGGAGAA GGTGCAGAAC 540
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 AAGCAACACC TGGCCAGGCA GTTAAAGGCG ATAAAGCGA AAATGGATGA ACTTAGGCCT 720
 TTGATACAGT GTTGGAGA GTACAAGGCC GATGCCAAT TGGTATGCA GTTAAAGAG 780
 GAGGTCCAGA ATCTGACGTC AGTGTCTAAC GAGCTGCAG AGGAAATGG CGCCTATGAC 840
 TAGCTGAAC TTGAGAGCAG AGTGTCCAT CTGGAAGAAA GGCTCCGTGC ATGCATGCCA 900
 AAACATAGCT GCGGGAAGTT GACGGGCATC AGTGAACCCG TGACTGTCAA GACCTCGGCG 960
 TCGAGGTTCG GATCTCGGAT GACAGACCTT CTGCGCCCTG AAGGCGATAA CCGGCTGTGG 1020
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 ATGAACACGG ACAATTTTAC CTCCCAAGCT CTCCCAAGCC CCTGCTCGGG CAGCGGGCAG 1140
 GTGGTCTACA ACGGTTCAT CTACTTCAAC AAGTTCAGG GCCACATCAT CATCAGGTTT 1200
 GACCTGAAGA CAGAGACCAT CCTCAAGACC CGCAGCCTGG ACTATGCCGG TTACAACAAC 1260
 ATGTACTACT ACGCTCGGG TGGCCTACTG GACATGACC TCATGGTGGG CAGAGACCGG 1320
 CTGTGGGCGG TGTACGCCAC CAACAGAAC GCTGGCAACA TCGTGGTCAG TAGGCTGGAC 1380
 CCGCTGTCCC TGCAGACCTT GCAGACCTGG AACACAGCT ACCCAAGCG CAGCGCCGGG 1440
 GAGGCTTCA TCATCTCGGG CACGCTGAC GTCAACCAAG GCTACTCAGG GGTACCCAG 1500
 GTCCACTATG CATACAGAAC CAATGCCCTC ACCTATGAAT ACATCGACAT CCAATCCAG 1560
 AACAAATACT CCAACATCTC CATGCTGGAC TACAACCCCA AGGACCGGGC CCGTATATGC 1620
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 GAGTTGTAGC TCCCTCTCTC TGGAAAGCAA GGGCCCAAGT CCTCACCAAC AAGGAGCTCC 1740
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 CAGCAGTGGG GATTCTGACA TCGAGGGATG GCATTACCTC CGTGTCTTTC CTTTCCAGC 1860
 CGGCGGGGCA CAGACGTGGG AAGAACTCC CGTATTGCA GCTGGAACTG CAGGCCAGG 1920
 CGCCCGGTT TCTCTCCCG CCGCTCCCT CTCTGGTCAA ACAACATACT AAGAGGGGGA 1980
 GGCATGACT GTTGCCAGT TCTCACCGGG GAAAAACCA CTGTTAGGAT GGCATGAACA 2040
 TTTCTTAGA TGTGTGTGAG CTCCGAGGAA TGTGGGCTCC AGGCTCTTTC AGAGCCATGG 2100
 GCTGCACCGG GCGTAGGCT AGTGTAACTC GCATCCCAT GCAGTCCGT TTCTTACTG 2160
 TGTGTCTGTC TCTTAGATTA ACGTGTCTGA GGCTCCCAT AGCTCCTGGA CCTGTGCTA 2220
 GTACATCTG AAGCATGGT CAGAGTGTGT AGAGTGAAGT TGTGTGTGCC ACATTGTGTG 2280
 AACTGCGGTA CCGGTAGAT ACATTGTGCA ACGTCTCTCT GTTATTCCTT TGAGGTGTA 2340
 ACTGTGATG TTCAGTTTAT GCGATGATTG TTGTAATGC AATGCGTAG TTTGGATTAA 2400
 TAAGTGGATG GTTTTGTGTT CTAAAAAGAA AAAAAAATC AGTGTTCACC CTTATAGABA 2460
 CATAGTCAAG TTCATGTGTA TAATAATCAA AGGAATTAAT CTCTCTCTGT TAAATTAGCT 2520
 AATCATGTA ACGCAGATA GGAAGGGCTC ACTTGGGGAA ACTTGGTTT CCGATGGGAC 2580
 AGGAAAGTCA TACGGGCAAC AGTATGCGGA AAGTACGTTT TTTAAGTAA AAAACAAAGG 2640
 CAAACTTTGT ACTATCCAGT TATCTAAGGA ACATAAAAAA CATTAGGAGA AAAAAAATAA 2700
 AAAAAAATAA AAAAAAATAA AAAAAAATAA AAAAAAATAA A

Seq ID NO: B36 Protein sequence
 Protein Accession #: NP_055094.1

1 11 21 31 41 51
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 APQQTMCSSD ARTKQLRQLL EKVQMSQSI EVLDRRTQRD LQYVEKMEVQ MKGLESKPKQ 120
 VEEGHQQLA RQFKAIKAKM DSLRPLIPVL EKYKADAKLV LQFKKEVQNL TSVLNLQEE 180
 IGAIDYDELQ SRVENLEERL RACMQLACG KLTGISDFVT VKTSGSRFSG WMTDFLAPEG 240
 DNRVHYMDGY HNRFPVREYK SMVDPMWTDN FTSERLPHPW SGTGQVYVNG SIYFNKFSH 300
 IIRFDLKT ETLKTRSLDY AGYNWYHYA WGHSDIDL M VDSGLWAVY ATNQNAGNIV 360

5 Seq ID NO: B37 DNA sequence
Nucleic Acid Accession #: NM_006334.1
Coding sequence: 286..653

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	CG	CG	CG	CG	CG	CG	180
	CG	CG	CG	CG	CG	CG	240
	CG	CG	CG	CG	CG	CG	300
15	AG	AG	AG	AG	AG	AG	360
	AT	AT	AT	AT	AT	AT	420
	AT	AT	AT	AT	AT	AT	480
	AT	AT	AT	AT	AT	AT	540
	AT	AT	AT	AT	AT	AT	600
20	AA	AA	AA	AA	AA	AA	660
	AG	AG	AG	AG	AG	AG	720
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	AG	AG	AG	AG	AG	AG	900
25	AA	AA	AA	AA	AA	AA	960
	AA	AA	AA	AA	AA	AA	
	AA	AA	AA	AA	AA	AA	
	AA	AA	AA	AA	AA	AA	
	AA	AA	AA	AA	AA	AA	

Protein Accession #: NP_006325.1

1 11 21 31 41 51
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APQQTMCSDR ARTKQLRLQL EKVNMSQSI EVLDRRTQRD LQYVKMSNQ MKGLSEKFEQ 120
VEESHKCHLLA ROFGK

	Coding sequence: 286..795						
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	GGGA/CACGAG	CCAGBGCGCG	CGCGCGGAGC	CAGCGGAGCC	CGGCGCCAGG	CCGAGGCGCG	240
	TCCGCGTCCA	CGGCGCGCGC	GGCGGCGCAG	CACCAGGAGC	CCTCATGTCC	AGGTGATTTGG	300
	AGGTGGCAGC	GAAACATGCA	CCCGGCCCGG	AGCTCCTCTA	GCCTTCCTTT	CCATCTCTTG	360
	ATGGGCACTG	AACTCACTCA	AAATAAAGA	GAACAACAA	CAGAGAAGAT	GGGAGGGCCA	420
50	GAGAGCGAGA	GGAAGAACAC	GAGAGAGAG	ACACTGAAGC	AGCTTCCCTT	TTTTTGCTTG	480
	GAAGCCCAAG	CTGGCTTCCT	GGCTCTGCC	AGGATGTGCA	GTCCAAATTC	CAATCCAGCA	540
	GTEGGGTAT	GTCCTCOGCT	TACCTCTGCT	AGCCCTTCTC	GTCGTCCTCG	CGAGCGATGC	600
	AGCCAGTCCC	TCTCTGAGAG	GTCCTGATGC	GCCTCTAGGA	GAGAASTTTT	CTTGGCCCCA	660
	GGAAAGGCTG	GTEGAGGGTG	GTGGTCTGTG	ATGTTGCTG	GACACGATCA	TTCACTCATG	720
55	TGCACACACA	CACACACACA	TGCACACACA	GSGAGGCAGA	TACCTGAGCA	GAGAGGCCAA	780
	CCAGGTCTCT	ATTAGTGCCA	AGCTGCCCCA	CAGAAGGGCA	TGCCGTGTCT	TTATTGGAGC	840
	ACCTTGGCAA	AGAGATGGCT	GATTCCTGGT	GGTCTTGGAC	ATGGCCGCGC	CCAGAGGGCC	900
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60	TAAAAA	AAAAA					

65

1	11	21	31	41	51	
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LPFLCEAHAG	SLALPRMCSP	NFNPAVGLCR	PAYPQSPSPG	AAQTSQSLL	ERFCMASRRE	120
VFLAPGRPGG	GNWLCTVAG	MHSFMCITHH	THAHTGEQIP	AEKSQPGPD		

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	ATGCGGGTTC	TGGGAGCGCG	CCGAGAGCTT	CTGCTCTCGG	TGACCGACCG	CCGCGAACC	180
80	GAAAGGCGG	TGCAAGGCTC	CCCTAAGAGC	AGCAGCGCCG	CGCTCGAGCG	CGAGCTGCAC	240
	CTGCCGCCCA	AGCTGCGGGC	CCTGTACGCG	CGGGGCGGGG	GCGGCTCTCT	TACAGGTCGG	300
	CGAGCGCGCG	CGGCGCGCGC	GGCGCGCGCG	CGGGCAGCTG	CCGCTCACGC	CACGCGGGGT	360
	CCAGCGCGGG	AGCGCCCTCC	GCGCGCACCG	CCAAAGCGCG	GCGCGCGGGA	ACGCGCGGAC	420
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	ATCAGCGAGG	CGCGCGCGGT	GAGCATCAGC	GCGAGCAAGT	CGTACCGCGA	GAAACGGGGC	540

5
 10
 15
 20

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CCCTTCGTGC CGCCGCGGCC CGGCTGGAC GAGCTGGGCG GCGCGGGGGG CGTCACGCAC 600
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GAGGAACTGC TGGAGGACGA CGAGGAGGAG CTGCTGGAGG ACCACGCCCG CGCGCTGCTC 780
AAGGAGCCTC GCGCTGTCTT TGTGGCGGCC ACTGGGCGCG TGGCCGCAGC AGCTGCCGCT 840
GCACTGGCCA CAGAGGGGCG GGAGCTGTCA CCAAGGAGG AGCTGTGCT GTACCCGGAA 900
GACGCTGAGG GCAAGGACGG CGAGGACAGC GTGTGCTCT CTGCGGCGAG CGACTCGGAG 960
GAGGGGCTGC TGAAACGCAA ACAGAGGCGC TACCGACCCA CGTTCACCAG CTACCAGCTG 1020
GAGGAACTGC AGCGGCGCTT CCAGAGAGCG CACTACCCGG ACCTCTTCA CAGGAGGAA 1080
CTGGCCATGA GGTCTGACTT GACCGAGGCC CGAGTCCAGG TCTGGTTCCA GAACGCTCGG 1140
GCCAAGTGGC GCAAGCGGGA GAAGGCGAGC GCGCAGACCC ACCCCCTTG GCTGCCCTTC 1200
CCGGGCGCGC TCTCCGCCAC CCACCCGCTC AGCCCTTACC TGGACGCCAG CCCCTTCCCT 1260
CCGACCAACC CGCGCTCGA CTCCGCTGG ACTGCGCTG CCGCGCGCGC CGCGCGCGC 1320
TTCCGAGGCC TACCTCCGCC TCCGGGCTCG GCCAGCTCC CGCCGAGCG GCGCGCGCTG 1380
GGCCTGAGCA CTTTCTCGG AGCGGCGAGG TTCCGACACC CAGCTTTCAT CAGCCCGGCA 1440
TTCCGCGAGC TCTTTTCAC AATGCGCCCC CTGACACCG CGTCGACCG GCGCGCGCTC 1500
CTGAGACGC CCAACCCGCG CGTGGAGGGC GCACTGGCAT CCGCGCGCTT GCGCGACCG 1560
GCCACGGCG CCGCAGACAG ACGCGCTCT AGCATAGCG CCGTGAAGCT CAAGGCCAAG 1620
GAGCACGCG CGCAGCTCAC GCAGCTCAAC ATCTGCGCG GCACCAGCAC GGGCAAGGAG 1680
GTGTGC
  
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Seq ID NO: B42 Protein sequence
Protein Accession #: AAK93901.1

25
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 35

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1 11 21 31 41 51
M9NQYEEGC SERPECKSKS PTLSSYCID SILGRRSPCK MRLGAAQSL PAPLTSRADP 60
EKAVQGSFKS SSAPFAEELH LPPKLRLRYG PGGRLIQA AAAAAAATA AAAAAATAG 120
PRGEAPFPFP PTARPERFD GAGAAAAA AAAAAWTLK ISQAPQVSI RSKSYRENGA 180
PFVPPPPALD ELGGPGGVTH PEBRLGVAGG PGSAPAAGGG TGTEDDEEL LEDEEDDEE 240
BELEEDDEE LLEDDARALL KEPRRCVPAV TGAVAAAAA AVATEGGELS PKEELLHPE 300
DAEKDGEDS VCLSGSDSE BGLLKRKQRR YRTTFTSYQL EELERAFQRT HYPLVFTREE 360
LAMRLDITEA RVQVWFQNR AKNRKREKAG AQTHPPGLPF PGLSATHEPL SPYLDASFPF 420
PHEPALDSAW TAAAAA AAA FESLPPFPFS ASLPPPGAPL GLSTPLGAAV FEHPAFISPA 480
FGRLEFSTMAP LTSASTAAL LRQPTFAVEG AVASGALADP ATAAADRRA SIAALRIKAK 540
EHAALQLN ILEGTSTGKE VC
  
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Seq ID NO: B43 DNA sequence
Nucleic Acid Accession #: CAT cluster

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1 11 21 31 41 51
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CTGCTCTCTT CCGCTCTCAT GCGCTCTTCA GCTCTTACTT TGGTGTGCT CCGCTCTCT 180
GCTCGTTTCT CTGTTCTCTT TCTTTCGCGG TCGGTGTCTT GCTTCTGCT GTTCTCTCT 240
GTCTGTGTTT GTGGGTCCTC CTCTGCGTCC TGCTCTTTC TCTTGTGCTT CCGCGGCTT 300
CCGTTTGTGG TCCCTCTGCT TCTGCGCGCG TTCTGTGTGC GCGGCGCGCC CCGTCTTTC 360
TTGTTGCTTT GCTCTGCTC TCTGTCTGCT GTTCTGCGC GTCTGTGCTT TCTCTCTTT 420
ATCTTCTGTT TTCTCTTTT CTGTTTCTT CTGTTTCTT TTGTCTTTT TTTCTCTTA 480
GCTGAGGTTT GGGAGAGATA ACGCTGATA CTTTATTTT TCAGGAAATC TGGAAACCTA 540
CAGTCTCTAG CCGCTCTCAG CCAAGAAAGA GCTCACTGTG GGCACCAAG ACAGGAGACC 600
AATGTGAGGA CCGTGTAGCC TGTGTCCGCG CCGTAACCTT CAGCACAGG GCAGGCTTCC 660
TGAGCNTTGA AGAGAATATG TGGAGAAACA AAACAGAAAC TGAAGAATA TGCAGGTGT 720
CTTCTTGGGA TGTATTCCA TGATAGATAG TAGGGGCGAG AGTGAGAGAG GCTGACTAGG 780
TCTGGACATG GAGCTCGGAA GAGTCAGGGT GTGATTCCGA GAGGCGCATG AGAAGGAAGG 840
TGGATTTTAA GCGTGGAAAT CTGAGGCTCA GTGGTCCAG TCACTCAGAG ACAGAAATCAG 900
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Seq ID NO: B44 DNA sequence
Nucleic Acid Accession #: NM_014421.1
Coding sequence: 718..1497

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1 11 21 31 41 51
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AGTGGCGCTG TGGGGGACCT CGATTCTCTT CAGATCTCGA GGATTGCGTC CCGGGACGTC 180
TCTGATCCG CTACTAAAGC GCTGCTAAC TTTGAAAGG AGCACTGTGT CCGCAAGGT 240
TTGACACATA AAGGATAGGA AAGAGAGGA GAGAAAGCA ACTGAGTTGA AGGAGAGGA 300
GCTGATGCGG GCTTCTGAT CAATTAAGAG GAGAGTTAAA CCGCGGAGAT CCGGGCGGGA 360
CCAGGAGGCT GCGGGGCAAG AAGGAACGGA AGCGGTGCGA TCCACAGGGC TGGGTTTCT 420
TGCACTTGG GTACGCGCTC CTGCGGAGA AAGCGCTCTG CATTGTATG CTTCCAGTTA 480
TTGCAAGACT TCCGTCTCTG GTGAGAAGC GGTCTGCTT TGGGTTCCGC TAATTTCTGT 540
CCTGAGGCGT GAGACTGAGT TCATAGGGTC CTGGGTCCCC GAACAGGAA GGGTTGAGGG 600
AACCAATCT GCAAGCCGCC GCGACCCAG TGAGGGGCC CGTGTGTTGG TCTTCTCTCC 660
CTTGTCAATC CCAACCCCTC GCGCTTTCG TCTTCTGCG GACCCCTCG CCGGGAGATG 720
GCGCGCTTGA TCGGAGCAA GGATTCTGTC TGCTGCTGCT TCTTACTGCG CCGGCTGCTG 780
ATGTTGGGA GCTCAAGAT CGGCAGTTC GCGGCCAAC TCACTCCAT CAAGTCTCT 840
CTGGGCGCGG AGACGCTCTG TCAGGCCGCC AATCGATCTG CCGGCATGTA CCAAGGACTG 900
GCATTGCGCG GAGTAAGAA GGGCAAAAC CTGCGGCGAG CTAACCTTGT TAGCAGTGAT 960
AAGGAGTGTG AAGTTGGGAG GTATTGCGAC AGTCCCGACC AAGGATCATC GGCCTGCATG 1020
GTGTGTCGGA GAAAAAGAA GCGCTGCGAC CGAGATGGCA TGTGCTGCC CAGTACCGGC 1080
TGCAATAATG GCATCTGTAT CCCAGTTACT GAAAGCATCT TAACCCCTCA CATCCCGGCT 1140
  
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CTGGATGGTA CTCGGCACAG AGATCGAAGC CACGGTCATT ACTCAAACCA TGACTTGGGA 1200
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 CCTTGCCTAC GATCATCAGA CTGCATTGAA GGGTTTGGCT GTGCTCGTCA TTTCTGGACC 1320
 5 AAAATCTGCA AACCACTGCT CCATCAGGGG GAAGTCTGTA CCAACAACG CAAGAAGGAT 1380
 TCTCATGGGC TGGAAATTTT CCAGCGTTGC GACTGTGCGA AGGGCCTGTC TTGCAAGATA 1440
 TGGAAAGATG CCACCTACTC CTCCAAAGCC AGACTCCATG TGTGTCAAGAA AATTTGATCA 1500
 CCATTGAGGA ACATCATCAA TTGCAGACTG TGAAGTTGTG TATTTAATGC ATATAGCAT 1560
 GGTGGAATAT AAGGTTCAAG TGCAGAAGAA TGGCTAAAT AAGAAACGTG ATAGAATAT 1620
 10 AGATGATCAC AAAAAGGGAG AAAGAAACA TGAAGTGAAT AGATTAGAAT GGCTGACAAA 1680
 TGCAGTGCAG CCAGTGTTC CATTATGCAA CTGTCTATG TAAATAATGT ACACATTGT 1740
 GGAAATGTCT ATTATTAAGA GAACAAGCAC ACAGTGGAAA TTAAGTATGA GTAGCATGTG 1800
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 15 AATAACTGT TATACAATAG GTTCTAAAA TAAAAATGCT AAACAAGAAA TGAAGACATG 1980
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 TAATGGCAG TTGTTAGGA AGGCCITTAG GAAGACAAAT AAATAACAA CAAACAGCCA 2160
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 25 GGATCTGAT TGCAGTGGG TAAGCAAGAA AATTGGGAAA ACTTTTCTG TTGTTCAAGT 2580
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 35 TTTAACTTT TGTAGACCAC AATTCACITT TTAGTTTCT TTTACTTAA TCCCATCTGC 3180
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 40 TTATATTTAC AATTGGGTT CTGCAATAT TTTCTATGT CCAOCCITTT AAAAATATT 3480
 ATTTGAAGTA ATTTATTAC AGGAATGTT AATGAGATGT ATTTCTTAT AGAGATATT 3540
 CTACAGAAA GCTTTGTAGC AGAATATAT TGCAGCTATT GACTTTGTAA TTTAGGAAAA 3600
 ATGTATAATA AGTAAATC TATTAATTT TTCTCCTCTA AAAACTGAAA AAAAAAATA 3660
 AAAAAAATA A

Seq ID NO: B45 Protein sequence
 Protein Accession #: NP_055236.1

1 11 21 31 41 51
 50 MAALMRKDS SCCLLLAAV LMVSSQIGS BRKLNSIKS SLGGETPGQA ANRSAGMYQS 60
 LAPGGSEKUK NLGQAYPCSS DKECEVGRYC HSHQGSASAC MYCRKKKRC HRDGMCCPST 120
 RCNIGICIPV TESILTPIHP ALDGTNRDR NHGHSNRLD GWNLGRPRT KMSHIKSHES 180
 DPCLRSSDCI EGFCARHFW TKICKPVLHQ GEVCTKQRK GSEGLEIFQR CDCAKGLSCK 240
 VWKDATYSSK ARLHVCQKI

Seq ID NO: 46 DNA sequence
 Nucleic Acid Accession #: NM_019885.1
 Coding sequence: 1..1539

1 11 21 31 41 51
 60 ATGCTCTTTG AGGGCTTGA TCTGGTGTGG GCGCTGGCCA CCTCGCCGC GTGCTGGTG 60
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 65 CCGCAGAGA GCTGCAAGCT GCCATCCCC AAGGATCCA TGGGCTTCC GCTCATCGA 180
 GAGACCGGCC ACTGCTGCT GCAGGTTCT GGCCTCCAGT CGTCGCGGAG GGAGAAGTAT 240
 GGCACGTTGT TCAAGACGCA TTTGTTGGGG CGGCCGCTGA TACGCTGAC CGGCGCGGAG 300
 AACGTGCGCA AGATCTCTAT GGGCGAGCAC CACCTCGTGA GCACCGAGTG GCCTCGCAGC 360
 ACCCGCATGT TGTGCGGCC CACACGGTGT TCCAAATCCA TTGGCGACAT CCACCGCAAC 420
 70 AAGCGCAAGG TCTTCTCAA GATCTTCAGC CACAGGCC CAGAGAGTTA CCTGCCAAG 480
 ATCCAGCTGG TGATCCAGGA CACACTGCGC GCTGGAGCA GCACCCCGA GGCCATCAC 540
 GTGTACCAGG AGGCGCAGAA GCTGACCTTC CGCATGGCCA TCCGGGTGCT GCTGGGCTTC 600
 AGCATCTCTG AAGAGGACCT TGGGCACTTC TTTGAGGTCT ACCAGCAGTT TGTGACAAAT 660
 GTCCTCTCCC TGCTGTGCA CCGTCCCTTC AGTGGCTACC GCGCGGCGAT TCAGGCTCGG 720
 75 CAGATCTGTC AGAAGGGGCT GGAGAAGGCC ATCGGGAGA AGCTGCAGTG CACACAGGGC 780
 AAGGACTACT TGGACGCCCT GGAACCTCTC ATTGAGAGCA GCAAGGAGCA CGGGAAGGAG 840
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 80 GGCACTGTC GCTCGACAC GCTCACTGGG CTGGCTTACC TGGACTGCGT CATCAAGGAG 1080
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5 ACCAGCCGCT TTGAGCTGGC TACACGGACC TTCCCCCGCA TCACCTTGGT CCCCGTCTG 1440
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 10 GAACIGCTCC CTTCCTCCG TTCTTTTCGG ACCCTTTTAG CTGGGTGGG GGGACGGAA 1920
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 15 GCGCCAGGCC CTGTCTCCG AGCATCTCTC CTGGTGGCCC TGGCAGCTG CACTGACACC 2220
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 20 GAAAGCGCTT CCGCGCTGCG GGCATTTATT GGGTTAATC TCGGAGCCTC ACTCTGGAC 2520
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 35 TGAATCTCAG ATGTCTCTT TATTTCTAC TTTTCCACTA CTAATAACA GTGTGAATA 3420
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 50 TAGTAATAA TGAATTTGC TCTATTGTA ACATGGTICA AAATATTAA ATGTTTATT 4320
 CACAGTGTG TTAATATTGA AAAAGCACTT GTGTGTTTG TTTTGATAG AAATGCTAC 4380
 CGTGTAGATG TTTTGTCTG COTGGTTTA ATCTGTATAT AATATCCAT GTTGCATATT 4440
 AAAAA

Seq ID NO: B47 Protein sequence
 Protein Accession #: NP_063938.1

1 11 21 31 41 51
 60 MLFEGLDLVS ALATIAACLV SVTLILAVSQ QLWQLRWAAT RDKSKLPIR KSGMGFPLIG 60
 ETGHWLLQSS GFQSSRRREKY GNVFKTHLG RPLIRVTGAE NVRKILMGE HLVSLEWPRS 120
 TRMLLGPNV SNSIGDIHRM KRKVFSPKIPS REALESYLPK IQLVIQDTLR AWSGHPERIN 180
 VYQEAQKLTF RMAIRVLLGF SIPEEDLGHF FEVYQQFVDN VPSLPVDLPF SGYRRGIQAR 240
 QILQKLEKA IREKLQCTQG KDYLDAIDL IESSKEHGEK MTMQELKDOT LELIFAYAT 300
 65 TABASTSLIM QLLKPTVLE KLRDELRAEG ILHSGGCPCE GTLELDLLEG LRYLDCVIKE 360
 VMRLFTPISS GYRTVLQTFE LDGFQIPKEW SVMYSIRDTH DPAFVFKDYN VFDPDRFSQA 420
 RSEKDKGRFH YLPFGGGVRT CLGKHLAKIF LKVLAVELAS TSRELELATRT PPRITLNPVL 480
 HPVDGLSVKF FGLDSNQNEI LPETRAMLSA TV

Seq ID NO: B48 DNA sequence
 Nucleic Acid Accession #: AB040527.1; AL136582.1
 Coding sequence: 94..2319

1 11 21 31 41 51
 75 GCGGCTGCGG GGTTCCTGGT GCTGAGGAGG GACGCCATTG GAGTTCGCGA GAAGCATGGC 60
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 80 GGGTCCAGGC CTTGCTCTCT TATCGAATGA GCGCTGGGAA CTGGAAGAAC CTGTGCTGGC 300
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CGAGGCTCCG GCAACCTCCG CACAGTCCCA GACAGGCTCC CGGCCCCAGG AGGCTGCTAC 660
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GAAGATCCCC AACAGCAACC CACCTGAGTA TGAATTCCTC TGGGCGCTGC GAGCCCGCCA 1800
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ACAGCACCTT AGCGGCTTC TTCTGTCTG TCGGAGGTGG CATGCAAGAT GAAGCTCTCT 2400
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TTACATTAAA GTTGCATAAT TAAA
  
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Seq ID NO: B49 Protein sequence
 Protein Accession #: BAB33378.1; CAB66517.1

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1 11 21 31 41 51
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SLGPGILRLS NEEWELNENPV LAQTLVEALQ LDPETLANET AARANNVARA AASNRAARAA 120
AAAARTAFSQ VVASHRVATE QVSGEDTQPT TYAAEAQGFY PEPPLASQPT SQMLVTSKMA 180
APEAPATSAQ SQTGSFAQEA ATEGESSACA FSGAPCAREV DANRPFATFL QQNDVDFDTQ 240
PAGVSWAFPP RFRPPAPQZS AATEGESSAS GVPQTGFERE VAATRPKTKK SKKALAKTRW 300
VEPQNVAAAS AAKAKMATESI PEPGGAARAT AQHSAEPNAR MGGKRTKSKK HLDDYEESSE 360
EERETPAVPP TWASQPSLT VRAQLAPREP MAPRSQIPSR HVLCLPFRNV TLLOERANKL 420
VKYLMIKDYK KIPKIRADML KIVIREYDEH FFEIIRATY TLEKKPGIHL KEIDKREHLY 480
ILVCTRDSAA RLGLKTKDTP RLSELLVLILG VIFMNGNRAS EAVLWEALRK MGLRPGVRHP 540
FLGLDLKLIT DDFVQKYLE YKIPNENFP EYEFNLGLRA RHETSKMRVL RFIQNMQRND 600
PREWKAHLE AVDDAFKTMV VDMAEESHARA QMRAGMNIGD EALLGRWSND DIQVZLLTWD 660
EDGDEGDAWA RIPPAPFARY HQYILNENRA NRRATWRAGV SSGTNGGAST SVLDGFSSTSS 720
TIRTEAARA GASFFSWIQH R
  
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Seq ID NO: B50 DNA sequence
 Nucleic Acid Accession #: XM_084965.1
 Coding sequence: 356..2014

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 65
 70
 75
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1 11 21 31 41 51
GACCTAGCST GTGCTCAGCT CTGGACAAGA CATGGATGTA GGCAGACATG CTTCTGCTCT 60
GCTGGGCTTA GTGACCAAAAT GCTAAGGACA GACATGAAGG GCTTGGGAAA GGCATGAAGA 120
TGACGGGAGT CTAGGAGAGA GGATAAGAAA AACAAGCATT TTGTGGTGGG TTGAATTGCG 180
TTGTGCTTTT TAGAGGCATT TCGTGATCCA TGGTTCGCTT CCGGTGAAGA GCGAGTCTAG 240
AGAAGGAATC CGAAGCGGCG GCGGCGAGCG CCGCTCAGGT TGATTAGAAA TACGGGTGAC 300
AGTGGGCTTG CCGAGAGCCA CTGCTGACGA AAGCGGCTTA TCCCGCGCGG TTTCATGGA 360
GAGAGCCGG AGCGCGGCGG GCGGCGGGGG TGTGAGCGAG CGCGGCGGAG CTGGCGCTC 420
CGTGGGGGTC TGCAAGAGGA AGCGGAGGCG CCGGCGCGGG ACCGGGACCC TCGCGGCGGA 480
CATGGACTTG CATTTGACT GTGCGCCGA AACGCGGCG CCGAGGCGCG CTTGCGGGA 540
GATTAAATAA GCTGCTTCA AATTATTCAA GAGAGGAAA TCGGTGGCA CCATGCCAG 600
CATTTTGGG GTCAAAAACA AAGGGGACGG GAAGAAGCTC GGTCCGACGG GGTGCTGAG 660
GAGCAGGAGC CAGCAGGAGC TTGCGAGGT GCTGTGCTG GAGAGCGCA GGAAGGAGGA 720
GCCGCGCGCG CCGCGGCGCA GCGCGGGGG CCGCGGCGGG CCGCGGAACC CGGGGCCGCC 780
CAGAGCCGCA GGGCGCGCG GGGGCTCCCT CCGCAGCAGC TCGGTGGCCA AGTCGACAG 840
CTTCTTCTCG CTGCTGAGA AGAACGCGCG CTCGGAARAC GGCAGGGGAG AGCTGTGGA 900
CGCGGACAG CGCGCGCGCA AACAAAAGCG GGGCTGCGG GGGCTGTTCA CGGCATGCG 960
CTGGCAGAGC AAGACAGAG GGGCCAAGGC GAGGCGCGCG GAGGGGCGCG CGCCCGGGG 1020
CBGCTGATC CTACCGGCT CACTCACCC CAGCTGAGG TCGCTCAAGG AGGAGACGCC 1080
CAGAGCCGCG CCGCGGCGG AGGAGCCAG CAGGAGCGC CCGCGAGACC CAGCAGGCTG 1140
TGAGATATT ATTGCAAGC AAGAGGAGA GGCAGGTCCC AGCTGTGACA AGCATGTCC 1200
CGGGCAGGC AAGCGGCTC TGTCTAAAA GAACCCCGG CTTGGTGGCT ACCAAGGAG 1260
CGGGAGAGG ATGGCCAGCC CGGACGAGG GAGCAGACCC TATCTACAGG AGTCTCGGA 1320
CATGCTCTCC CAGAGCGAG AGCAGGAGC CAGGCGCGG GAGGCGCGG CTAAGGTGG 1380
AGCTGCGCTG GAAACCAAG TGGTGCCGA GACCCCAA GACACAGGT GTGTGGAAGC 1440
GGCCAGGAG CCGTCTCGG TCAAGCGAG GAGGCTCAAC CGGATTCCCA TCGAGCCCCA 1500
TCTAAGGAG GAGCCCAAG ACCCGGAGA GGAGCAGAG GAGGCGTCC CCAACAGCGA 1560
  
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 10
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CGAGGGCTAC TGGGACTCCA CCACGCCAGG CCCAGAGGAA GACAGCTCGA GCAGCGGGAA 1620
GAAGGCGGGC ATCCCCCGGG ATAGCTACAG OGGGGACGCG CTCTATGATC TCTATGCTGA 1680
CCCGGACGGTA AGTCCAGCAA CCCTTCCTGG AGGGAAGBAC AACGAGGAGA CGTCCCTCCCT 1740
GTCCCGGTAA AGCCCGTAT CTCCAGGCAC CATCACCTGT CCACTGCGAA CAOCAGGCAG 1800
CTTGCTGAAG GACTCTAAGA TCCCTATTAG CATCAAGCAC CTGACCAACC TTCCATCTAG 1860
CCATCCCGTG GTGCACCAGC AACCTCCAG GAGTGAGATG CCCAGAACAA AAATCCCGGT 1920
TTCCAAAGTG CTGGTCCGCA GAGTCAGCAA CCGGGGCTTG GCTGGGACCA CCATCAGAGC 1980
AACGGCTGTC CACGACAGTG CCAAAAAGTT GTGAGGCTTT CCAGGCCAAG GTGGATGGGC 2040
CCCATGCCAA GGAATACAAC TTTTCCCTGG AAACCACTAA AGTAAGTTT GCTTTTCCTA 2100
AAGAAAGTCT TTTAGGACAC CACCGGTCCC CCGCCCTGCT CCAGAGCGTG GACCGAGGAG 2160
GTCTTTGTGC CTTGAGCAGG GACCGGATAA CACCAGAAAG AGGGATGCTA CACGGGGGTT 2220
TCTCCTCTCA AGATAAGTCC CTGAGAATTA TTTTCAAGCA CTTTTTCTT TTTTACCTTT 2280
AAGTTTTTCT TCTTTTGTCT TTAATATACT GAACACTTGG AAGTCACCTT TACTTGCCTT 2340
TGCAGAAAAC AGAAGCTTAGC CAAACCTAAG TAAGAGTCAT GCTTGATAT TGGGATAAGC 2400
CAGTGTCTAG AGGCCTGAAG GAACCGCTGA AGAACCAGAG GAGATCTCCT CTTCACAGAC 2460
ACGTTTCTT CTTTCCCTTC TTTCTCTTT CTTTCCAGT T
  
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Seq ID NO: B51 Protein sequence
 Protein Accession #: XP_084965.1

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 25
 30

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1 11 21 31 41 51
| | | | |
METSRSRGGG GAVSERGGAG ASVGVCRRA EAGAGTGTLA ADMDLHCDCA AETPAAEPPS 60
GKINKAAFKL FKRRKSGGTM PSIFGVKNKG DGKSSGPTGL VRSRTHDGLA EVLVLESGRK 120
EPEPGGGDSG GCGGGRPNPG PFRAAGPGGG SLASSSVAKS HSFFSLKKK GRSENGKEGP 180
VDASKAGGKQ KRLRLGLFSG MRWHRKDKRA KAERAEGRAP GGGILILPGSL TASLECVKEE 240
TPRAAREPEE PSQDAPRDPA GCGDIIADQF EEAGPSCKKH VFGPGKPLS KKNPGVVAYQ 300
GGGEEMASGD EVDITLYQEF WDMLSQTEBQ GEPEQEGAAK VAAALETKV PETPKDTRCV 360
EAAKDASVRK RRLRLRLPIE PHPKERPKEP EKEQEGVEN SDEGYNDSTT PGEEDSSSS 420
GKKAGIFRDS YSGDALYDLY ADPDGSPATL PGKDNNEETS SLRLKPVSP GTITCPLRTP 480
GSLLEKDSKIP ISIKHLINLP SEHPVVRQQP SRSEMPRTKI PVSXVLVVRV SNRGLAGTTI 540
RATACHDSAK KL
  
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Seq ID NO: B52 DNA sequence
 Nucleic Acid Accession #: FGENESH predicted
 Coding sequence: 1..2016

35
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 45
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 55
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1 11 21 31 41 51
| | | | |
ATGGAGACGA GCGGAGCCCG CGCGCGCGGC GGGGCTGTCA CGGAGCGCGG CCGAGCTGGC 60
GGGTCCGTGG GGGTCTGTCAG GAGGAAGGCG GAGGCGGGGG CCGGGACCGG GACCTCTGCG 120
GCAGACATGG ACTTGCATTG TGACTGTGCC GCGAAACGC CGCTCGCGGA GCCCGGTGCG 180
GGGAAGATTA ATAAAGCTGC CTTCARATTA TTCAAGAAGA GGAATATGGG TGGCACCATG 240
CCAGCATTTT TTGGGCTCAA AACAAGAGG GACGGGAAAA GCTCGGGTCC GACGGGGCTG 300
GTGAGGAGCA GGAACCAAGA CGGACTTGCC GAGGTGCTGG TGCTGGAGAG CGGCAGGAAG 360
GAGGAGCCGC GCGCGCGGGG CACAGCGGCG GGGGGCGGGG GGGGCGGGCC GAACCCGGGG 420
CCCCACAGAG CGCAGAGGCC OGGCGGGGCG TCCTCTCCCA GCAGCTCGGT GGCCTAAGTCG 480
CACAGCTTCT TCTCGCTGCT GAAGAAGAAC GGGCGCTCGG AAAACGGCAA GCGAGAGGCT 540
GTGAGCGCGA GCAGAGCGCG CGGCAACCAA AAGCGGGGGC TGCGGGGGCT GTTCAGCGGC 600
ATGCGCTGGC ACAGGAAAGA CAAGCGGGCC AAGCGCGAGG CCGCGAGGG GCGCGCGCCC 660
GGGGCGGGCT TGATCTTACC CGGCTCTGCT ACCGCCAGCC TGAGTGTGCT CAAGGAGGAG 720
ACGCCACAGG CCGCGCGCGA GCGGAGGAG CCCAGCCAGG ACGCCCGCGG AGACCCAGCA 780
GGTAGACCCG CAGGGGAGAG GGAAGTGCCG GCGCCCGCGG ACCGCGCGCC AGCGCGGAGC 840
TGCCGAGAGG CAGAAGGCGCT CGCGCACCCC GCGCACACCG GCGCGCGGGG AGAGGAGCGC 900
GCGGGGCATC GCGCGCGCGA GCGCGGGCCC GGGGAGGTCC GCAAGCGCAG GACGCTTCC 960
AGGACGGGGG CGGTTCCTGT AAAGACGGTC CCCCTTGTGG ACTCGGAAGG CGGCAGCGGC 1020
CGCGCGCGCG CGCGCCCGAG CCTTGGCTCT TCGATGCCAC CCTCAGACCC GTCCGCGATG 1080
CGTATTGTGT TTATGTTTTC TGAAGTGAAT TCACTGAAAA GCTTTGACTC TCTTACAGGC 1140
TGAGGAGATA TTATTGACGA CCAAGAGGAA GAGGAGGTC CCAAGTGTGA CAAGCATGTC 1200
CCCGGGCCAG GCAAGCGGCG TCTGTCTAAA AAGAACCCTG GGTGTGTGTC CTACCAAGGA 1260
GGCGGGGAAG AGATGGCCAG CCCGACGAG GTGAGACACA CCTATCTACA GGAGTTCTGG 1320
GACATGTCTT CCCAGACCGA GAGGACAGGA CCGGAGCCCC AGGAGGGGCG GGCTAAGGTG 1380
GCAGCTGCGC TGGAACACAA GGTGTGTGCC GAGACCCCCA AAGACACCCG GTGTGTGGA 1440
GCGGCCAAGG ACGCTCTCTT GGTCAAGCGC AGGAGGCTCA ACCGATTCC CATCGAGCCC 1500
CATCTAAGG AGGAGCCCAA GCACCGGAG AAGGAGCAGC AGGAAGCGT CCCAACAGC 1560
GACGAGGGCT ACTGGGACTC CACCAAGCCA GGCACAGAG AAGACAGCTC GAGCAGGGG 1620
AAGAGGGCGG GCATCCCGCG GATAGCTAC AGCGGGGACG CGCTCTATGA TCTCTATGCT 1680
GACCGGAGCG GAAGTCCAGC AACCTTCTCT GGAGGGAGAG ACAACAGGA GAOGTCTCT 1740
CTGTCCCGGT TAAAGCCCGT ATCTCCAGGC ACCATCACCT GTCCACTGCG AACACAGGC 1800
AGCTTGTGTA AGGACTCTAA GATCCCTATT AGCATCAGC ACCTGACCAA CCTTCCATCT 1860
AGCCATCCCG TGGTGACACA GCAACCTTCC AGGAGTGAGA TGCCAGAAC AAAATCCCG 1920
GTTTCCAAAG TGCCTGTCCG CAGAGTCAGC AACCGGGGCT TGCTGCGGAC CACTATCAGA 1980
GCAACGGGCT GCAACAGCAG TGCCAAAAG TTGTGA
  
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Seq ID NO: B53 Protein sequence
 Protein Accession #: FGENESH predicted

80

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1 11 21 31 41 51
| | | | |
METSRSRGGG GAVSERGGAG ASVGVCRRA EAGAGTGTLA ADMDLHCDCA AETPAAEPPS 60
GKINKAAFKL FKRRKSGGTM PSIFGVKNKG DGKSSGPTGL VRSRTHDGLA EVLVLESGRK 120
EPEPGGGDSG GCGGGRPNPG PFRAAGPGGG SLASSSVAKS HSFFSLKKK GRSENGKEGP 180
VDASKAGGKQ KRLRLGLFSG MRWHRKDKRA KAERAEGRAP GGGILILPGSL TASLECVKEE 240
TPRAAREPEE PSQDAPRDPA GEPAGGEFVP APADRAPARS CREABGLAHP GTGARGEDA 300
  
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AGHRAEPGP GEVRAEDAS RTGAVPVKTV FLVDSBGGSG RAPAAPDFAS VDPFSDPSAD 360
 RICLMFSDVT SLKSFDSLTG CGDILADQEE EAGPSCDKHV PGPGKPAISK KNPVVVAYQG 420
 GGEEMASPE VDDTYLQEFW DMLSQTEEQG FEPQEGAAKV AAALBKVVP ETPKIDTRCUE 480
 AAKDASSVKR RLNRIPLEP HPKEEPKHPE KEQEGVPHS DEGYWDSTTP GPEDSSSSSG 540
 KKAGIPRDSY SGDALYDLXA DFDGSPATLF GSKDNEETSS LSRLKPVSPG TITCPLRTFG 600
 SLKDSKSIPI SLKHLTNLFS SRPVVHQQPS RSEMPRTKIP VSKVLVRRVS NRGLAGTTIR 660
 ATACHDSAKK L

Seq ID NO: B54 DNA sequence
 Nucleic Acid Accession #: NM_014138.1
 Coding sequence: 60..854

1 11 21 31 41 51
 CTGCAGAGAC TTCCACAGGAA GGTCCAGGCG CCTCTCAGCC TTGCTACTCA GAACAGCOGA 60
 TGATGGGCTT CAGTAACCTG AGCCCCGGTC CTGGCCCCAG CCAGGCCGTG CCTCTCCAG 120
 AGGGGCTGTG CCCTCAGCGG TACAGAGAGG AGAAGACCCT GGAAGAGCGG CGGTGGGAGA 180
 GGCTGGAGTT CCTTCAGAGG AAGAAAGCAT TCCTGCGGCA TGTGAGGAGG AGACACCCCG 240
 ATCATGTGCG CCCCCTATGCT GTTGGGAGGG AAGCCAGAAT CTCCTCATTA GGTGACAGAA 300
 GTCAGAAATG ATTCCGATGT GAATGTCGAT ACTGCCAGAG CCACAGGCCG AATCTTTCTG 360
 GGATCCCTGG GAGAGATTAAC AGGGCCCCAC ATCCCTCCTC CTGGGAGACG CTGGTGACGG 420
 GCCTCAGTGG CTGACTCTTC AGCCTAGGCA CCAACAGAGC CGGGCTCTG CTGGAAGCGG 480
 CACTCCAGCC ACAGGAGACA GAGGAGAGC GCCAGCGAGA GAGGCAGCAG GAGAGCAAAA 540
 TAATGTTTCA GAGGCTGCTC AAGCAGTGGT TAGAGGAAAA CTGAGACGTG CACCCCTATG 600
 GGATGAGAGC CCGAAGGGAC TCAGACGGAG CCGCCGTGTT GGCAGCGCCT GGGTGTGGGC 660
 CCATTTTGGG GACCAACAGC CAAGCTGTGG TCGATGAGT GCCAGGACCT GTGTACCCGG 720
 ACAAGTGGGA GTCTCTCCAG CATGATGCTT GACTGACCG AGGAAGGTCC TCATGTTTCG 780
 TGCTCTGCTT TCTCGATGCT CTGTGAGGCA TTCTTTGGCA AAGGACGCTG CBTACACCGC 840
 GTCTCACCGC CATCTCATAT GGTCTCTGTG ATGCATGTTG TCGCTTTCCG ACCCGGATC 900
 TCCATCTCTC TTCCCTTCTT GCTGTCACTA AGAGATCACA TGTCGTGTGA GTGTGAATGC 960
 CTGTGTGCTG TCCTGTGCTT TTGCACCATT GAGTTGACTG CCTCTGAGAA GCAGCACTAG 1020
 GCTGTGTGAA ATGCAATGTG CTGCCCTGAG ATCCAGTTTC AAGAATGGGC AGGTAAACGC 1080
 AGTGTGGGAA AGGAATGTGG AATGAGAATC TGGTGTGTCA CCGCTGTACT ATTGTGTAA 1140
 ATGTTTACTG ATGTGATTAAG CTACATGTAT GTAAATGTTG CAATACCCCT AACAGTCGAG 1200
 TAGTAGTCTC CCTTACAGGA ATTTTGTAGC GGGTTCCTCA TCATCAATAC CAAATAATA 1260
 TATGTAGGAA TGGAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA 1320
 AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA 1380
 AAAAAAAA AAAAAAAA AAAAAAAA AAAAAA

Seq ID NO: B55 Protein sequence
 Protein Accession #: NP_054857.1

1 11 21 31 41 51
 MMGLSNLSPG PGPSQAVPLP EGLLRQRYRE EKTLEERRNE RLEFLQKKA FLRHVRRRHR 60
 DDMAPYAVGR EARISPLGDR SQNRFRCSER YCQSHRPNLS GIPGESNRAP EPSSWETLVQ 120
 GLSGLLSLSG TNQPSPLPEA ALQPOETEER RQRRERQESK IMFORLLKQW LEEN

Seq ID NO: B56 DNA sequence
 Nucleic Acid Accession #: NM_000025.1
 Coding sequence: 198..1424

1 11 21 31 41 51
 GCTACTCCTC CCCCAGAGAC GGTGCAACCG AGGAGATTGG GGTGGGGGGA GGCTGAGCGC 60
 TCTGGCTGGG ACAGCTAGAG AAGATGGCCC AGGCTGGGGA AGTCGCTCTC ATGCTTGTCT 120
 GTCCCTCTCC CTGAGCCAGG TGATTTGGGA GACCCCTCTC TTCTCTCTTT CCTACCGGC 180
 CCACGCGCGA CCGCGGGATG GCTCCGTGGC CTCACAGAAA CAGCTCTCTT GCCCATGGC 240
 CGGACCTCC CACCTCTGGG CCAATAACG CCAACACGAG TGGGCTGCCA GGGGTTCCT 300
 GGGAGGCGGC CCTAGCCGGG GCCCTGCTGG CGCTGGCGGT GCTGGCCACC GTGGGAGGCA 360
 ACCTGTCTGT CATGTGTGGT ATGCGCTGGA CTCGAGACT CAGACCATG ACCAACGTGT 420
 TCGTGACTTC GCTGGCGGCA GCGGACCTGG TGATGGGACT CTGGGTGGTG CCGCCGGCGG 480
 CCACCTTGGC GCTGACTGGC CACTGGCGCT TGGGCGCCAC TGGCTGCGAG CTGTGACCT 540
 CGGTGGACGT GCTGTGTGTG ACCGCCAGCA TCGAAACCTT GTGCGCCCTG GCGGTGGACC 600
 GCTACCTGGC TGTGACCAAC CCGCTGCGTT ACGGCGCACT GGTACCAAG CGCTGCGCCC 660
 GGAAGCTGT GGTCTGGTGT TGGGTGCTGT CGGCGCGGT GTCTTTGGG CCTATCATGA 720
 GCCAGTGTGT GCGGTAGGG GCGGACGCG AGGCGCAGGG CTGCACTCC AACCCGCGCT 780
 GCTGTGCTTT CCGCTCCAAC ATGCCCTACG TGTGCTGTCT CTCTCTCTCT TCTTCTTACC 840
 TTCTCTCTCT CGTGTATGCT TTGCTTACG CGCGGCTTTT GTGTGTGGCT ACGCGCCAGC 900
 TCGCTTGTCT CGCGGGGAG CTGGGCGCT TTCCGCGGGA GAGTCTCTCG CCGGCGCGCT 960
 CGGCTCTCTT GCGCCCGGCC CCGGTGGGGA CGTGGCGTCC GCGCGAAGGG GTGCGCGCT 1020
 GCGGCTGGCG GCGGCGCGCG CTCCTGCTCT TCGGGAACA CCGGCGCTGT TGCACCTTGG 1080
 GTCTCATCAT GGGCACCTTC ACTCTCTGCT GGTTCGCTTT CTCTCTGCTT AACGTGCTGC 1140
 GCGGCTGGG GCGGCTCTCT CTAGTCCGCG GCGCGGCTTT CTTTGGCTGT AACTGCTTAG 1200
 GTTATGCCAA TTCTGCTTTC AACCGCTCA TCTACTGCGG CAGCGCGGAC TTTCGAGCG 1260
 CCTTCCGCGG TCTTCTGTGC CGCTGCGGCC GTCGCTGTCC TCGGAGGCC TGGCGCGCG 1320
 CCGGCGCGCG CCTCTTCCCG TCGGCGGTTC CTGCGGCGCG GAGCAGCCCA GCGCAGCCCA 1380
 GCGTTTGCCA AGGCTCTGAC GGGGCTCTCT GGGGAGTTTC TTAGGCTTGA AGGACAAGAA 1440
 GCAACAATC TGTGATTCAG AACCTGTGGA AAACCTCTGG CCTCTGTCTA GAATGAGTGC 1500
 CATGGAATTC CCGGCTGTGT AACTCTTACC CTCGAGAAC TGACGACTGG GCGATGTGAC 1560
 CCAAGGAGGG ATCCTTACCA AGTGGGTTTT CACCTCTCTT TTGCTCTCTG TCTGAGAGAT 1620
 GTTTTCTAAA CCGCAGCCTT GAATCTCACT CCTCCCTCAG TGGTAGTGTG CAGGTGCCGT 1680
 GGAGCAGCAG GCTGGCTTGT GTAGGGGCAC CCATCAACCG GCTTGTCTGT GCACTCAGTG 1740
 AGTGTCTTAG GCAAGAGAG CTCCCTGTGT TCCATCTCTT CTGCAACCCA AACCTGATG 1800

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AGACCTTAGT GTTCTCCAGG CTCTGTGGCC CAGGCTGAGA GCAGCAGGGT AGAAAAGACC 1860
AAGATTGGGG GTTTTATCTC TGTTTCCCTT ATTACTGCTC TCAGACAGTG GCCTCTCTCA 1920
CITTAGGCAT GGAATGGCTC CGATCTAOCCT CACAGCAGTG TCAGAGGAGC TTCGCCAGGG 1980
TTTGGGGAGC TCAGGGGTTT ATAAGARGGT GAAACCATTAG AACAGATCCC TTCTTTCTCT 2040
TTTGCAATCA GATAAATAAA TATCACTGAA TCCAGTTCAT CCTGGGCCCA CTTCCTCTCC 2100
GTTGTTTTTC TTTTCATAAT CCACTTACTC CTTTCCCTTC TACTCTGCGC TGGCTTTTGA 2160
CAGAGGCAGT AATTAGGCC TAATCCTCAC TCTTTCTTTC CTAATCTTCA TCAAAACAAA 2220
AATGAAAAGT CTGTCTGGAC GAAGGGGAGT GAGCTTGAGC CTTTGATATC TTGCTCCCCC 2280
ACCCCTCCCTG AAATCTCTGA AATCCAGTTG CCATTGAGTA GCAAAGCCAC GCTCCCCACA 2340
GGACTTGGAC AGAGGGGCCA CAGGGGGATG GGCTGGCTGT GGCCAGGTTT AGGGCAGGGG 2400
GCATTGTGTC CCTTCATGCT ATAATCCAGT GGTGCTTAC ATGGTGTGTG TGTGTGTGTG 2460
TGCGTGTGTG TGTGTGTGTG TGTGTCTGGA GGCACAGGCA CAAAGCATTT CTGGGTTTGG 2520
TCAAATGTCT TGTGTCTATA ATATATTCTG ATGTTTCCCA GCCTTTCAC AACCTCTACC 2580
TTCCACTCA CCTTCCCCAG CTACAAAAT CTGTATTATC CTCTTAAAT AAAACTGGAG 2640
TTAC

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Seq ID NO: B57 Protein sequence
Protein Accession #: NP_000016.1

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1 11 21 31 41 51
MAPWPHENSS LAPWFDLPTL APNTANTSGL PGVPWEAALA GALLALAVLA TVGNNLLNIV 60
AIANTPRLQT MINVFTSLA AADLVMLLV VPPAATLALT GHWPLGATGC ELWTSVDVLC 120
VTASITLCA LAVDRYLAVT NPLRYGALVT KRCARTAVVL VVVVSAVVSF APIMSQWWEV 180
GADABAQRCH SNPRCCAFAS NMPVVLLESS VSFYLLPLVM LEVYARVFWV ATRQLRLLRG 240
ELGRFPPEES PFAPSRSLAP APVGTCAFFE GVPACGRRA RLLPLREHRA LCTGLGLWGT 300
FTLCMLPPFL ANVLRALGGP SLVPGPAFLA LNWLGYSANSA FNPPLYCRSP DFRSAFRRLL 360
CRGRRLPFE PCAARPALF PSVPEARSS PAQPRLCQRL DGASHGVS

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Seq ID NO: B58 DNA sequence
Nucleic Acid Accession #: NM_032553.1
Coding sequence: 37..1038

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1 11 21 31 41 51
CACCATTAGG CAAAGATAGT TTCTCTAGAG ASAATCATGC CTGCTAATTA CACGTGTACC 60
AGGCCAGATG GAGACAATAC AGATTTTCGA TACTTTATTT ATGCAGTGAC ATACACTGTC 120
ATTCTTGTGC CAGGCTCATAT AGGGAATATA TTAGCCCTGT GGGTATTCTA TGGTTATATG 180
AAGAAACAA AACGAGCTGT GATATTTATG ATAAACTTAG CCATTGCTGA CTTACTACAA 240
GTCTTTCTCT TGCCACTGAG GATCTTCTAC TACTTGAATC ATGACTGGCC ATTTGGGCCT 300
GGTCTCTGCA TGTCTGTGTT CTACCTGAGG TATGTCAACA TGTATGCAAG CATCTACTTC 360
TTGCTCTGCA TCAGTGTGCG ACGATTTTGG TTTCTCATGT ACCCCTTTGG CTTCCTAGAC 420
TGCAAAACAG AATATGACCT GTACATCAGC ATTGCTGGCT GGCTGATCAT CTGCCCTGCC 480
TGTGTACTCT TTCCACTCCT CAGAACCACT GATGATACCT CTGGCAATAG GACCAATGCC 540
TTTGTGATC TTCTTACCAG GAATGTCAAC CTGGCCCACT CGTTTGTAT GATGACCATT 600
GGCGAGTTGA TTGGGTTTGT AACTCCGCTT CTGATTGTCC TATATTGTAC CTGGAGACG 660
GTTTATACAC TGCAAGATAA ATATCCCATG GCCCAAGATC TTGGAGAGAA ACAGAAAGCC 720
TIGAGATGA TTCTAACCTG TGCAAGGGTA TTCTAATTT GCTTTGCACC TTATCATTTT 780
AGTTTCTCTT TAGTATTCCT GGTGAAGTCC AATGAAATTA AAAGCTGCCT AGCCAGAAAG 840
GTGATTCTAA TATTTCTATC TGTGGCATTG TGTCTTGCEA GTCTGAATTC ATGTCTTGAC 900
CCAGTCATAT ACTACTTTTC CACTAATGAG TTCGAAAGAC GGCCTTCAG ACAAGATTTC 960
CATGACAGCA TCCAACCTCA TGCAAAATCC TTTGTGAGTA ACCATACAGC TTCCACCATG 1020
ACACCTGAAT TATGCTAATA CAAAACCA AACTGAATGT GACCTGAAAT GCAAGTACAT 1080
CAGAACATAT TATGCTAATA CAAAGCACAG GGAAGAACTT GCAAAACAA ACAGCTTTTC 1140
AGTTCTGCTC TATCTTACTG CTATGGGGAA TTCACTTCTT CAAAGCAGGA CCTATTGGA 1200
GCATTACAT CCACGATTAT TGATGTTGAC ATGTCCATGT AGTAATTTTT CTTCAGT

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Seq ID NO: B59 Protein sequence
Protein Accession #: NP_115942.1

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1 11 21 31 41 51
MPANYCTRP DQNDIDERYF IYAVTYTVIL VPGLIGNILA LNVFYGYMKE TKRAVIFMIN 60
LAIDLQLVL SLPLRIFFYL NHDWPFPGPL CMFCFYLYKV NMYASTYFLV CISVREFWFL 120
MYPRFHDCK QKDYLYISIA GWLIICLACV LFPLLRSTDD TSGNRTKCPV DLETRFVILA 180
QSVVMTIGE LIGFVTPILLI VLXCTWKTIV SLQDKYPMAG DLGERQKALK MLITCAGVFL 240
ICFAPYHBSF PLDFLVKSNK IKSLARKVI LIFESVALCL ASLNSCLDPV IYFSTNEFR 300
RLLSRQDLSD SIQLHAKSFV SNHTASTMT ELC

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Seq ID NO: B60 DNA sequence
Nucleic Acid Accession #: CAT cluster

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80

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1 11 21 31 41 51
GATTGGGATT TTAATCCGAC TCACTATAGG GAATTTGGC CCTCGAGGCC AAGAATTCGG 60
CCCGAGGGTT AGACATTAA CTGAGTCTT TTCATATCAC GGTATGCTTT TATTTTACC 120
TCATATATAA TTAATTTTCA TCTGGGCATA TATTTCCAGA TTAGAAATCA TTTCTTTTCA 180
TACATTTTAA GGAATTTATA CATTTGCATC TGAAATTTGA TTCAATATCT TCTAGAAACC 240
AAGAGTGGAC TTGATATCCG TCTGATATA TTTTCTTGT TGGTAAAGAG CCTCTTTT 300
CCCTTTTAT TTTCACTTC TCTTCTCTA GTGTTTATA TCTTATTTT ATGAATGTAG 360
TCTAATTAAT TAGAACACTG TCTCCGAGTA TGTGTTTAT TGGGTTTGT TTTGACAT 420
TGCTCCAGG TCGAGTTTA TGTGTGTTA TGTTCCTAT TTGAGGTTG ACACCTAGAA 480
AATTTTCTCA ATTCGAAAC TATTTTCTT CAGCACTCAG AAATTTTAT CAAAGATTAT 540
TTCCACGATT ATTTCTCTTC CTGGTTTCT CGTGTCTTA ACCTAGATT CAATTGTTA 600

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ATGTTAGACC TTACACATCT TCAATGTATC ATATATATTT CACTCATATT ATTTATGTTC 660
 ATATCTTTTG GACTATTGTG TGAARGCAAT AAATGTATAT TACTTTAAAA AAAAAAATAA 720
 AAAACTECAT TTTCAAATTT AATACACACA AATTGTGCAT ACCACACAC ATATACCACA 780
 GATATATCCA TTTTCAGGAT TTCTTTAAGT GTTATTTTAA AAATAATCAT ATTCCTATTT 840
 TGTGAACGTG GGGATTCTCT GAAACTTTTT GAAACCTCTC ATTAGTCTGT GTTGTGTGG 900
 TTCTTTTAAA TTAATCTCTC CTTCAGAATT ACTTTGTGTG TTTGAATTG AGTCTTTGCC 960
 ATTATAAGG CGGGCTTTCC TTGAATACCA GATAACTCTG AGTTTCTCTG TCATATTTAA 1020
 GAATAAATAA CCTAATTTGA AAAAAAATAA AAAAA

Seq ID NO: B61 DNA sequence
 Nucleic Acid Accession #: NM_014522.1
 Coding sequence: 846..3911

1 11 21 31 41 51
 15 CTGGTGGTCC AGTACCTCCA ARGATATGGA ATACACTCCT GAAATATCCT GAAAACTTTT 60
 TTTTTCAGA ATCCTTTAAT AAGCAGTTAT GTCAATCTGA AAGTTGCCTA CTGTACTTTT 120
 ATATTAATAG CTATTCCTGT TTTTCTTATC CAAAGAAAAA TCCTCTAATC CCTTTTTCAC 180
 ATGATAGTTG TTACCATGTT TAGGCATTAG TCACATCAAC CCTCTCCTC TCCCAAACTT 240
 20 CTCTCTCTCA AATCAAACTT TATTAGTCCC TCCCTTATAA TGATTCCTTG CCTCGTTTAA 300
 TCCAGATCAA TTTTTCCTCA CTTTGATGCC CAGACCTGAA GAATGAGCT ACTGTATAAA 360
 TTATTCATTG CCAAGAGAAAT AATTGCATT TAAACCCATA TTATAACAAA GAATAATGAT 420
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Seq ID NO: B62 Protein sequence
 Protein Accession #: NP_055337.1

1 11 21 31 41 51
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Seq ID NO: B63 DNA sequence
 Nucleic Acid Accession #: XM_059180.2
 Coding sequence: 276..3740

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40	AGCTTACATC ACCAAGGTCT CTGTGTCAA CCTGTGCCCA CTCTATATGC ACTTTGTTTA 5040
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Seq ID NO: B64 Protein sequence
Protein Accession #: A39577

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	DGHDIEHCL GMAYLAISEY AMMKMQLPE LPKDLSYKRY IPETLANKSIR QRNLTKMRI 240
	NNVFEDFLKE FNNKTICDSS VSTHDLKVY LATLETLMH XGASIPETEM LLISSSENMN 300
	WFSNDGGWV LYYEVMVTGN LGIQWREKPN VVSVEKERNE LKRKLEENKO KKDEERNKIR 360
	ESWNNFSFPF EITHIVIKES VVSINKQDNK KMLKLSHBE EALSFVSLVD GYFRLTADAH 420
55	HYLCTDVAPP LIVHNIQNGC HPCICTEYAI NKLRQEGSEE GMVYLRWSTF DFDNIMATVI 480
	CFKBSQVQG AQKQPKNFQI EVQKGRYSLH GSDRSFPLG DLSHLKQI LRTDNISFMI 540
	KRCQPKPKE IENLLVATKK AQWQPVYPM SLSFDRIK KDLVQGEHLG RGRTHIYSG 600
	TLMDYKDDG TSEEEKIKVI LKVLDPHRD ISLAFPEAAS MMRQVSHKHI VYLYGVCVRD 660
	VENINVEEFV RGGPLDLFME RKSDVLTTPN KFKVAKOLAS ALSYLEDKDL VHGNCVCKNL 720
60	LLAREGIDSE CGPFIKLSPP GIPITVLSRQ ECLEIFPLA PECVEDSKML SVAADKNSFG 780
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65	DFGLTKALET DKREYTVKDD RDSPVFWYAP ECLMQSKFYI AEDVNSFQVT LHELLTYCDS 1080
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Seq ID NO: B65 DNA sequence
Nucleic Acid Accession #: NM_004867.1
Coding sequence: 140..931

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Seq ID NO: B66 Protein sequence
 Protein Accession #: NP_004858.1

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Seq ID NO: B70 Protein sequence
Protein Accession #: NP_002966.1

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5      1      11      21      31      41      51
      |      |      |      |      |      |
      MQAANLLGAL VVPQLLGFH GARGAEREWE GGWGGAQEEE REREALMLKH LQEALGLPAG 60
      RGDENPAGTV EGKEDWEMEE DQGESESEEA TPTPSSGFSP SPTPEDIVTY ILGRLAGLDA 120
10     GLHQLHVRLE ALDTRVVELT QCLRLRLNAA GUTRDAVOAL QEAQGRAERE HGRLEGCCLKG 180
      LRLGHKCPLL SRDFFAQAAA QARCTARGGS LAQPADRQOM EALTRYLRAA LAPYNWFVWL 240
      GVHRRRAEGL YLFENGQRVS FFAWHRSPRP ELQAQPSASP HPLSPDQPNG GTLENCVAQA 300
      SDDGSWRDHD CQRRLYVVCB PFP

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Seq ID NO: B71 DNA sequence
Nucleic Acid Accession #: BC000839.1

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15     1      11      21      31      41      51
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      CTGGCCAGGG CGACTGGCGG ATAAGGTCTT GTGCGTGGCC TCGAGGCTTA AAAGTAGCAG 60
20     TGGGCTTTTB TGAAGGACAA AATGGCGATG GCGGGCCGTG TAGGTCCCCC TTCCTATGAT 120
      GAGGACCTTT TCACAGACCT GTACTGAGCT CCGTGAGGAT AGTTAACTCT GAGGAGATGG 180
      GCGCTGCAAG CCTCCTTCTT AGCCGTCTGT TCAGAAATA GCGTTTTCGA AATGCCCTGA 240
      GTTGACCTAA TGTCTTATTG GGTCTCTGTC TGCAGGATTT ACGGCGACGT TGAACCGGAA 300
      GAGAGCTCTG TTGTTGCAAT GTTCAGCCCA CAAGAGCTTA CTGCTGAAGG AATGGGACAA 360
25     GACCCATCTT TATGCAAAGC CAGCGTTACA GTAAATGTTCC AGCATCTCAT AATCTATCCT 420
      GGGGAATTCG GCTGCCCTCC AGGGTGAATA CAGGTATTCC TGATGACAGT CTGCTCTAT 480
      CTTACAGAGC AGCTTGTGTC TATATACCAT TGAAGAAGCT TCAGAGCTGA GAGGTACTAC 540
      TAACCAATAA CCTGCTGGG TCAAGGGGCC AGCACCTTCT CTCTAAAGCC CAAGAGGAGT 600
      TTGAGGAAAA CTAGGTGTCT GTGTTCACTC CAGGCTGAAG TTACAGGTCT GAGCAATAAA 660
30     GGTGTATAAA AATAGGAATC TGTCTGGAG GACATCAGAA GGTGAATTTT CCAAGTTCTT 720
      GGACAACTTA GCTGTTGAAA AGCTTCTCG GTTTGGGGGG TATTTCAGAT GTACCTTAAA 780
      GTGTTAGCAG ATACAGATTA AGACACTGGG AGCCAATGAA ACAGCAGTTG AGGGTTGCT 840
      GTGTATCA CA TTTCTGATT TTATCACCCC CTCTCTGCAA CATTATTAT CTGGAATCTA 900
      CCTGCCCCCT TGTCTTTTAT ATACAAGGCG TTGGTFTTGT TACCCAGGCT GGTTCAGG 960
35     CCATAGCTTT AAGAGATCCT CTCACACAG ATTTCCAAAG TGCTGGGATT GCAGGTGTGA 1020
      TTCATGGCAC CCAGACTTTG CTGCTTCTCT TACATGATCC AGGCCAGAA CCCAACTCA 1080
      GGCATGATC AGATGACAC TTTGTAAAC TACTGACCTA GCTGTGTCG AATGTGTGAT 1140
      TGAACCTCC ATAACCTCAC TTCTGTCTG TTCTCTGTA TACAGCCACC TTCGTGTC 1200
40     GTCATGAGCC TTTAGGTCTC CATTTGCATA TTGCAAATAC TATGTTCCAT GTAGGTAGCT 1260
      CATTCAAGGC CTGTCTCTTC ACTTCAAAAA AGGTTCCCTT GAGGACTGGC TGTCAATTTG 1320
      TGTGCTGTG TTGTTGTTG ATGAAAAATA TAAATGATT GATTACATAA AAAAAAATA 1380
      AAAAAA

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Seq ID NO: B72 DNA sequence
Nucleic Acid Accession #: CAT cluster

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      TGTCTAGTAG GCTCTGGGTA ATCGGCCGAB GGTGGCTTGG TGGTCTTTAT AGCTGTACT 60
50     CTTGTACTT GTCTTTTCT TTTATTTCT TTTGAGCGAT TGTGGAACA TAGCATAGCA 120
      CGCACTATGG CACGAGGCTC GTGCTGCCG GCGAGGGGGA CTGGCGGATA AGGTCTTGT 180
      CGTGGGCTCG AGGCTTAAAA GTAGCAGTGG GCTTTGTGA AGGACAAAT GGCGATGGG 240
      GGCGGTGTAG GTCCCTCTTC CTATGATGAG GACCTTTCA CAGACCTGTA CTGAGCTCG 300
      TGAGGATAA TTAATCTGAG GAGATGGGCC CTGCAAGCCT CTGCTTAGC GGTCTGTTCA 360
55     GAAAAATAGG TTTTGAAT ATCCCTGAGT GACCTAATGT CTTATGGGC TCCTGCTGTC 420
      AGGATTTAG CACAGCTTGG AACCGAGAG AGCTCTGTT TGTCAATGTT CAGGCCACAA 480
      GAGCTTACT GTGAAGGAAT GGGACAAGAC CCATCTTAT GCAGAGCCAG GGTACAGTA 540
      ATGTTCCAGC ATCTCATAT CTATCTGGG GAATTCAGCT GCTTCCAGG GTGAATACAG 600
      GTATTCTGA TGACAGCTG CCTCTATCT ACAGAGCAGC TTGTTGCTAT ATACCATGA 660
60     AAGGCTTCA GAGCTGAGAG GTACTACTAA CCATAACCT GCTTGGCTCA AAGGCCAGC 720
      ACCTTCTCTC TAAAGCCCAA GAGGAGTTG AGGAAAACTA GGTGTCGTG TTCCTCCAG 780
      GCTGAAGTTA CAGGTCTGAG CAATAAGGT GTATAAAAA TGAATCTGT CTGGAGGAC 840
      ATCAGAGGT GAATTTTCCA AGTCTTGGG CAACCTAGCT GTTGAAGAG TTTCTGGTT 900
      TGGGGGGTAT TTAGATGTA CCTTAAAGT TTAGCAGACA CAGATTAAGA CACTGGGAGC 960
65     CAAAGABACA GCAGTTGAGG GTTTGCTGTG TATCAGATT CTGTATTTA TCACCCCTT 1020
      CCTGCAACAT TATTTATCTG GAATCTACCT GCGCTTTGT TTTTAGATA CAGGGCTTG 1080
      GTTTGTATC CAGGGCTGGT TTCAAGGCCA TAGCTTTAAG AGATCCTCTC ACCACAGAT 1140
      TCCAAAGTGC TGGGATTGCA GGTGTGATC ATGCAACCCA GACTTTGCTG CCTTCTTAC 1200
      ATGATCAGG CCGCAAGACC AAATCAAGC ACTGTATAGA TGACCACTT GTTAACTAC 1260
70     TGACCTAGCT TGTGCAAT TGTGATTGA ACTTCCATA ACTCCACTTC GTGTCTGTT 1320
      CTCTGTATAC AGCCACCTTC TGTTCCTGTC ATGAGCCTT AGGTCTCCAT TTGCATATT 1380
      CAAATACAT GTTCCATGTA GGTAGCTCAT TCAGGGCTT GCTCTTCACT TCAAAAAAG 1440
      TTCTCTTGA GACTGGCTGT CAATTTGTGT TGTCTGTGT GTTGTGATG AAAATAATA 1500
75     AATGATTGAT TACATAAAA AAAAAAATA AAAAAAATA AAAAAAATA CAAAAAAC 1560
      CGCGGCGCTT TTTCCCGGCC GCACAAAGTT ATAAACGCC GTCCATC

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Seq ID NO: B73 sequence
Nucleic Acid Accession #: NM_000222.1
Coding sequence: 22..2952

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      GATCCCATCG CAGCTACCCG GATGAGAGGC GCTGCGCGCG OCTGGGATTT TCTCTGCGTT 60
      CTGCTCTTAC TGTCTGGGCT CCAGACAGGC TCTTCTCAAC CATCTGTGAG TCCAGGGGAA 120

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	CCGTCCTCCAC	CATCCATCCA	TCCAGGAAAA	TCAGACTTAA	TAGTCCGCGT	GGGCGACGAG	180
	ATTAGGCTGT	TATGCACTGA	TCCGGGCTTT	GTCAAAATGGA	CTTTTGAGAT	CCTGGATGAA	240
	ACGAATGAGA	ATAAGCAGAA	TGAATGGATC	ACGGAAGG	CAGAGGCCAC	CAACACCGGC	300
5	AAATACACGT	GCACCAACAA	ACACGGCTTA	AGCAATTCCA	TTTATGTGTT	TGTTAGAGAT	360
	CCTGCCAAAG	TTTTCCCTGT	TGACCGCTCC	TTGTATGGGA	AAGAAGACAA	CGACACGCTG	420
	GTCCGCTGTG	CTCTCACAGA	CCCAGAAATG	ACCAATTATT	CCCTCAAGGG	GTGCCAGGGG	480
	AAGCCTCTTC	CCAAGGACTT	GAGGTTTATT	CCTGACCCCA	AGCGGGGCAT	CATGATCAAA	540
	AGTGTGAAC	GGCCTTACCA	TCGGCTCTGT	CTGCAATTGT	CTGTGGACCA	GGAGGGCAAG	600
10	TCAGTGTGTT	CGGAAAAATT	CATCCTGAAA	GTGAGGCCAG	CCTTCAAAGC	TGTGCTGT	660
	GTGTCTGTGT	CCAAAGCAAG	CTATCTTCTT	AGGGAAGGGG	AAGAATTAC	AGTGACGTGC	720
	ACAATAAAG	ATGTGTCTAG	TTCTGTGTAC	TCAACGTGGA	AAGAGAAAA	CAGTCAGACT	780
	AAACTACAGG	AGAAATATAA	TAGCTGGCAT	CACGGTGACT	TCAATTATGA	ACGTACAGCA	840
	ACGTTGACTA	TCAGTTCAGC	GAGAGTTAAT	GATTCTGGAG	TGTTTATGTG	TTATGCCAAT	900
15	AATACTTTTG	GATCAGCAAA	TGTCACAACA	ACCTTGGAA	TAGTAGATAA	AGGATTCAAT	960
	AATATCTTCC	CCATGATAAA	CACTACAGTA	TTTGTAAACG	ATGGAGAAAA	TGTAGATTG	1020
	ATTGTGAAAT	ATGAAGCATT	CCCCAAACCT	GAACACGAGC	AGTGGATCTA	TATGAACAGA	1080
	ACCTTCACTG	ATAAATGGGA	AGATTATCCC	AAGTCTGAGA	ATGAAGATGA	TATCAGATAC	1140
	GTAAGTGAAC	TTCACTTAAC	GAGATTAAAA	GGCACCAGAG	GAGGCACTTA	CACATTCTTA	1200
20	GTGTCCAAAT	CTGACGTTAA	TGCTGCCATA	GCATTTAATG	TTTATGTGAA	TACAAAACCA	1260
	GAATCTCTGA	CTTACGACAG	GCTCGTGAAT	GGCATGCTCC	AATGTGTGGC	AGCAGGATTC	1320
	CCAGAGCCCA	CAATAGATTG	GTATTTTGTG	CCAGGAACTG	AGCAGAGATG	CTCTGCTTCT	1380
	GTACTGCCAG	TGATGTGCA	GACACTAAAC	TCATCTGGGC	CACCGTTTGG	AAAGCTAGTG	1440
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25	TACAAAGATC	TGGCAGAGAC	TTCTGCCAT	TTTAACCTTG	CATTAAAGG	TAAACACAAA	1560
	GAGCAAAATC	ATCCCCACAC	CCGTTCACCT	CCTTGTCTGA	TTGGTTTGGT	AATCGTAGCT	1620
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	GAAGTACAGT	GGAAATGGTT	TGAGGAGATA	AATGGAAACA	ATTATGTTTA	CTAGACCCCA	1740
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30	ACCTTGGGTG	CTGAGGCTTT	CGGGAAGGTT	GTGAGGCCAA	CTGCTTATGG	CTTAATTAAG	1860
	TCAGATGGGG	CCATGACTGT	CGCTGTAAAG	ATGCTCAAGC	CGAGTGCCCA	TTTGACAGAA	1920
	CGGGAGGCC	TCATGTCTGA	ACTCAAAGTC	CTGAGTTACC	TTGGTAAATCA	CATGAATATT	1980
	GTGAATCTAC	TTGAGGCTCG	CACCAATTGA	GGGCCCAACC	TGGTCATTAC	AGAAATTTGT	2040
	TGCTATGGTG	ATCTTTTGAA	TTTTTTGAGA	AGAAAACGTG	ATTCATTAT	TTGTTCAAAG	2100
35	CAGGAAGATC	ATGCAAGAGC	TGCACCTTAT	AAGAATCTTC	TGCATTCAAA	GGAGTCTTCC	2160
	TGCAGCGATA	GTACTAATGA	GTACATGGAC	ATGAAACCTG	GAGTTTCTTA	TGTTGTCCCA	2220
	ACCAAGGCGG	ACAAAAGGAG	ATCTGTGAGA	ATAGGCTCAT	ACATAGAAAG	AGATGTGACT	2280
	CCCGCATCA	TGGAGGTGTA	CGAGTTGGCC	CTAGACTTAG	AAGACTTGCT	GAGCTTTTCT	2340
	TACCAAGTGG	CAAAAGGATC	GGCTTTCTCT	GCCTCCAAGA	ATTGTATTCA	CAGAGACTTG	2400
40	GCAGCCAGAA	ATATCTCTCT	TACTCATGGT	CGGATCACAA	AGATTGTGTA	TTTTGTCTA	2460
	GCCAGAGACA	TCAAGAAATGA	TTCTAATTAT	GTGGTTAAGG	GAACGCTCG	ACTACCTGTG	2520
	AAGTGGATGG	CACCTGAAAG	CATTTFCAAC	TGTTATACA	CGTTTGAAGG	TGACGTCTGG	2580
	TCTATGGGAA	TTTTCTTTTG	GGAGCTGTTT	TCITTAGGAA	GCAGCCCTCA	TCTTGAATG	2640
	CGGTGTGATG	CTAGATTCTA	CAAGATGATC	AAGGAAGGCT	TCCGGATGCT	CAGCCCTGAA	2700
45	CACGCACTTG	CTGAAATCTG	TGACATAATG	AAGACTTGCT	GGGATGCAGA	TCCCTAAAA	2760
	AGACCRACAT	TCAAGCAART	TGTTACGCTA	ATTGAGAGGC	AGATTTCAGA	GAGCACCAAT	2820
	CATATTACT	CCAACCTTAC	AATCTGCAGC	CCCAACCGAC	AGAGGCGCGT	GGTAGACCAT	2880
	TCTGTGCGGA	TCAATCTCTG	CGGCAGCAC	GCCTCTCTCT	CCAGCCCTCT	GCTTGTGCTC	2940
	GACGATGTCT	GAGCAGAATC	AGTGTGTTGG	TCACCCCTCC	AGGAATGATC	TCTTCTTTTG	3000
50	GCITTCATTA	TGGTTATTTT	CTTTCTTTTC	AACCTTGATC	CACCTCCAGG	ATAGTGGGCA	3060
	CCCCACTGCA	ATCCGTGCTT	TCTGAGCACA	CTTTAGTGGC	CGATGATTTT	TGTCTATCAG	3120
	CACCATCTCT	TGCAAAAGGT	TCCAACCTGA	TATATTCCCA	ATAGCAACGT	AGCTTCTTAC	3180
	ATGAACAGAA	AACATCTCTG	TTTGGAAAAA	GAGAGGGAGG	TATGGACTGG	GGCCAGAGT	3240
	CCTTTCCAG	GCTTCTCCAA	TTCTGCCCCA	AAATATGGTT	GATAGTTTAC	CTGAATAAAT	3300
55	GGTAGTAAT	ACAGCTTGCC	TTCAAGACCA	TCCATAGTAG	TATGATGATA	CAGATTAGA	3360
	AGCTGAAAAC	CTAAGTCTCT	TATGTGGAAA	ACAGAACATC	ATTAGAACAA	AGGACAGAGT	3420
	ATGAACACCT	GGGCTTAAGA	AATCTAGTAT	TTCATGCTGG	GAATGAGACA	TAGGCCATGA	3480
	AAAAATGAT	CCCCAAGTGT	GAACAAAAGA	TGCTCTTCTG	TGGACCACTG	CATGAGCTTT	3540
	TATACTACCG	ACCTGGTCTT	TAAATAGAGT	TGCTATTAG	AGCATTGAAT	TGGAGAGAG	3600
60	GCCTCCCTAG	CAGCACTTGG	TATATACGCA	TCTATAAAT	GTCCGTGTTT	ATACATTGTA	3660
	GGGGAACAA	CCATAGAGTT	TGCTTCTGTT	ATACAAACCT	GGCATTAATG	CCACTGTGTA	3720
	TAGAAGTAGA	TTAAGAGCCA	TATAAGTTTG	AAGGAACAG	TTAATACCAT	TTTTTAAGGA	3780
	AACAATATAA	CCACAAAGCA	CAGTTTGAAC	AAAATCTCCT	CTTTAGCTG	ATGAACCTTAT	3840
	TCTGTAGATT	CTGTGGAACA	AGGCTATCAG	CTTCAGAAATG	GCATTGACT	CAATGGATTT	3900
65	GATGCTGTTT	GACAAAGTTA	CTGATTCACT	GCAATGGCTCC	CACAGGAGTG	GGAAAAACAT	3960
	GCCATCTTAG	TTTGGATTCT	TATGTAGCAG	GAATAAAGT	ATAGGTTTAG	CCTCTCTCC	4020
	AGGCATGTCC	TGGACACCGG	GCCAGTATCT	ATATATGTGT	ATGTAGCTTT	GTATGTGTGT	4080
	AGACAAATAT	TTGGAGGGGT	ATTTTGTCCC	TGAGTCCAAG	AGGTTCTTTT	AGTACCTGAA	4140
	AAGTAACCTG	GCTTTTCAAT	TAGTACTGTC	TCTTGTTTCT	TTTCACATAG	CTGTCTAGAG	4200
70	TAGCTTACCA	GAAGCTTCCA	TAGTGGTGCA	GAGGAAGTGG	AAGGCATCAG	TCCCTATGTA	4260
	TTTGCACTTC	ACCTGCACCT	AAGGCACCTT	GTTATTAGA	CTCATCTTAC	TGTACCTGTT	4320
	CCTTAGACCT	TCCATATATG	TACTGTCTCA	CTGAACATT	TAAATTTTAC	CCTTTAGACT	4380
	GATGCTTGG	TATATTCTCT	GATGTTTACC	TCTTTAAAAA	CAAAACAAAA	CAAAACAAAA	4440
	AACCTCCCTT	CTCATCTGCC	CAATATAAAA	GGCAAAATGT	TACATGGCAG	AGTTTGTGTG	4500
75	TTGCTCTGAA	AGATTACAGT	ATGTTGCCCT	TATGGTTTCC	CCCTTCTCAA	TTTCTTAGAG	4560
	TACATTTAGA	GAACTGTGGC	CGTTATCTGG	AAGTAACCAT	TTGCACTGGA	GTTCTATGCT	4620
	CTGCACTTCT	TCCAAAGTTA	ACAGATTTTG	GGGTGTGTTT	GTCAACCAAG	AGATTGTGTT	4680
	TGCACTACT	TTGTCTGAAA	AATTCCTTGG	TGTTCTTATT	GACTTCAATG	ATAGTAAGAA	4740
	AAGTGGTGT	TAGTTATAGA	TGCTAGGTA	CTTCAGGGGC	ACTTCATTGA	GAGTTTGTCT	4800
80	TTGCACTACT	TTGTCTGAAA	AATTCCTTGG	TGTTCTTATT	GACTTCAATG	ATAGTAAGAA	4860
	AAGTGGTGT	TAGTTATAGA	TGCTAGGTA	CTTCAGGGGC	ACTTCATTGA	GAGTTTGTCT	4920
	AATGCTTTTT	GAATATTTCC	AAGCCCATGA	GTCTTGAAA	ATATTTTTTA	TATATACAGT	4980
	AACITTAGTG	GTAAATACAT	AAGCGGCGTA	AGTTTAAAGG	ATGTTGGTGT	TCCAGTGT	5040
	TTATTCCTGT	ATGTTGTCCA	ATTGTTGACA	GTTCTGAAGA	ATTC		

Seq ID NO: B74 protein sequence
Protein Accession #: NP_000213.1

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5      1      11      21      31      41      51
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MRGARGANDF LCULLLLLRV QIGSSQPSVS PGRPSPPSIH PGKSDLIVRV GDEIRLLCTD 60
PGFVKWTFEI LDETENENKQW EWIETKAEAT NTGKYTCNTK HGLNSIYVF VRDPAKLFLV 120
DRSLYGEKEDN DTLVRCLPTD PEVTNYSLEK CQKRLPKDL RFIEDPKAGI MKSVKRAYH 180
RLCLHCSVDQ EGKSVLSSEK ILKVRPAFKA VPVSVSKAS YLLREGSEFT VTCTIKDVSS 240
SVYSTWKREN SQTKLQEKYN SWHGDENYE RQATLTSSA RVNDSGVFMC YANNTFGSAN 300
VTTLLEVVDK GFNIFPMIN TTVFVNDGEN VDLIVEYEAF PKPEHQWYIY MNRITFDKWE 360
DYPKSENEEN IRVYSELHIA RLKGTGGTY TFLVNSSDVN AALAFNVYVN TKPEILLYDR 420
LVNGLMLQVCA AGFPEPTIDH YFCPGTEQRC SASVLPVDVQ TLNSSGPFPG KLVVQSSIDS 480
SAPKHNGTVE CKAYNDVGKT SAYFNFAFKG NNKEQIHPT LFTPLLIGFV IVAGMMCIIV 540
MILTYKYLQK PMYEVQWKVV KEINGNNYVY IDPTQLPYDH XWEFFRNRLS FGKTLGAGAF 600
GKVVEATVAG LLIKSDAMTV AVIKMLKPSAH LTEREALMSE LKVLSYLGNH MNIVNLLGAC 660
TIGGPTLVIT FYCCYGLLLN FLRRKRDSFI CSKQEDHAEA ALVKNLLESK EBSGSDSTNE 720
YMDMKPGVSY VVPTKADRRR SVRIGSYIER DVTPAIMEED ELALDLEDLL SFSYQVAKGM 780
APLASKNCTH RDLAARNILH THGRITKICD FGLARDIKND SNYVVKGNAR LPVKWMAPEY 840
IFNCVYTFES DVWYGTGIFW ELFSLGSSPY PGMPVDSKPY KMKEGFRML SPEHAFARMY 900
DIMKTCWDAD PLKRPYFQI VQLIEKQISE STNHIYSNLA NCSFNRQKPV VDHSVRINSV 960
GSTASSSQFL LVHDDV

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Seq ID NO: B75 DNA sequence
Nucleic Acid Accession #: NM_004456
Coding sequence: 58..2298

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30      1      11      21      31      41      51
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GGCCGAGACTG GGAAGAAATC TGAGAAGGGA CCACTTTGTT GGCCGAAGCG TGTAAAATCA 120
GAGTACATCG GACTGAGACA GCTCAGAGAG TTCAGACGAG CTGATGAAGT AAAGAGTATG 180
TTTAGTTCCCA ATCGTCAGAA AATTTTGGAA AGAACGGAAA TCCTAAACCA AGAATCGAAA 240
CAGCGAAGGA TACAGCCTGT GCACATCCTG ACTTCGTGTA GCTCATTCGG CGGGACTAGG 300
GAGTGTTCGG TGACCAAGTA CTGTGATTTT CCAACACAAG TCATCCCATT AAAGACTCTG 360
AATGCACTTG CTTCACTACC CATAATGTAT TCTTGTCTC CCCTACAGCA GAATTTTATG 420
TTGGGAAGATG AAACGTGTTT ACATAACATT CCTATATGG GAGATGAAGT TTTAGATCAG 480
GATGGTACTT TCATTGAAGA ACTAATAAAA AATTATGATG GGAAAGTACA CGGGGATAGA 540
GAATGTGGGT TTATAAATGA TGAAATTTTT GTGGAGTTGG TGAATGCCCT TGGTCATAT 600
AATGATGATG ACGATGATGA TGATGGAGAC GATCCTGAAG AAGAGAGAAG AAAGCAGAAA 660
GATCTGGAGG ATCACCAGGA TGATAAAGAA AGCCGCCAC CTGGGAATTT TCCTTCTGAT 720
AAAATTTTGG AGGCTATTC CTCATGTGTT CCAGATAAGG GCACAGCHGA AGAACTAAG 780
GAAAAATATA AAGAACTCAC CCAACAGCAG CTCCAGCGCG CACTTCCTCC TGAATGTACC 840
CCCAACATAG ATGGACCAAA TGCTAAATCT GTTCAGAGAG AGCAAGCCTT ACCTCCTTT 900
CATACGCTTT TCTGTAGCG ATGTTTTTAA TATGACTGCT TCCTACATCC TTTTCATGCA 960
ACACCCAACA CTTATAAGCG GAAGAACACA GAACAGCTC TAGACAACAA ACCTTGTGGA 1020
CCACAGATTC ACCAGCTTTC GGAGGAGAGA AAGGAGTTTG CTGCTGCTCT CACCGCTGAG 1080
CGGATAAAGA CCCCACCAA AGSTCCAGGA GSCCGAGAA GAGGACGGCT TCCCAATAAC 1140
AGTAGCAGGC CCAGCAGCCC CACCATTAAT GTGCTGGAAT CAAAGGATAC AGACAGTAT 1200
AGGGAAGCAG GACATGAAC GGGGGGAGAG AACAAATGATA AAGAGAGAAG AGAGAAGAAA 1260
GATGAACATT CGAGCTCCTC TGAAGCAAA TCTCGGTGTC AAACACCAAT AAGATGAAG 1320
CCAAATATTG AACCTCTTGA GAATGTGGAG TGGAGTGGTG CTGAAGCCTC AATGTTTAGA 1380
GTCCCTCATG GCACTTACTA TGACAATTC TGTGCCATTG CTAGGTTAAT TGGGACCAAA 1440
ACATGTAGAC AGGTGTATGA GTTTAGAGTC AAAGAATCTA GCATCATAGC TCCAGCTCCC 1500
GCTCAGAGATC TGGATATCTC TCACAAGAAA AAGAAAGGGA AACACCGGTT GTGGGCTGCA 1560
CACTGCGAAG AGATACAGCT GAAAAGGAG GSCCTCTCTA ACCATGTTTA CAACATCAA 1620
CCCTGTGATC ATCCACGGCA GCCTTGTGAC AGTTCGTGCC CTGTGTGTAT AGCAAAAAT 1680
TTTTGTGAAA AGTTTGTGCA ATGTAGTTCA GAGTGTCAA ACCGCTTCC GGGATGCCGC 1740
TGCAAAACAC AGTGACACAC CAAGCAGTGC CCGTGCTACC TGGCTGTCCG AGAGTGTGAC 1800
CCTGACCTCT GTCTTACTTG TGGAGCCGCT GACCATGGG ACAGTAAAAA TGTGTCTGTC 1860
AAGAACTGCA GTATTACAGC GGGCTCAAAA AGSCATCTAT TGCTGGCACC ATCTGACGTC 1920
GCAGGCTGGG GGATTTTAT CAAAGATCCT GTGCAGAAAA ATGAATTCAT CTCAGAATAC 1980
TGTGGAGAGA TTATTCTCA AGATGAAGCT GACAGAAGAG GGAAGTGTGA TGATAAATAC 2040
ATGTGCAGCT TTCGTTCAA CTGGAACAT GATTTGTGG TGGATGCAAC CCGCAAGGCT 2100
AACAAAATTC GTTTTGCAAA TCATTGGTA AATCCAACT GCTATGCAAA AGTTATGATG 2160
GTTAACGGTG ATCAGAGGAT AGGTATTTT GCCAAGAGAG CCTCCAGAC TGGCGAAGAG 2220
CTGTTTGTG ATTACAGATA CAGCCAGGCT GATGCCCTGA AGTATGTGG CATCGAAGA 2280
GAATGGGAA TCCCTTGACA TCTGCTACT CTTCCCTCTC CTCGAAACA GCTGCTTAG 2340
CTTCAGGAAC CTCAGTACT GTGGGCAAT TAGAAAAAGA ACATGCACTT TGAATTTCTG 2400
AATTTGCAAA GTACTGTAG AATAATTTAT AGTAATGAGT TTAATAATCA ACTTTTATT 2460
GCTTCTCAC CAGCTGCAAA GTGTTTGTGA CCAATGAAT TTTGCAATAA TGCAGTATGG 2520
TACATTTTTC AACTTTGAAT AAAGAATACT TGAATTTGAA AAAAAAATAA AAAAAA

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Seq ID NO: B76 Protein sequence
Protein Accession #: NP_004447

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80      1      11      21      31      41      51
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KQRIQPVHII LTVSSSLRGT RECSVTSDDL FPIQVIPLNT LNAVASVPIM YSWSPQQNPF 120
MVDEETVLHN IPYMGDEVLQ QDGTFLLELI KNYDGKVBGD RECGFINDEI FVELVNALGQ 180
YNDDDDDDDG DDFEERBEKQ KMLEDRRDDK ESRPERKFTS EKILEAISM FPDKGTAEL 240
KEKYKELTEQ QLPALPPEC TPNIDGNPAK SVORBSLSHS FTLEFCRRCP KYDCFLHPFH 300
ATPNTYKRWK TETALDNKPC GPQCYQHLEG AKEFAAALTA BRITPPRRP GRRRRGRLEN 360

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NSSRPSTPTI NVLESKDTDS DREAGTETGG ENNDKEEEEEK KDETSSSSSEA NSRCQTPFKM 420
 KPNIEPPENV EWSGAESMF RVLISTYYDN FCAIARLIGT KTCRQVYEPR VKESSIIAPA 480
 PAEDVDTPPR KKKRKHRLWA AHCRIQLKK DGSSNHVYNY QPCDEPRQPC DSSCPCVIAQ 540
 NPKCKPQCS SECQNRFFGC RCKAQCNTRQ CPCYLAUREC DPDLCLTCGA ADHWDKKNVS 600
 CKNCISIQRS KKHLLAPSD VAGWGFIFKD PVQKNEFISE YCGEIIISQDE ADRRGKVYDK 660
 YMCSEFLNLM NDFVVDATRK GNKIRFANHS VNPNCYAKVM MVNGDHRIGI FAKRAIQTGE 720
 BLFVYRYYSQ ADALKYVGIE REMEIP

Seq ID NO: B77 DNA sequence
 Nucleic Acid Accession #: NM_007015
 Coding sequence: 1..1005

1 11 21 31 41 51
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 15 ATBACAGAGA ACTCOGACAA AGITCCCATT GCCCTGGTGG GACCTGATGA CGTGGGAATTC 60
 TGCAGCCCCC CGGCGTACGC TACCTGACG GTGAAGCCCT CCAGCCCCGC GCGGCTGCTC 120
 AAGGTGGGAG CCGTGGTCCT CATTCGGGA GCTGTGCTGC TGCTCTTTGG GGCCATCGGG 180
 GCCTTCTACT TCTGGAAGGG GAGCGACAGT CACATTTACA ATGTCCATTA CACCATGAGT 240
 ATCAATGGGA AACTACAAGA TGGGTCAATG GAAATAGACG CTGGGAACAA CTTGGAGACC 300
 20 TTTAAATGG GAATGTGAGC TGAAGAAGCA ATTGCAGTTA ATGATTTCCA GAATGGCATC 360
 ACAGGAATTC GTTTTGTCTG AGGAGAGAAG TGCTACATTA AAGCGCAAGT GAAGGCTCGT 420
 ATTCTGAGG TGGGCGCCGT GACCAACAG AGCATCTCCT CCAACTTGA AGGCAAGATC 480
 ATGCCAGTCA AATATGAAGA AATTTCTCTT ATCTGGGTGG CTGTAGATCA GCCTGTGAAG 540
 GACAACAGCT TCTTGAGTTC TAAGGTGTTA GAACCTCTGC GTGACCTTCC TATTTTCTGG 600
 25 CTTAAACCAA CCTATCCAAA AGAAATCCAG AGGGRAAGAA GAGAAGTGGT AAGAAAAATT 660
 GTTCCAACTA CCAACAAAGG ACCACACAGT GGACCCAGGA GCACCCAGG CGCTGGAGAA 720
 CTGAATAATG AAACCAAGCC CAGTGTTCRA GAGGACACAC AAGCCTTCAA TCCTGATAAT 780
 CCTATCATC AGCAGGAAGG GGAAGCATG ACATTGCAAC CTAGACTGGA TCACGAAGGA 840
 ATCTGTTGTA TAGAATGAG GCGGAGCTAC ACCCACTGCC AGAAGATCTG TGAACCCCTG 900
 30 GGGGCTATT ACCCATGACC TTATAATTAT CAAGGCTGCC GTTCGGCTCG CAGAGTCATC 960
 ATGCCATGTA GCTGGTGGGT GGCCGCTATC TTGGGCTATG TGTGAAATCA CTTTATATAT 1020
 CACGTGCTGT AAATAATGAA CTAGCTGAAG AGACACCAA AGAAGCATT AGGCAGGTG 1080
 ATGCTGATGG GACCATATAA TATTTTACA CGCAGCCTGA GCGGTTATTC TTGACACTCT 1140
 35 TAACAGAATT TTTTAAATCG TTTTCCAGAA CTTTATATTA TGCAAATCCA CTGAAAGCGT 1200
 AGTTCAAGTC TAAATATGCA TAACCCCGTT ATTGTGTTAT TTTTATTTGC ATTGATTGTC 1260
 CATAAGTCTT CCCTTGCTTG CATCTTCCA AGCTATTTG AAATAAACAC GAAATTTTAC 1320
 AGTTTGCC

Seq ID NO: B78 Protein sequence
 Protein Accession #: NP_008946

1 11 21 31 41 51
 | | | | |
 45 MTENSDKVP I ALVGPDDVEF CSPPAYATLT VKPSSPARLL KVGAVVLISS AVILLFGAIG 60
 AFYFWKGSDB HTYNVHYTMS INKGLQDGSB BIDAGNNLET FPMGSGABEA IAVNDPQNGI 120
 TGRFAGGEEK CYIKAQVKAR IPEVGAVTKQ SISSKLEBKI MEVKYEENSL IWVAVDQPVK 180
 DNGFLSSKVL ELCSLDLPYF LKPTYPKEIQ RERREVRVKI VPTTTRKPHS GPRSNPQAGR 240
 50 IANNETREPSVQ EDSQAFNFDN FYHQQEGESM TPDFRLDHEG ICCIECRRSY THCQKICEPL 300
 GGYYPWPYNY QGCRSACRVI MPCSNWVARI LGMV

Seq ID NO: B79 DNA sequence
 Nucleic Acid Accession #: NM_012449.1
 Coding sequence: 66..1085

1 11 21 31 41 51
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 55 CCGAGACTCA CGGTCAAGCT AAGGCGAAGA GTGGGTGGCT GAAGCCATAC TATTTTATAG 60
 AATTAAATGGA AAGCAGAAAA GACATCACAA ACCAAGAAGA ACTTTGGAAA ATGAAGCCTA 120
 60 GGAGAAATTT AGAAGAAGAC GATTATTTCG ATAAAGACAC GGGAGAGACC AGCATGCTAA 180
 AAGAGACCTGT GCTTTTGCAT TTGCACCAA CAGCCCATGC TGATGAATTT GACTGCCCTT 240
 CAGAACTTCA GCACACACAG GAACCTTTTC CACAGTGGCA CTTGCCAAAT AAAATAGCTG 300
 CTATTATAGC ATCTCTGACT TTCTTTTACA CTCTCTGAG GGAAGTAATT CACCCTTAG 360
 CAACCTTCCA TCAACATAT TTTTATAAAA TTCCAATCCT GGTCATCAAC AAAGTCTTGC 420
 65 CAATGGTTC CAATCACTTC TTGCAATGG TTTACCTGCC AGGTGTGATA GCAGCAATG 480
 TCCAACCTTA TAATGGAACC AAGTATAAGA AGTTTCCACA TTGGTTGGAT AAGTGGATGT 540
 TAACAAGAAA GCAGTTTGGG CTCTCAGTT TCTTTTATGC TGACTGCAT GCATTTTATA 600
 GTCTGTCTTA CCCAATGAGG CGATCCTACA GATACAAGTT GCTAAACTGG GCATATCAAC 660
 AGGTCCACAA AAATAAGAA GATGCCCTGA TTGAGCATGA TGTTTGGAGA ATGGAGATTT 720
 70 ATGTGTCTCT GGGAAATGTG GGAATGGCAA TACTGGCTCT GTTGGCTGTG ACATCTATTC 780
 CATCTGTGAG TGACTCTTTG ACATGGAGAG AATTTCACTA TATTCAGAGC AAGCTAGGAA 840
 TTGTTTCCCT TCTACTGGGC ACAATACACG CATTGATTTT TGCCCTGGAT AAGTGGATAG 900
 ATATAAACA ATTGTATGG TATACACCTC CAACITTTAT GATAGCTGTT TTCCTTCCAA 960
 TTGTGTCTCT GATATTAAAA AGCATACTAT TCCTGCCATG CTTGAGGAG AAGTACTGTA 1020
 75 AGATTAGACA TGGTTGGGAA GACGTACCA AAATTAACAA AACTGAGATA TGTTCCTGAT 1080
 TGTAGAATTA CTGTTTACAC ACATTTTGT TCAATATTGA TATATTTTAT CACCAACATT 1140
 TCAAGTTTGT ATTGTGTAAT AAAATGATTA TTCAGGAAA AAAAAAAAAA AAAAA

Seq ID NO: B80 Protein sequence
 Protein Accession #: NP_036581.1

1 11 21 31 41 51
 | | | | |
 80 MRSRKDITNQ EELWQMKPRR NLEEDDYLRK DTGETSMLKR FVLLHLHQTA HADEFDQPSB 60
 LQHTQELFFQ NMLPIKIAAI IASLTFLYTL LREVIHPLAT SHQQYFKKIP ILVINKVLPM 120

VSITLLALVY LPGVIAAIVQ LHNQTKYKCF PHWLKRWMLT RKQFGLLSFF FAVLHAIYSL 180
 SYPMRRSYRY KILNWAYQQV QONKEDAMIE HDVVRMEIYV SLGIVGLAIL ALLAVTSIPS 240
 VSDSLWREF HYIQSKLQIV SLILGTIHAL IFAWNKWIDI KQFVWYTPPT FMLAVFLPTV 300
 VLIFKSILFL PCLRRKILKI RHGNEDEVTKI NKTEICSQL

Seq ID NO: B81 DNA sequence
 Nucleic Acid Accession #: NM_000684
 Coding sequence: 87..1520

10 1 11 21 31 41 51
 TGCTACCCCG GCGCGGGCTT CTGGGGTGTG CCCCAACCAC GGCCACGCC TGCCACACCC 60
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 AGCCCGGTAA CTTGTCTGCG GCGGCACCGC TCCCGGACCG GCGGCGCACC GCGGCGCGGC 180
 TGCTGGTGCC GCGCTGCGCG CCGGCTCGGT TGTGCTCTCC CGCCAGCGAA AGCCCCGAGC 240
 CGCTGTCTCA GCAGTGGACA GCGGCGATGG GTCTGTGTAT GCGGCTCATC GTGCTGCTCA 300
 TCGTGGCGGG CAATGTCTGG GTGATCGTGG CCATCGCCAA GACGCGCGGG CTGCAGAGCG 360
 TCACCAACCT CTCATCARG TCCCTGGCCA GCGCGACCT GTCATGGGG CTGCTGGTGG 420
 TGCGGTTTGG GCGCAACATC GTGGTGTGGG GCGGCTGGGA GTACGGCTCC TTCTTCTGG 480
 AGCTGTGGAC CTCAGTGGAC GTGCTGTGCG TGACGGGACG CATCGAGACC CTGTGTGTCA 540
 TTGCGCTGGA CCGCTACCTC GCGCATCACT CGCCCTTCGG CTACCGAGAG CTGCTGAGCG 600
 GCGGCGCGGG GCGGCGGCTC GTGTGACCGG TGTGGGCCAT CTCGCGCTGG GTGTCTCTCC 660
 TGCCCATCTT CATGCACTGG TGGCGGGCGG AGAGCGACGA GCGCGCGCGC TGCTACAAGG 720
 ACCCCAGTGG CTGCGACTTC GTCAACCAAC GGGGCTACGC CATCGCTCTG TCCGTAGTCT 780
 CCTTCTACGT CTCAGTGGAC ATCATGGGCT TCGTGTACCT GCGGGTGTTC GCGAGGCGCC 840
 AGAAGCAGGT GAAGAAGATC GACAGCTGGG AGCGCGCTTT CCTCGCGCGC CCAGCGCGGC 900
 CGGCTCGCGC CTGCGCTCGC CCGGTCCCGG GCGCGCGCGC GCGCGCGCGA CCGCGCGCGC 960
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 CGCGCGCTGT GCGCGCTACG GAGCAGAAAG CGCTCAAGAC GCTGGGCATC ATCATGGCG 1080
 TCTTCAAGCT CTGCTGGCTG CCTTCTTCC TGCGCAACGT GGTGAAGGCC TTCCACCGCG 1140
 AGCTGGTGCC CAGCGCGCTC TTCTGTCTCT TCACTGGCT GGGCTACGCC AACTCGGCT 1200
 TCAACCCCAT CATCTACTGC CCGAGCCCGG ACTTCGCAA GGCCTTCCAG GGACTGCTCT 1260
 GCTGCGCGCG CAGGCGCTGC GCGCGCGCGC AGCGACCTCA GCGAGACCGG CCGCGCGCTT 1320
 CGGGCTGTCT GCGCGCGCGC GAGCCCGCGC CATCGCGCGG GCGCGCGCTG GAGCGCGAGC 1380
 ACGACGATGT CBTGCGGGCC ACGCGCGCGC GCGCGCTGCT GGAGCCCTGG GCGCGCTGCA 1440
 ACGCGCGGGC GCGCGCGGAC AGCGACTCGA GCTTGAGCGA GCGGTGCGCG CCGCGCTTCC 1500
 CTTGGAATC CAGGTGTAG GCGCGCGCGC GCGCGCGCGA CTCGCGCGAC GGCCTTCCAG 1560
 GCGAACGAGG AGATCTGTGT TTAATTAGAA CCGATAGCAG GTGAATCTGA AGCCCAAT 1620
 CTTGCTGTA ATCATCGAG GCAAGAGAA AAGCCAGGA CCGTTCGACA AAAAGGAAAG 1680
 TTTGGGAAGG GATGCGAGAG TGGCTTGTG TTT

Seq ID NO: B82 Protein sequence
 Protein Accession #: NP_000675.1

45 1 11 21 31 41 51
 MGAGVLVLGA SEPGNLSAA PLPDGAATAA RLIVPASPEA SLLPPASESP EPLSQQWTAG 60
 MELLMALIVL LIVAGNVLVI VAIKTPRLQ TLNLFIMS L ASADLVMLL VVPFGATIVV 120
 WGRWEYGSFF CELWTSVDVL CVTASISTLC VIALDRYLAI TSPFRYQSL TRARARGLVC 180
 TVWALISALVS PLPIIMBNWR AEDDEARECY NDEKCCDFVT NRAYAIASSV VSFYVPLCIM 240
 AFVYLVVFRE AQKQVKKIDS CERFLGPPA RPPSPSPSPV PAPAPPPGPP EPAAAAATAP 300
 LANRAGKRRL PRLVALREQL KALKTLGLIM GVFTLCWLPF FLANVVKAEH RELVDELFLV 360
 FFMNLGYANS AFNPITYCRS EDRKAFQGL LCCARAAAR RHATGDRFR ASGCLARPPG 420
 PPSPGAASOD DDDDVVGATP PARLLEPWAG CNGGAARDSD SLDDEPCRFQ PASESKV

Seq ID NO: B83 DNA sequence
 Nucleic Acid Accession #: NM_000729.2
 Coding sequence: 2..421

60 1 11 21 31 41 51
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 AGCCATGAAC AGCGGGGTGT GCGGTGCGGT GCTGATGGCG GTACTGGCGG CTGGGCGCCT 120
 GACGACGCGG GTGCTCTCCG CAGATCCCGC GGGCTCGGGG CTGCACCGGG CAGAGGAGGC 180
 GCGCGGTAGG CAGCTGAGGG TATCGCAGAG AACGGATGGC GAGTCCCGAG CGCACCTGGG 240
 CGCCCTGCTG GCAAGATACA TCCAGCAGGC CCGGAAAGCT CCTTCTGGAC GAATGTCCAT 300
 CGPTAAGAAC CTGCAGAAAC TGGACCCGAG CCACAGGATA AGTGACCGGG ACTACATGGG 360
 CTGGATGGAT TTGGGCGGTC GCGATGCCGA GGAGTATGAG TACCCCTCCT AGAGGACCCA 420
 GCGGCCATCA GCGCAACCGA AGCAACCTCC CAACCCAGAG GAGGCAGAAAT AAGACAACAA 480
 TCACACTCAT AACTCATTTG CTGTGAGATT TGACATTGAA TGTATCTATT TATTAGTTTC 540
 TCAATGTGAA AATGTGTCT GTAGATTGT OCACTGCAAC CACACACGCT CACCAGAGT 600
 TGTGCAACT GAAGACAAA CTGTTTCTT CATCTGTGAC TCCTGTTCTG AAAATGTTGT 660
 TATGCTATTA AAGTGATTTC ATCTGCTC

Seq ID NO: B84 Protein sequence
 Protein Accession #: NP_000720.1

80 1 11 21 31 41 51
 MNSGVCLCVL MAVLAAGALT QVPPADPAG SGLQRAEAP RRQLRVSRQT DGESRAHLGA 60
 ELARYIQAR KAPSGRMSIV KNLQNLDPSE RISDRDYNGW MDFRRSARE YEYPS

TABLE 74 Gene Sequences Up- or Down-Regulated in Cancer

Angiogenesis

5

A1 DNA SEQUENCE

Gene name:endothelial differentiation, sphingolipid G-protein-coupled receptor, 1

Unigene number:Hs.154210

Probeset Accession #:M31210

Nucleic Acid Accession #:M31210

Coding sequence:251-1396

10

TCTAAAGGTCGGGGCAGCAGCAAGATGCGAAGCGAGCCGTACAGATCCC

GGGCTCTCCG

60

AACGCAACTTCGCCCTGCTTGAGCGAGGCTGCGGTTTCCGAGGCCCTCTC

CAGCCCAAGGA

120

AAAGCTACACAAAAGCCTGGATCACTCATCGAACCACCCCTGAAGCCAG

TGAAGGCTCT

180

CTCGCTCGGCTCTCTAGCGTTCTGCTGGAGTAGCGCCACCCGGGCTTCT

GGGGACACAG

240

GTTTGGCACCATGGGGGCCCAACAGGTCCTCGTGGTCAAGGCCCAACGCA

GCTCGGTCTC

300

TGACTACGTCAACTATGATATCATGTCGCGCATTTACAAC

TACACGGGAAAGCTGAATAT

360

CAGCGCGGACAAAGGAGAACGCAATTAAACTGACCTCGGTGTGTTTCATTC

TCATCTGCTG

420

CTTTATCATCTGGGAGAACATCTTTTGTCTTGCTGACCATTTGGAAAAACA

AGAAATTCCA

480

CCGACCCATGTACTATTTTATTTGGCAATCTGGCCCTCTCA

GACCTGTTCG

540

CTACACAGCTAACCTGCTCTTGTCTGGGCGCACCACCTAC

AAGCTCACTC

600

GTTCCTGCGGGAAGGGAGGTA

TGTTTGTGGC

660

CATCGCCATTGAGCGCTATA

TCACAATGCT

720

CTTCGCGCTCTTCCTGCTAA

TCAGCGCTG

780

GCCTATCATGGCTGGAAGTGCATCACTGC

GCTGTCCAGC

840

CTACCAAGAGCACTATATCTCTCTGTCACACGCTCTC

ACTCTGCTTC

900

CGTCACTCTGTACTGTCAGAA

TCTACTCCTT

960

CCGCAAGAACATTTCCAAGG

CCAGCGCGAG

1020

AATTATGCTCTGAGCGCTCT

TCATCGCTG

1080

GGATGTGGGCTGCAAGGTGA

AGACCTGTGA

1140

GTTAGCTGTGCTCAACTCCG

GCAACCAACCC

1200

GCCTGCGGCGTTTACTCGGA

TCATGTCTCG

1260

CAAAATTCAGCGACCCATCA

TGCGCGCAT

1320

CTCCACCGCC

CAGAAAGAC

1380

CAACTCTCTCTCTCTAGAACT

GGAGCTGTG

1440

CTGGCCACCC

CAGTGTCTTG

1500

GCTGCAAGCC

AGAGGGAGGA

1560

TGGGTAGAGT

TAGTTCTCTGT

1620

GGAAATATATATTTCAACCC

CTGGAGCTTT

1680

GTCAAGCTCC

TAAAGGTTTC

1740

CGTCTCTCTTG

TCTGAGCTT

1800

GAGTGTGTG

ACTTCTGCTT

1860

TCCTCTCATA

CCCTCTCTCA

1920

AGAGCTGGGG

TTGTGGAATG

1980

GCTGTGGGAA

GATGAAGATG

2040

TTTCATGTA

AGCGGATCC

2100

AAAACATCTTTCAATGAAA

TGTGTTACCA

2160

AAGGAAGCCC

ACTTATCTTA

2220

GACAAGCAAA

ACAAAGTGA

2280

TAGCAATGTA

GTCTAACAAA

2340

AGAACTCTGTGTGATTCATT

TCAAGCAACA

2400

TTTTCTTGAT

TTTTGATGT

2460

CGGTGTTAAC

TTTTCTAGAA

2520

GGAAAGCCAG

AACTTTTAAG

2580

TATTACAAG

AATAAAATA

2640

CGAGAGATGT

CTTGTTTTTT

2700

TCATTTTGCA

CATAGCTTTA

TCACCTTTTA

AACATTAATA

AACTGATTTT

TTTAAAG

60

A1 Protein sequence:

Gene name:endothelial differentiation, sphingolipid G-protein-coupled receptor, 1

Unigene number:Hs.154210

Probeset Accession #:M31210

Protein Accession #:AAA52336

Signal sequence:none found

Transmembrane domains:50-71, 92-110, 122-140, 160-177, 202-222, 251-269, 283-301

Cellular Localization:plasma membrane

70

1121314151

MEPTSVPLVKARRSSVSDYVNYDIIVRHYN

YTGKLNISAD

KENSIKLTSV

VFILICCFII

60

LENIFVLTLIWKTKKFRHFM

YFIGNLALS

DLLAGVATTA

NLLSGATTY

KLTPAQWFLR

120

EGSMFVALSA

SVFSLALAI

ERYITMLRMK

LHNGSNFRL

PLLISACNVI

SLILGGLPIM

180

GNICISALSS

CSTVLPVYHK

HVILFCTTVF

TLLLLSIVIL

YCRISLVRT

RSRLTFRKN

240

ISKASRSSEN

VALLKTVIIV

LSVPLACWAP

LPILLLLDVG

CKVKTCDILF

RAEYFLVLAV

300

LNSGTNPFIY

TLTNKEMRRA

FIRIMSCKCK

PSGDSAGKFK

RPIIAGMBFS

RSKSDNSSHP

360

QKDEGDNPET

IMSSGNVNSG

S

80

A3 DNA SEQUENCE

Gene name:G protein-coupled receptor 51

Unigene number:Hs.198612

Probeset Accession #:AA452928

Nucleic Acid Accession #:NM_004624.1

A5 DNA SEQUENCE

Gene name:

ESTe

Unigene number:

Hs.293616

Probeset Accession #:

AW043782

Nucleic Acid Accession #:

none found

Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

10 1 11 21 31 41 51
 AGCAACGACG CGGCGCAGCG GGAGCGGCGG COGCGCCATG TGGCTGCTGG GCGCGCTGTG 60
 CCTGCTGCTG AGCAGCGCGG CGGAGAGCCA GCTGCTCCCG GGGAACTACT TCACCAATGA 120
 GTGCAACATA CCAGGCAACT TCATGTGCAG CAATGGACGG TGCATCCCGG GCGCTGGCA 180
 GTGTGACGGG CTGCTGACT GCTTCGACAA GAGTGATGAG AAGGAGTGCC CCAAGGCTAA 240
 15 GTCGAAATGT GCGCCAACTT TCTTCCCTCG TGCCAGCGGC ATCCATTGCA TCATTGGTGG 300
 CTTCCGGTGC AATGGGTTTG AGGACTGTCT CGATGGCAGC GATGAAGAGA ACTGCACAGC 360
 AAACCCCTCG CTTTGTCTCA CGGCCCGCTA CCACTGCAAG AACCGGCTCT GTATTGACAA 420
 GAGCTTCATC TGGATGGAC AGAATAACTG TCAAGACAAC AGTGATGAGG AAAGCTGTGA 480
 AAGTTCTCAA GAACCCGGCA GTGGGCAAGT GTTTGTGACT TCAGAGAAC ACCTTGTGTA 540
 20 TTACCCGAGC ATCACCCTATG CCATCATCGG CAGCTCCGTC ATTTTGTGTC TGGTGGTGGC 600
 CCTGCTGGCA CTGCTCTTGC ACCACCAGCG GAAGCGGAAC AACCTCATGA CGCTGCCCGT 660
 GCACCGGCTG CAGCAGCGTG TGTCTGTCTC CGGCTGGTGG GTCCCTGGAC ACCCCACCA 720
 CTGCAACGCT ACCTACAACG TCAATAATGG CATCCAGTAT GTGGCCAGCC AGGCGGAGCA 780
 GAATGCGTGG GAGTAGGCT CCCCACCTCT CTACTCGAG GCTTGTCTGG ACCAGAGGCC 840
 25 TGGTGGTAT GACCTTCTCT CACCGCCTTA CTCTCTGAC ACGGAATCTC TGAACCAAGC 900
 CGACCTGGCC CCTTACCGCT CCGGCTCCGG GAGTGCCAC AGTGCCAGCT CCCAGGACG 960
 CAGCAGCGCT CTGAGCGTGG AAGACACCGG CCACAGCCCG GGGCAGCTCG GCCCCAGGA 1020
 GGGCACTGCT GAGCCGAGGG ACTCTGAGCC CAGCCAGGGC ACTGAAGAAG TATAAGTCCC 1080
 AGTTATTTCA AAGTCCATAT GGGTTAATCT GCTCTGACTT GTTGCCATTG TAACAATTG 1140
 30 TGCTCATGGG AAGCTCTTTA AGCACCCTGA AGGATGCTCT AAGTTACAGT TTGGGATATT 1200
 AACTATCTCT GCATTCCTCT CTTCCGCCAG ACTTCAGAGA TGTTTTCTG GCGTCTCAGT 1260
 TGACATGATC TGTGTGCGT CTTTCTGTCT AGGTCACTCT TCCCTGGGA CCGAGATCA 1320
 CACCTCTATT TTTACATTA TTTCTGTCT GTTGGAGAGA CAGCATATAA AACAGTATTG 1380
 35 AAATAGCGTG GGAGTAGGCA ATGTTTCTGT GCTATATTGG ATGCTCAGAA GTGCAGGAGA 1440
 CGCTGGACCC AATCTCTCT GCTGGGTAGT TACCTTATAG CATTGGGGA TTTGGGTAG 1500
 ATGATCTAAC CAGGAGGCCA TCACCTGGATG GTCAACCCCG CAAAAAATT CCATTGAGC 1560
 ATCAAAAGCT GCTTGTGACA ATCCTATTGG ATGCCCCAG TTCAGCAGAG TCAGTGGCCA 1620
 AAGAAACTT TGGACGTGAG TAACACCTTT CAGCAGTGGC AAGCTTATT TGGTTTGTG 1680
 40 AAGGACTCTG AAACCATCTA CCTGTATATA ATTCTGGCTT TAGAAATTG CCCAAGATG 1740
 CTCATTCTGA GAGCTTCTCT CAGCAGCATA TATCATCAGC CTCATCTCTA AATAGGCAGG 1800
 GAGCCCTTCC CATGATTTTA TCCAAGTTCT CAGCTCCTAA AATGCAGGCT GCGAAGACCC 1860
 TACACCTGCT CAGCTCTTAC AGCCACTTAC CTGGTTCTG GACTGTCACT CTCOCAGCTG 1920
 ACCTGCTGCT AGCCAGGAA TGGAGACCTA ACTTGAGTGG GCCCAAGTGC TGACCTGGCT 1980
 45 GTATGTCCT CTGGCCACA CCGAGCCTGT CTGCTCAT CTATGAGCCT CAACACTGGC 2040
 CTCCAAAGTT CCCCTAACAC TTGCAAAATC CTTTCTAAGT GTGCATTGG ACTTGAGGAC 2100
 ACTGTTTCT ATCAGAGTGT AGAGCCATGT TCAATACCTC CAGCAGCTCT TCTTGGCTCC 2160
 CTGACCTGTC CACCTCTCTG TTCCCAAGGT CCCAATACCA GCACCTCTAG TTAGAGTTAG 2220
 GGTGAGGTC AGGCTCTTCC CAACATCCCA GTAGTTCTC CTCTGAGACA CATGGGCAAG 2280
 50 AGCAATTTG GATCAAGAT TTTCCATTG GATCTATTG AAATCTTTA GAAATGCATT 2340
 TGAACAGTG TGTGTGTTT TTCCCTCTA GTTAAGGGAC TATTATATG TGTATAGGAA 2400
 AGCTGTCTCT TTTTGTGTT TTCTTTTAA AGGTCCAAA GAAAGATGA AAAGGAGATC 2460
 ACACCTCTG CCGCTCTGAG CCGTGATAA CAGTCACTC CAGACTAAC TGTGTGCCAG 2520
 ACATTGTGTC ATTGTGACG TTTGAGGTTA TTATTATCA AGTCTTGAA GGAAGCAGAA 2580
 55 AGAGGAGCTC CTCTCTCCT CGTGTATAG TCTCTATGT TGTGCTAGT TTTCTTTT 2640
 TTCTCTGTG CCAGTCAGCC ACGGGGCCG CCTCCCTGCA GGAATAAGG GTAAAAGCTT 2700
 AGGTGTGTT TGGCAAGAAA CCACACTGAC TGATGAGGGG TAAATGGAA CCAGGTAGAG 2760
 CCACCTCGGG CAGCTGTGAC CCATTGAGG CTTCTTCCG CAGCTGAAGA AATGTTCAAG 2820
 AACCTGTTG ACGCTAATTA AAACAGAGCC TGCAGGAAGT GGGGCTAAG TGGCATTGAG 2880
 60 TGATCTGCT CTGTAGACTT TCTTCTCTT TTTTAACCA ATCCAAAGG TGTACAGAA 2940
 AAGCTAGCCA CTGCTATTG GTTTTGTGTA AAAAAAAGA GAAAGAAAG AAGAAAGAAA 3000
 AACGGAAGG AACCTAGCTG CCTGTATCTT TCATTTTAA AATAGCACTT GAGTTATTTT 3060
 CTGAGTAAT CAATAAAGAA CTTTGTATGA CAGCCAGAA GTGTTAGAAC TCTGGCTGAA 3120
 CATTTTCATCT CCGTGTAGTC AGAAGGGCTT TATTTCTCCC TTGATGGGG CCCCTCTCTC 3180
 65 TTTCTGCTG CTGTGAAGTT GTTTAGAGGA AAGAACTCTA ATTTAATTA ATTGCGCAGT 3240
 GAGTTAATCT CACTGCTTT TCTGCTTCCA GGCATCTTAG GAAAAAAGA TGGTTTGTG 3300
 AGATAAGGGA TGCTTACTAA TGCTTTTTA AAACARACAG GGACATTTT ATTATAGATT 3360
 TGATTTTCTT AATGAATGTT TTTAAATAA TATAATAGG ACACCAAGC GCGAGGTTT 3420
 70 TTTTGGGGG GAGGGGGTT GTTTTCCAA TCAAGATGGC ACATTAGTGG CCAGCAATAT 3480
 TTTTAACTC ATTCCAACCA GGAAGCTTTT TTATACATT CCTAATCTA CCGCAACCA 3540
 ABAATAGTCT CATCTCTTT TTTCTCAAT GAGATCGTG TTTTATTTA GCATTAAAT 3600
 AGTTACACTG TGATGACTGG CCTATTACCT GACTCAGCTC CCTTACCTT GAAATGACA 3660
 TTTTAAAAA ATGCAACTAA GTGGTTAATA GTGTGTGAGC CTCAGGTTA ATGTAACTG 3720
 GAAAGGTTG GTGTGCTGTC TTTTGTGTT TTGGTGGGC TGGGTTTGT TTTTAAATT 3780
 75 TTATCTTTC TAATAAATT GCAGTTTCT TCTTCTGTT TGTGCAAAAG GWMCTAMARM 3840
 AAMMAAAAC AWYWTGGGG GGGCTTGGGC CTCGAAAAA GTTTTAAACA CCATTTCGG 3900
 TGGGGCGGG GGGCCACAGT AGGTACGGG ACCACGGGG CCACAAAGG ACCCCAGAG 3960
 GAAACCTGG CCAAGAAAAA GGTGCGAGA ATTCTCCACA CCAGAAAAA ACGCGCCGG 4020
 80 GGAACCGCA GAGTPTTGG TAAACCAAC CCGAAGAGAG AACTCAGAAG CACACAAGCG 4080
 GGACTCAACC AGGAGGACCC AAGGGAACCC GATAGAGTAC G

A6 Protein sequence:

Gene name:

ESTe

Unigene number: Hs.293616
 Probeset Accession #: AN043782
 Protein Accession #: none found
 Signal sequence: 1-17
 Transmembrane domains: 169-191
 LDLa domains: 28-66, 70-108, 112-149
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 MLLLGPICLL LSSAAESQLL PGNNFTNECN IPGNFMCENG RCIPGAWQCD GLEDCFDKSD 60
 EKECPKAKSK CGPTFPFCAS GIHCIIGRFR CNGFEDCPDG SDEENCTANP LLCSTARYHC 120
 KNGLCIDKSF ICDGQNNQD NSDEESCESS QEPOSGQVVF TSENQLVYYP SITYALIGSS 180
 VIFVLVVALL ALVLHHQRKR NNLMTLFPVR LQHPVLLSRL VULDEPHRCN VTYNVNNGIQ 240
 YVASQAQNA SFVGSPPSYS EALLDQRFAP YDLPPPPYS DTESLNQADL PPRSRSGSA 300
 NSASSQAASS LLSVEDTSHS FGQFGPQEGT ABERDSEPSQ GTEEV

A7 DNA SEQUENCE

Gene name: Integrin, alpha 5 (fibronectin receptor, alpha polypeptide)

Unigene number: Hs.149609
 Probeset Accession #: X06256
 Nucleic Acid Accession #: NM_002205
 Coding sequence: 1-3150 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 ATGGGGAGCC GGAGGCCAGA GTCCCTCTTC CACGCCGTGC AGCTGCGCTG GGGCCCCGGG 60
 CGCCGACCCC CGCTSSSTGCC GCTGCTGTTG CTGCTSSSTGC CGCCGCCACC CAGGGTCGGG 120
 GGCITCAACT TAGACGGGGA GGGCCAGCA GTACTCTCGG GGGCCCCGGG CTCCTTCTTC 180
 GGATTCTCAG TGGAGTTTTA CGGCCGGGA ACAGACGGGG TCAGTGTGCT GGTGGGAGCA 240
 CCGAAGGCTA ATACCAAGCA GCCAGAGTG CTGCAGGGTG GTGCTGTCTA CCTCTGTCTT 300
 TGGGGTGCCA GCGCCACACA GTGCACCCCC ATTGAATTTC ACAGCAAGG CTCCTCGGCTC 360
 CTGGAATCCT CACTGTCCAG CTCAGAGGGA GAGGAGCGTG TGGAGTACAA GTCCITGTCAG 420
 TGGTTCGGGG CAACAGTTGG AGCCCATGGC TCCTCCATCT TGGCATGCGC TCACCTGTAC 480
 AGCTGCGGCA CAGGAAGGA GCCACTGAGC GACCCCGTGG GCACCTGTCT CCTCTCCACA 540
 GATAACTTCA CCGGAATTCG GAGTATGCA CCTGCGCGCT CAGATTTCAG CTGGGCAGCA 600
 GGACAGGGTT ACTGCCAAGG AGGCTTCAGT GCGGAGTTCA CCAAGACTGG CCGTGTGGTT 660
 TTAGGTGGAC CAGGAAGCTA TTTCTGGCAA GGCCAGATCC TGTCTGCCAC TCGGAGCAG 720
 ATTGCAGAA CTATTATCCC CGAGTACCTG ATCAACCTGG TTCTGGGACA GCTGCAGACT 780
 CGCCAGGGCA GTTCCATCTA TGATGACAGC TACCTAGGAT ACTCTGTGGC TGTGTGTGAA 840
 TTCACTGGTG ATGACACAGA AGACTTTGTT GCTGTGTGTC CCAAGGGGAA CCTCACTTAC 900
 GGCTATGTCA CCATCTTAA TGGCTCAGAC ATTCGATCCC TCTACAACTT CTCAGGGGAA 960
 CAGATGCGCT CTACTTTTGG CTATGCAATG GCGCCACAG AGCTCAATGG GAGCGGCTG 1020
 GATGACTTGC TGGTGGGGGC ACCCTGCTCT ATGGATCGGA CCCCTGACGG GGGGCTTCAG 1080
 GAGTGGGCA GAGACTAGT CTACCTGACG CACCCAGCGG GCATAGAGCC CAGGCCACCC 1140
 CTTACCTTCA CTGCCCATGA TGAGTTTGGC CGATTTGGCA GCTCCTTBAAC CCCCTTGGG 1200
 GACCTGGACC AGGATGGCTA CAATGATGTG GCCATCGGG CTCCCTTTGG TGGGAGACC 1260
 CAGCAGGAG TAGGTGTTGT ATTCTCTGGG GGCOCAGGAG GGCTGGGCTC TAAGCCTTCC 1320
 CAGGTTCTGC AGCCCCCTGG GGCAGCCAGC CACACCCAG ACTTCTTTGG CTCTGCCCTT 1380
 CGAGGAGGCC GAGACTGGA TGCAATGGA TATCTTGATC TGATTGTGGG GTCCCTTTGGT 1440
 GTGACAAAGC CTGTGSTAT CAGGGGCGCG CCCATCTGTT CCGCTAGTGC CTCCCTCACC 1500
 ATCTTCCCGG CATGTTCAA CCCAGAGGAG CGGAGCTGCA GCTTAGAGGG GAACCTGTG 1560
 GCGTGCATCA ACCCTAGCTT CTGCTTCAAT GCCTCTGAA AACACCTTGC TGACTCCATT 1620
 GGTTCACAG TGAACCTTCA GCTGGAGTGG CAGAGCAGA AGGGAGGGGT ACGGCGGGCA 1680
 CTGTTCTTGG CCTCCAGGCA GGCACCCCTG ACCCAGACCC TGCTCATCCA GAATGGGGCT 1740
 CGAGAGGATT CGAGAGAGAT GAAGATCTAC CTCAGGAACG AGTCAGAAAT TCGAGACAAA 1800
 CTCTGCGCGA TTCACATGCT TCTCAACTTC TCCTTGGACC CCGAGCTTCC AGTGGACAGC 1860
 CACGGCCCTCA GGCAGCCCTT ACATTATCAG AGCAAGAGCC GGTAGAGGA CAGGCTCAG 1920
 ATCTTGTGCG ACTGTGGAGA AGACAACATC TGTGTGCGTG ACCTGCAGCT GGAAGTGTTC 1980
 GGGGAGCAGA ACCATGTGTA CTTGGGTGAC AAGAATGCCC TGAACCTCAC TTTCATGCC 2040
 CAGAATGTGG GTAGGGGTGG CGCCTATGAG GCTGAGCTTC GGGTCACTCC CCTCCAGAG 2100
 GCTGAGTACT CAGGACTCGT CAGACACCCA GGAACCTTCT CCGGCTGAG CTGTGACTAC 2160
 TTTGCCGTGA ACCAGAGCGG CTGCTGGTG TGTGACCTGG GCAACCCCAT GAAGGAGGA 2220
 GCCAGTCTTG GGGTGGCCT TCGGTTTACA GTCCCTCATC TCCGGGACAC TAAGAAAACC 2280
 ATCCAGTTTG ACTCCAGAT CTTCAGCAGG AATCTCAACA ACTGCAAG CGACGTGTTT 2340
 TCCTTTGGCG TCTCGTGA GGTCTAGGCC CAGGTCAACC TGAACGTTGT CTCCAGCCT 2400
 GAGGCACTGC TATTCCAGT AAGCGACTGG CATCCCGAG ACCAGCTTCA GAAGGAGGAG 2460
 GACCTGGGAC CTGCTGTCCA CCAATGCTAT GAGCTCATCA ACCAAGGCC CAGCTCCATT 2520
 AGCCAGGGTG TGCTGGAAT CAGCTGTCCC CAGGCTCTGG AAGGTACAGC GCTCCTATAT 2580
 GTGACAGAG TTAAGGAGT CACTGCAACC ACCAATCACC CCATTAAACC AAAGGCGCTG 2640
 GAGTTGGATC CGAGGGTTC CTTGACACAC CAGCAAAAC GGGAGCTTCC AAGCCGCGAG 2700
 TCTGCTTCTT CCGGACCTCA GATCCTGAAA TGCCCGGAGG CTGAGTGTTC CAGGCTGCGC 2760
 TGTGAGCTCG GGCCTCTGCA CCAACAAGAG AGCCAAAGTC TGCACTTGCA TTTCGAGTC 2820
 TGGGCAAGA CTTCCTGCA GCGGAGCAC CAGCCATTTA GCTGCACTG TGAGGCTGTG 2880
 TACAAGCCC TGAAGATGC CTACCGAATC CTGCTCGGCG AGCTGCCCA AAAAGAGCTG 2940
 CAGGTGGCCA CAGCTGTGCA ATGACCAAG GCAGAGGCA GCTATGGCGT CCACTGTGG 3000
 ATCATCATCC TAGCCATCCT GTTTGGCTTC CTGCTCTAG GTCTACTCAT CTACATCTC 3060
 TACAAGCTG GATTCTTCAA ACGTCCCTC CCATATGGCA CGGCATGGA AAAAGCTCAG 3120
 CTCAGCCCTC CAGCCACCTC TGATGCCCTGA

A8 Protein sequence:

Gene name: Integrin, alpha 5 (fibronectin receptor, alpha polypeptide)
 Unigene number: Hs.149609
 Probeset Accession #: X06256
 Protein Accession #: NP_002196
 Signal sequence: 1-42
 Transmembrane domains: 998-1020
 Integrin alpha domains: 56-115, 268-318, 322-384, 388-444, 452-503, 1022-1036
 Cellular Localization: plasma membrane

	1	11	21	31	41	51	
15	MGSRTTPEPL	HAVQLRWGPR	RRPFLLPLLL	LLLPPPPRVG	GFNLDRAEAP	VLSGPPGSFF	60
	GFSEVFYRPG	TGVSFVLVGA	PKANTSQPGV	LQGGAVYLCP	WGASPTQCTP	IEFDSKGSRL	120
20	LESSLSSEEG	KEPVEYKSLQ	WFGATVRAHG	SSILACAPLY	SWRTEKEPLS	DPVGTCTYLS	180
	DNFTRILEYA	PCRSDFSWAA	GGYCCGGFS	AEFTKTGRVV	LGGPGSYFWQ	GQILSATQEQ	240
	IAESYYPEYL	INLVQQQLQT	RQASSTYDSD	YLGYSVAVGE	FSGDDTEDFV	AGVPEKMLTY	300
	GYVTILNGSD	IRSLYNFSGE	QMASYFGYAV	AATDVNGDGL	DDLVLGAPLL	MDRTPDGRPQ	360
	EVGRVYVYLG	HPAGIEPTPT	LTLTGEDEFG	RFGSSLTPLG	DLQDQGYNDV	AIGAPFGGET	420
25	QQGVVVFVPG	GGGGLGSKFS	QVLQPLWAAS	HTPDFFGSAL	RGGRLDNGG	YPLIVGSFG	480
	VDKAVVYRGR	PIVSASASLT	IFPAMFNPEE	RSCSLGNPNV	ACINLSPLCN	ASGKHVADSI	540
	GFTVELQLDH	QKQKGVRRRA	LFLASRQATL	TQTLLIQNGA	REDCREMKTY	LRNSESFRDK	600
	LSPIHIALNF	SIDPQAPVDS	HGLRPALHYQ	SKSRIEDKAQ	ILLDCGEDNI	CVPDLQLEVF	660
	GEQNHVYLG	KNALNLTIFA	QNVGEGGAYE	AELRVTAPEE	AEYSGLVRHP	GNFSSLSQDY	720
30	FAVQSRLLLV	COLGNEMKAS	ASLWGSRLRFT	VPHLRDTKKT	IQDFPQILSK	NLNNSSQSDVV	780
	SFRLSVEAQA	QVTLNGVSKP	EAVLEFVSDW	HPRDQPKKEE	DLSPAHEBVY	ELINQGPSSI	840
	SQGVLELSCP	QKQKGVRRRA	VTRVTGLNCT	TNEPINFKGL	ELDDEGSLEH	QKREAPSRSS	900
	SASSGPQILK	CPEAKCFRLR	CELGLHQQE	SQSLQLHFRV	WAKTFLQREH	QPFSLQCEAV	960
35	YKALKMPYRI	LPRQLPQKER	QVATAVQNTK	AECSYGVPLW	IIILAILFGL	LLGLLIYIL	1020
	YKLGPFKRSI	PYGTAMEKAQ	EKPPATSDA				

A9 DNA SEQUENCE

Gene name: Integrin, beta 1 (fibronectin receptor, beta, antigen CD29 includes MDF2, MSK12)
 Unigene number: Hs.287797
 Probeset Accession #: X07979
 Nucleic Acid Accession #: NM_002211.1
 Coding sequence: 1-2397 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
45	ATGAATTTC	AACCAATTTT	CTGGATTGGA	CTGATCAGTT	CAGTTTGCTG	TGTGTTTGCT	60
	CAAACGATG	AAAATAGATG	TTTAAAGCA	AATGCCAAT	CATGTGGAGA	ATGTATACAA	120
	GCAGGGCCAA	ATTGTGGGTG	GTGCACAAAT	TCAACATTTT	TACAGGAAGG	AATGCCTACT	180
50	TCCTGACGAT	GTGATGATTT	AGAAGCCTTA	AAAAAGAAGG	GTTCCTCTCC	AGATGACATA	240
	GAATATCCCA	GAGGCTCCAA	AGATATAAAG	AAAAATAAAA	ATGTAACCAA	CCGTAGCATA	300
	GGACACGACG	AGAACTCCAA	GCCAGAGGAT	ATTACTCAGA	TCCACCCACA	GCAGTTGGTT	360
	TTGCGATTAA	GATCAGGGGA	GCCACAGACA	TTTACATTAA	AATTCAGAG	AGCTGAAGAC	420
	TATCCCATTT	ACCTCTACTA	CCTTATGGAC	CTGTCTTACT	CAATGAAGA	CGATTGGAG	480
55	AATGTAAAAA	GTCTTGAAC	AGATCTGATG	AATGAAATGA	GGAGGATTAC	TTCCGACTTC	540
	AGAAATGGAT	TTGCTCTATT	TGTGGAAAAG	ACTGTGATGC	CTTACATTAG	CACAACACCA	600
	GCTAAGCTCA	GGAACTCTTG	CACAAGTGAA	CAGAACTGCA	CCAGCCCTTT	TAGCTACAAA	660
	AATGTGCTCA	GTCTTACTAA	TAAAGGAGAA	GTATTTAATG	AACCTGTGAG	AAAACAGGCG	720
	ATATCTGGAA	ATTTGGATTC	TCCAGAGGAT	GGTTTCGATG	CCATCATGCA	AGTTGCAGTT	780
60	TGTGGATCAC	TGATTGGCTG	GAGGAATGTT	ACACGGCTGC	TGGTGTTCCT	CACAGATGCC	840
	GGGTTTCACI	TTGCTGGAGA	TGGGAATCTT	GGTGGCATTG	TTTTACCAA	TGATGGACAA	900
	TGTCACCTGG	AAAAATAAT	GTACACAATG	AGCCATTATT	ATGATTATCC	TTCTATTGCT	960
	CACCTTGCTC	AGAACTGAG	TGAAATAAT	ATTCAGACAA	TTTTTGCACT	TACTGAAGAA	1020
	TTTCAGCCTG	TTTACAAGGA	GCTGAATAAC	TTGATCCCTA	AGTCAGCAGT	AGGAACATTA	1080
65	TCCTGCAAT	CTAGCAATGT	AATTCAGTTG	ATCATTGATG	CATACAAATC	CCCTTCTCTA	1140
	GAAGTCATTT	TGGAAAACGG	CAATTTGTCA	GAAGGAGTAA	CAATAAGTGA	CRAATCTTAC	1200
	TGCAAGAACG	GGGTGAATGG	AACAGGGGAA	AATGGAAGAA	AATGTTCCAA	TATTTCCATT	1260
	GGAGATGAGG	TTCAATTTGA	AATTAGCATA	ACTTCAATA	AGTGTCCAAA	AAAGGATTCT	1320
	GACAGCTTTA	AAATTAGGCC	TCTGGGCTTT	ACGAGGGAAG	TAGAGGTTAT	TCTTCTGATC	1380
70	ATCTGTGAT	GTGAATGCCA	AAGCGAAGGC	ATCCCTGAAA	GTCCCAAGTG	TCATGAAGGA	1440
	AATGGACAT	TTGAGTGTGG	CGCGTGCAGG	TGCAATGAAG	GGCGTGTGG	TAGACATTGT	1500
	GAATGCAGCA	CAGATGAAGT	TACAGTGAAA	GACATGGATG	CTTACTGCAG	GAAGAGAAAC	1560
	AGTTCAGAAA	TCTGCAGTAA	CAATGGAGAG	TGCGTCTGCG	GACAGTGTGT	TTGTAGGAAG	1620
	AGGGAATAAT	CAATGAATAT	TTATTTCTGC	AAATTTCTGC	AGTGTGATAA	TTTCACTGT	1680
75	GATAGATCCA	ATGGCTTAAT	TTGTGGAGGA	AATGGTGTTC	GCAAGTGTGG	TGTGTGTGAG	1740
	TGCAACCCCA	ACTACACTTG	CAGTGCATGT	GACTGTTCCT	TGGATACATG	TACTTGTGAA	1800
	CCAGCAACCG	GACAGATCTG	CAATGGCCGG	GGCATCTGCG	AGTGTGGTGT	CTGTAAAGTGT	1860
	ACAGATCCGA	AGTTTCAAGG	GCAAACTGT	GAGATGTGTC	AGACCTGCCT	TGGTGTCTGT	1920
	GCTGAGCATA	AAATATGTGT	TCAGTGCAGA	GCCTTCAATA	AAGGAGAAAA	GAAGAGACAA	1980
80	TGCACACAGG	AATGTTCCTA	TTTAAACATT	ACCAAGGTAG	AAAGTCCGGA	CAATTAACCC	2040
	CAGCCGTTCC	AACCTGATCC	TGTGTCCCAT	TGTAAAGGAG	AGGATGTGTA	CGACTGTGTG	2100
	TTCTATTATC	CGTATTTCAT	GAATGGGAAC	AACAGGTTCA	TGTTTCAATG	TGTGGAGAA	2160
	CCAGAGTGTC	CCACTGGTCC	AGACATCATT	CCAATTTGTAG	CTGGTGTGTT	TGCTGGAATT	2220

GTTCCTATTG GCCCTGCATT ACTGCTGATA TCGAAGCTTT TAATGATAAT TCATGACAGA 2280
 AAGGAGTTTG CTAATTTTGA AAAGGAGAAA ATGAATGCCA AATGGGACAC GGGTGAAAAT 2340
 CCTATTATTA AGAGTGCCGT AACAACTGTG GTCAATCCGA AGTATGAGGG AAAATGA

A10 Protein sequence:

Gene name: Integrin, beta 1 (fibronectin receptor, beta, antigen CD29 includes MDF2, MSK12)
 Unigene number: Hs.287797
 Probeset Accession #: X07979
 Protein Accession #: NP_002202.1
 Signal sequence: 1-21
 Transmembrane domains: 732-754
 INB domain: 34-464
 PSI domain: 26-76
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 1 MNLQPIFWIG LISSVCCVFA QIDENRCLKA NAKSCGECIQ AGPNCGWCTN STFLQEGMPT 60
 2 SARCDLRLAL KKKGCFDDI ENPRGSKDIK KKNKVNRSK GTAELKPED ITQIQPOQLV 120
 3 LRLRSGEPQT FILKFKRAED YPIDLYLMD LSYMKDDLE NVKSLGTDLM NEMRRITSDP 180
 4 RIGFGSPFEK TUMPYISTTP AKLRNPCTSE QNCTSPFSYK NVLSLTNKGE VFNELVGRQR 240
 5 ISGNLDSPEG SHYDYMVAV CGSLIGWRNV TRLLVPSTDA GFHPAGDGKL GGIPLPNDGQ 300
 6 CHLENNMYTM SHYDYPSIA HLVDKLSENN IQTIFAVTEE PQPVYKELN LIPKSAVGTL 360
 7 SAMSSNVIQL IIDAYNSLES EVILENGKLS EGVTSYKSY CKNGVNGTGE NGRKCSNISI 420
 8 GDEVQPEISI TSNKCPKDS DSKFIRPLGF TSEVEVILQY ICECECQSEB IPBSEPKCHSG 480
 9 NGTFECGACR CNEGRVGRHC BCSTDEVNSE DMDAYCRKEN SBEICSNNGE CVCGQCVCBK 540
 10 RDNTHBYSG KFCBCDNFMC DRENGLICGG NGVCKCRVCE CNPNYTSBAC DCSLDTSTCE 600
 11 ASHGQICNGR GICECGVCKC TDPKPOGQTC EMCQTCLGVC ASHKCVQCR AFNKGEKKOT 660
 12 CTQECSTFNI TKVESRDKLP QPVQDPVSH CKEDVDDCW FYFTYSVNGN NEVMVHVVEN 720
 13 PECFTGEDII PIVAGVVAGI VLIGLALLLI WKLLMIHDR RRFAXFEKEK MNAKWDGTEN 780
 14 PIYKSAVTTV VNEKYEGK

A11 DNA SEQUENCE

Gene name: selectin E (endothelial adhesion molecule 1)
 Unigene number: Hs.89546
 Probeset Accession #: M24736
 Nucleic Acid Accession #: NM_000450
 Coding sequence: 1-1833 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 1 ATGATTGCTT CACAGTTTCT CTCAGCTCTC ACTTTGGTGC TTCTCATTTA AGAGAGTGGA 60
 2 GCCTGGTCTT ACACACCTTC CACGGAAGCT ATGACTTATG ATGAGGCCAG TGCTTATTGT 120
 3 CACCAAAAGT ACACACACCT GGTGTCAATT CAAACAAAAG AAGAGATTGA GTACCTAAAC 180
 4 TCCATATTGA GCTATTACAC AAGTTATTAC TGGATTGGAA TCAGAAAGT CAACAATGTG 240
 5 TGGGCTCTGG TAGGAACCCA GAAACCTCTG ACAGAAAGAG CCAGAACCTG GGCTCCAGGT 300
 6 GAACCCACAA ATAGGCCAAA AGATGAGGAC TGGGTGGAGA TCTACATCAA GAGAGAAAAA 360
 7 GATGTGGGCA TGTGGAATGA TGAGAGGTGC AGCAGAAAGA AGCTTGCCCT ATGCTACACA 420
 8 GCTGCTGATC CCAATCATTC CTGAGTGGC CACGCTGAAT GTGTAGAGAC CATCAATAAT 480
 9 TACACTTGCA AGTGTGACCC TGGCTTCAGT GGACTCAAGT GTGAGCAAT TGTGAAGTGT 540
 10 ACAGCCCTGG AATCCCTGTA GCATGGAGC CTGGTTTGCA GTCAACCACT GGGAAACTTC 600
 11 AGCTACAAAT CTTCCTCTCT TATCAGCTGT GATAGGGGTT ACCTGCCAAG CAGCATGGAG 660
 12 ACTATGCAGT GTATGTCTCT TGGAGAATGG AGTGCTCCTA TTCCAGCCTG CAATGTGGGT 720
 13 GAGTGTGATC CTGTGACAAA TCCAGCCAAT GGGTTCGTGG AATGTTTCCA AAACCCCTGA 780
 14 AGCTTCCCAT GGAACACAAC CTGTACATTT GACTGTGAAG AAGGATTGTA ACTAATGGGA 840
 15 GCCAGAGACC TTCAAGTGTAC CTCATCTGGG AATTGGGACA ACGAGAAGCC AACGTGTAAA 900
 16 GCTGTGACAT GCAGGGCCGT CCGCCAGCCT CAGAATGGCT CTGTGAGGTG CAGCCATTCC 960
 17 CTTGCTGGAG AGTTCACCTT CAAATCATCC TGCAACTTCA CCTGTAGGGA AGGCTTCATG 1020
 18 TTGCAGGGAT CAGCCAGGT TGAATGCACC ACTCAAGGGC AGTGGACACA GCAATCCCA 1080
 19 GTTTGTGAAG CTFTCCAGTG CACAGCCTTG TCCAACCCCG AGCGAGGCTA CATGAATTGT 1140
 20 CTTCCTAGTG CTCTGTCAG TTTCCTGTTT GGGTCCAGCT GTGAGTTCTC CTGTGAGCAG 1200
 21 GGTTTTGTGT TAAAGGGATC CAAAAGGCTC CAATGTGGCC CCACAGGGGA GTGGGACAAC 1260
 22 GAGAAGCCCA CATGTGAAGC TGTGAGATGC GATGCTGTCC ACCAGCCCCC GAAGGGTTTG 1320
 23 GTGAGGTGTG CTCATTCCCC TATTGGAGAA TTCACCTACA AGTCTCTTGT TGCTTTCAGC 1380
 24 TGTGAGGAGG GATTGTGAAT ATATGGATCA ACTCAACTTG AGTGACATC TCAGGGACAA 1440
 25 TGACAGAGAG AGGTTCCTTC CTGCCAAGTG GTAAATATGT CAAGCCTGGC AGTTCGGGGA 1500
 26 AAGATCAACA TGAGCTGCAG TGGGGAGCCC GTGTPGGCA CTGTGTGCAA GTTCGCTGT 1560
 27 CTTGAAGGAT GGAAGCTCAA TGGCTCTGCA GCTGGACAT GTGGAGCCAC AGGACACTGG 1620
 28 TCTGGCTGTC TACCTACCTG TGAAGCTCCC ACTGAGTCCA ACATTCCCTT GGTAGCTGGA 1680
 29 CTTTCTGCTG CTGGACTCTC CCTCTGACA TTAGCACCAT TTCTCTCTGT GCTTCGGAAA 1740
 30 TGCTTAAGGA AAGCAAGAA ATTGTGTCTT GCCAGCAGCT GCCAAGGCT TGAATCAGAC 1800
 31 GGAAGCTACC AAAGCCCTT TTACATCCTT TAA

A12 Protein sequence:

Gene name: Selectin E (endothelial adhesion molecule 1)
 Unigene number: Hs.89546
 Probeset Accession #: M24736
 Protein Accession #: NP_000441
 Signal sequence: 1-22
 Transmembrane domains: 555-573
 C-lectin domain: 23-139

Cellular Localization: plasma membrane

5 1 11 21 31 41 51
 MIASQFLSAL TLVLLIKESG AWSYNTSTEA MYDEASAYC QQRVTHLVAI QNKKEIEYLN 60
 SILSYSPSYW WIGIRKVN NVVWVGITQKEL TEEAKNNAPG EPNNRQKDED CVBIYIKREK 120
 DVGMNNDERC SKKALALCYT AACTNTSCSG HQECVETINN YTCCKDPGFS GLKCEQIVNC 180
 TALESPFEGHS LVCSPHPLGNF SYNSSCSISG DRGYLPSSME TMQCMSGGEW SAPLPACNVV 240
 10 ECDVNTNPAN GFVECFQNGF SFFWNTTCTF DCEBGFELMG AQSLQCTSSG NWDNEKPTCK 300
 AVTCRAVRQP QNGSVKCSHS PAGEFTFKSS CNPTCEBGFN LQBPQVBECT TQGGNTQQIP 360
 VCEAFQCTAL SNPERGYMNC LPSASGSPRY GSSCEPSCBQ GFVLKGSKRL QGGPTGEMDN 420
 EKPTCEAVRC DAVHQPQKGL VRCASPIGE FTYKSSCAPS CEEGFELYGS TQLECTSQGQ 480
 15 WTSEVPBQOV VKCSLAVPG KLNMCSCGEP VFGTVCKFAC PEGWTLNGSA ARTCGATGHW 540
 SCLLPTECAP TESNIPLVAG LSAAGLSLLT LAPFLNLRLK CLRKAKKFVP ASSCQSLES D 600
 GSYQKPSYIL

A13 DNA SEQUENCE

20 Gene name: G protein-coupled receptor 39
 Unigene number: Rs.85339
 Probeset Accession #: AA349893
 Nucleic Acid Accession #: NM_001508
 Coding sequence: 1-1362 (underlined sequences correspond to start and stop codons)

25 1 11 21 31 41 51
 ATGGCTTCAC CCAGCCTCCC GGGCAGTGAC TGCTCCCAA TCATTGATCA CAGTCATGTC 60
 CCGAGTTTG AGGTGGCCAC CTGGATCAAA ATCACCCITA TTCTGGTGTA CTTGATCATC 120
 TTGGTATGG GCGTCTCTGG GAACAGCGCC ACCATTCGGG TCACCCAGGT GCTGCAGAA 180
 30 AAAGGATACT TCGAGAAGGA GGTGACAGAC CACATGGTGA GTTTGGCTTG CTGGACATC 240
 TTGGTATTC TCATCGGCAT GCCCATGGAG TTCTACAGCA TCATCTGGAA TCCCTGACC 300
 AGGTCCAGCT ACACCCGTGC CTGCAAGCTG CACACTTTCC TCTTCGAGGC CTGCAGCTAC 360
 GCTACGCTGC TGCACGTGCT GACACTCAGC TTGAGCGCT ACATCGCCAT CTGTACCCCC 420
 TTCAAGTACA AGGCTGTGTC GGGACCTTGC CAGGTGAAGC TGCCTATTGG CTTGCTCTGG 480
 35 GTCACCTCCG CCTCGGTGCG ACTGCCCTTG CTGTTTGCCA TGGGTACTGA GTACCCOCTG 540
 GTGAACGTGC CCAGCCACCG GGGTCTCACT TGCAACCCCT CCAGCACCCG CCACCCAGAG 600
 CAGCCCGAGA CTTCAATAT GTCCATCTGT ACCAACCTCT CCAGCCCTG GACCGTGTTC 660
 CAGTCCAGCA TCTTCGGGCG CTTCTGGTTC TACCTGTGCG TCTGCTCTC CGTAGCCCTC 720
 40 ATGTGCTGGA ACATGATGCA GGTGCTCATG AAAAGCCAGA AGGGCTCGCT GGCCTGGGGC 780
 ACCGCGCCTC CCGACGTGAG GAAGTCCBAG AGCGAAGAGA GCAGBACCCG CAGGAGGCAG 840
 ACCATCATCT TCGTAGGCT GATTGTGTG ACATTGCGG TATGCTGGAT GCCCAACAG 900
 ATTCCGAGGA TCATGGCTGC GGCCAAACCC AAGCAGGACT GGACGAGGTC CTACTTCGG 960
 CGGTACATGA TCTCTCTCC CTTCTCGGAG ACGTTTTTCT ACCTCAGCTC GGTCTCATAC 1020
 45 CGCTCTCTGT ACACGATGTC CTGCGAGCAG TTTCGGCGGG TGTCTGTGCA GGTGCTGTGC 1080
 TGCCGCTCTG CCGTCGAGCA CGCCAAACAC GAGAAGCGCC TGGCGGTACA TGCCACTCC 1140
 ACCACGAGCA GCGCCCGCTT TGTGCGCGC CCGTGTCTCT TCGCTTCCG GCGCCAGTCC 1200
 TCTGCAAGGA GAAGTGAAG GATTTTCTTA AGCACTTTTC AGAGCGAGGC CGAGCCCGAG 1260
 TCTAAGTCCC AGTCATGAG TCTCGAGTCA CTAGAGCCCA ACTCAGGCGC GAAACCGACC 1320
 50 AATTCGTCTG CAGAGAATGG TTTCAGGAG CATGAAGTTT GA

A14 Protein sequence:

55 Gene name: G protein-coupled receptor 39
 Unigene number: Rs.85339
 Probeset Accession #: AA349893
 Protein Accession #: NM_001508, NP_001409
 Signal sequence: none found
 Pfam domains: 7tm_1 [72-172, 224-344]
 Transmembrane domains: 32-54, 68-90, 111-133, 151-173, 221-243, 280-301, 320-342
 60 Cellular Localization: plasma membrane

65 1 11 21 31 41 51
 MASPSLPGSD CSQIIDHSHV PEFEVATWIK ITLLIVYLII FVMGLLGNSA TIRVTQVLQK 60
 KGYLQKEVTD HNVSLACSDI LVFLIGMPME FYSIIMNBLT TSSTLSCKL HTLEFEACSY 120
 ATLLHVLTLF FERYIAICHP FRYKAVSGPC QVKLLIGFVW VTSALVALPL LFAMGTETPL 180
 VNVPSHRGLT CRRSSTRHEE QPETSNNMIC TNLSSRWTFV QSSIFGAPVV YLVVLLSVAF 240
 70 MCKNMQVLM KSQKSLAGG TRPEQLRKSE SEESRTARRQ TIIFRLRLIV TLAVCWMPNQ 300
 IRRIMAAAKP KHDWTRSYFR AYMLLPFSE TFFYLSSVIN PLLYTVSSQQ FRRVFVQVLC 360
 CRSLQVHANE EKRLRVHAYS TTOSARPVQR PLLFASRRQS SARRTKIFL STPQSEAEPQ 420
 SKQSLSLES LEFNSGAKPA NSAAENGFOE HEV

A1 ProstateA15 DNA sequence

80 Gene name: CBGP1
 Unigene number: Rs.222399
 Probeset Accession #: AA256485
 Nucleic Acid Accession #: AJ400877
 Coding sequence: 51-3080 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

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15
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|      |      |      |      |      |
GGGGTCCGCG | CACACCTCCC | GGGCCGCGCG | CGGCCACGCG | CGGCACTCCG | CGGCTCTGCG | 60
CGGCAACCCG | TGAGGCATCC | ATGGGGGTGG | CGGGCCGCAA | CGGTCCTGGG | GCGGCTGGGG | 120
CGGTGCTGCT | CTGCTGCTGG | CTGCTGCTGG | CACTGCTGCT | GCTGGCGGGG | GCGTCCCGCG | 180
CGGGTCCGGG | CGGTGCGCGG | GGGCCGCGAG | AGGATGTAGA | TGAGTGTGCC | CAAGGGCTAG | 240
ATGACTGCCA | TGCCGACGCC | CTGTGTCTGA | ACACACCCAC | CTCCTACAAG | TGCTCCTGCA | 300
AGCCTGGCTA | CCAAGGGGAA | GGCAGGCGAG | GTGAGGACAT | CGATGAATGT | GGAATGAGC | 360
TCAATGGAGG | CTGTGTCCAT | GACTGTTTGA | ATATTCCAGG | CAATTATCGT | TGCCTTGT | 420
TTGATGGCTT | CATGTTGGCT | CATGACGGTC | ATAATTGTCT | TGATGTGGAC | GAGTGCCTGG | 480
AGAACAAATG | CGGCTGCCAG | CATACCTGTG | TCAADGTCT | GGGGAGCTAT | GAGTGTGCT | 540
GCAAGGAGGG | GTTTTTCCTG | AGTGACAATC | AGCACACCTG | CATTCACTGC | TCAGGAGAGG | 600
GCCTGAGCTG | CATGAATAAG | GATCACGGCT | GTAGTCACT | CTGCAAGGAG | GCCCAAGGG | 660
GCAGGCTGCG | CTGTGAGTGC | AGGCTTGGT | TTGAGCTGGC | CAAGAACCAG | AGAGACTGCA | 720
TCTTGACCTG | TAACCATGGG | AACGGTGGGT | GCCAGCACTC | CTGTGACGAT | ACAGCCGATG | 780
GCCCGAGGTG | CAGCTGCGAT | CCACAGTACA | AGATGCACAC | AGATGGGAGG | AGCTGCTCTG | 840
ABCGAGAGGG | GCTCTGCTGG | GAGGTGACAG | AGAGCAACAC | CACATCAGTG | GTGGATGGGG | 900
ATAAGCGGGT | GAAACGGCGG | CTGCTCATGG | AAACGTGTGC | TGTCACCAAT | GGAGGCTGTG | 960
ACCGCACCTG | TAAGGATACT | TCGACAGGTG | TCCACTGCAG | TTGTCTCTGT | GGATTCACCTC | 1020
TCCAGTTGGA | TGGTAGAGCA | TGTAAAGATA | TTGATGAGTG | CCAGACCCGC | AATGGAGGTT | 1080
GTGATCATTT | CTGCAAAATC | ATCTGTGGCA | GTTTTGAAGT | CGGCTGCAGG | AAAGGATTTA | 1140
AATATTAAAC | AGATGAGGAG | TCTTGCCAAAG | ATGTGGATGA | GTGCTCTTTG | GATAGGACCT | 1200
GTGACCAACG | CTGCATCAAC | CACCTTGGCA | CATTTGCTTG | TGCTTGCAAC | CGAGGATACA | 1260
CCCTGTATGG | CTTCACCCAC | TGTGGAGACA | CCAATGAGTG | CAGCATCAAC | AACGGAGGCT | 1320
GTGACGAGGT | CTGCTGTGAC | ACAGTGGGCA | GCTATGAATG | CCAAGTCCAC | CTTGGGTACA | 1380
AGCTCCACTG | GAATAAAAAA | GACTGTGTGG | AAGTGAAGGG | GCTCTGCGCC | ACAAGTGTGT | 1440
CACCCGCTGT | GTCCTGCTGC | TGCGTAAGA | GTGGTGGAGG | AGACGGGTGC | TTCTCTAGAT | 1500
GTCACTCTGG | CATTCACTCT | TCTTCAGATG | TCACCACCAT | CAGGACAGAT | GTAACCTTTA | 1560
AGCTAAATGA | AGGCAAGTGT | AGTTTGAATA | ATGCTGAGCT | GTTCCCGAG | GGTCTGCGAC | 1620
CAGCACTACC | AGAGAAAGCA | AGCTCAGTAA | AAGAGAGCTT | CCGCTACGTA | AACCTTACAT | 1680
CGAGCTCTGG | CAAGCAAGTC | CCAGGAGGCC | CTGGCCGACC | AAGCACCCCT | AAGGAAATGT | 1740
TTATCATATG | TGAGTTTGAG | CTTGAAACTA | ACCAAAGGGA | GGTGACAGCT | TCTTGTGAC | 1800
TGAGCTGCAT | CGTAAAGCGA | ACGAGAGAGC | GGTCTCGTAA | AGCCATCCGC | ACGCTCAGAA | 1860
AGGCGGTCCA | CAGGGAGCAG | TTTCACTCCG | AGCTCTCAGG | CATGAACCTC | GACGTGGCTA | 1920
AAAGGCTCCC | CAGAACATCT | GAAAGCCAGG | CAGAGTCTTG | TGGAGTGGGC | CAGGTCATG | 1980
CAGAAACCCA | ATGTGTCAAT | TGCGGGCTG | GGACCTATTA | TGATGAGACA | CGAGAACGCT | 2040
GCATTTTATG | TCCAAATGGA | ACCTTCCAAA | ATGAGGAAGG | ACAATGACT | TGTGAACCAT | 2100
GCCCAAGACC | AGGAATTTCT | GGGGCCCTGA | AGACCCGAGA | AGCTTGGAT | ATGTCTGAAT | 2160
GTGGAGGTCT | GTGTCAACCT | GGTGAATATT | CTGCAGATGG | CTTTGCACTT | TGCCAGCTCT | 2220
GTGCCCTGGG | CAGCTTCCAG | CCTGAAGCTG | GTCGAAGCTT | CTGCTTCCCC | TGTGGAGGAG | 2280
GCCTTGCCAC | AAAACATCAG | GGAGCTACTT | CCTTTCAGGA | CTGTGAACCC | AGAGTTCAAT | 2340
GTTCACTGTG | CAATTTCTAC | AACACCAACA | CTCACCGATG | TATTCTGTGC | CCAGTGGGGA | 2400
CATACCGACC | TGAATTTGGA | AAAATAAATT | GTGTTTCTTG | CCCAGGAAT | ACTACGACTG | 2460
ACTTTGATGG | CTCCACAAAC | ATAAACCACT | GTAAAAACAG | AAGATGTGGA | GGGGAGCTGG | 2520
GAGATTTTAC | TGGGTACATT | GAATCCCAAA | ACTACCCAGG | CAATTACCCA | GCCAACACCG | 2580
AGTGTAGTGG | GACCATCAAC | CCACCCCCCA | AGGCGCGCAT | OCTGATCGTG | GTCCCTGAGA | 2640
TCTTCTGGCC | CAGTAGGGAC | GACTGTGGGG | ACTATCTGGT | GATGCGGAAA | ACCTCTTCAT | 2700
CCAATTCGTG | GACACATAT | GAAACCTGCC | AGAOCCTAGA | ACGCCCATC | GCCTTCACCT | 2760
CCAGGTCAAA | GAAGCTGTGG | AITCAGTTCA | AGTCCAAATG | AGGGAACMG | GCTAGAGGGT | 2820
TCCAGGTCCC | ATACGTGACA | TATGATGAGG | ACTACGAGA | ACTCATGAA | GACATAGTTC | 2880
GAGATGGCAG | GCTCTATGCA | TCTGAGAAC | ATCAGGAAAT | ACTTAAAGAT | AAGAAACTTA | 2940
TCAAGGCTCT | GTTGTATGTC | CTGGCCATC | CCCAGAACTA | TTTCAAGTAC | ACAGCCGAGG | 3000
AGTCCCGAGA | GATGTTTCCA | AGATGTTTCA | TCGATTGCT | ACCTTCCAAA | GTGTCCAGGT | 3060
TTTTGAGACC | TTACAAATGA | CTCAGCCAC | GTGCCATCA | ATACAAATGT | TCTGCTATAG | 3120
GGTGTGTGGG | ACAGAGCTGT | CTTCCTTCTG | CATGTACAGA | CAGTCCGGTA | TTGCTGCTC | 3180
CGGTATCAGT | GACTCATATG | AGTTCAATTT | TTATAGATAA | TACAGATATT | TTGTTAAATT | 3240
GAACCTGGTT | TTTCTTTCCC | AGCATCTGCG | ATGTAGACTG | AGAATGGCTT | TGAAGGCTAT | 3300
CAGCTTCTCA | CTGCTGTGGG | CGGATGTCTT | GGTATAGTCA | CGGCTGCTCT | GAGCTGGACT | 3360
TTGGTCAGCC | TAGGTGAGAC | TCACCTGTCC | TTCTGGGCTC | TTACTCTCTC | TCAAGGATC | 3420
TGTAGTGGAA | AGGAGGCCAC | AGAATAAGCT | GCTTATTCTG | AACCTTCAGC | TTCTCTAGC | 3480
CCGCCCCCTC | CTAGGGGAGC | CCTCTGCACT | CGTGTGACGG | CTCTGACCA | GCAGAACAGG | 3540
CAAGAGGGGA | GGGAGGAGGA | CCGCTGCAGG | CTCCCTCCAC | CCACTTGAG | ACCTGGGAGG | 3600
ACTCAGTTTC | TCCACAGCCT | TCTCCAGCCT | GTGTGATACA | AGTTTATATC | CAGGAACCTG | 3660
AGTTCTAAGC | AGTCTCTGTT | AAAAAAATAA | GCAGAAAGAA | TTAGAAATAA | ATAAAAACTA | 3720
AGCACTTCTG | GAGACAT

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Al6 Protein sequence

Gene name: CBGP1
Unigene number: Hs.222399
Probeset Accession #: AA256485
Protein Accession #: CAB92285
Signal sequence: 1-31
Transmembrane domains: none
PFAM domains: EGF-like domains [49-84,132-167,177-213,286-321,407-442]
CUB domain [809-918]
Cellular Localization: may be secreted

80
1
11
21
31
41
51
MGVAGRNRPQ AAWAVLLLLL LPLPLLLLAG AVFPGRGAA GPQEDVDECA QGLDDCHADA 60
LQNTPTSTYK CSCKGTYGGE GRQCEDIDEC GNELNGGCVH DCLNTPGMYR CTCFDGFMLA 120
HDGHNCLDVD ECLEENGGSCQ HTCVNVMSY ECKCKEGFPL SDNQHTCIHR SEBSLSCMNK 180
DEGCSHCKE AFRGSVACBC RPFELAKNQ RDCILTCNHG NGGCGHSCID TADGPECSCN 240
POYKMHIDGR SCLREDTVL BVTESNTTSV VDGDKRVKRR LLMETCAVNN GGDRTCKDT 300

STGVHCSCPV GFILQLDQKT CKDIDECQTR NGGCDHFCKN IVGSFDCGCK KGFRLITDEK 360
 SCQDVDECSL DRTCDHSCIN HPGTFACACN RGYTLVGFTH CGDTNECSIN NGGCCQVCVN 420
 TVGSYECCCH PGYKLNHNRK DCVSVKGLLP TSVSFVSLH CGKSGGGDCG FLRCH9GHL 480
 SSDVTTIRTS VTFKLMEGKC SLKNAELFFE GLRFPALPEKH SSVKESFRYV NLTCSGKQV 540
 FGAPGRPSTP KEMFITVRFB LETNQKEVTA SCDLSCIVKR TEKRLKKAIR TLRKAVHREQ 600
 FHLQLSGMNL DVAKKPPRTS ERQASSCGVG QGHAEQCVS CRAGTYDGA RERCILCFNG 660
 TFQNESQMT CEPKPRFQNS GALKTPFAWN MSECGLCQP GEYSADGFAP COLCALGTFQ 720
 PEAGRTSCFP CGGGLATKHQ GATSFQDCET RVQCSFGHPY NTHHRCIRC FVGTYQPEFG 780
 KNNCVSCPGN TTIDFDGSTN ITQCNRRCG GELGDFGTGI ESNYPGNYP ANTECTWTIN 840
 PPPKRRILIV VPBIFLPIED DCGDYLVMRK TSSNSVTYI ETCQTYERPI APTSRSKLW 900
 IQPKSNBGNB ARGFPVPYVT YDEDYQSLIE DIVRDGRLYA SENHQEILKD KKLKALPDV 960
 LAHPQNYFKY TAQESREMFY RSFIRLLR8K VSRLRPYK

A17 DNA sequence

Gene name: ESTs
 Unigene number: Hs.293102
 Probeset Accession #: AI951118, AW170035, AL044891, AI908272
 Nucleic Acid Accession #: none found
 Coding sequence: 1-489 (entire sequence is an open-reading-frame)

1 11 21 31 41 51
 CAAAAAGAAA TAGATAAAAT AAATGGAAAA TTAGAAGAGT CTCCTGATAA TGATGGTTTT 60
 CTGAAGGCTC CCTGCAGAAAT GAAAGTTTCT ATTCCAACCTA AAGCCTTAGA ATTGATGGAC 120
 ATGCAAACTT TCAAAAGCAGA GCTCCTCCGAG AAGCCATCTG CCTTCGAGCC TGCCATTGAA 180
 ATGCAAAAGT CTGTTCCAAA TAAAGCCTTG GAATTGAAGA ATGAACAAAC ATTGAGAGCA 240
 GATCAGATGT TCCTTCAGAA ATCAAAACAA AAGAAGSTTG AAGAAATTC TTGGGATTCT 300
 GAGAGTCTCC GTGAGACTGT TTTACAGAA GATGTGTGTG TACCCAAAGC TACACATCAA 360
 AAAGAATGG ATAAATATAG TGGAAAATTA GAAGATTCAA CTAGCCTATC AAAAATCTTG 420
 GATACAGTTC ATTCCTGTGA AAGAACAAGG GAACCTCAA AAGACCCCTG TGACCCACGT 480
 TCAGGAAAA

A18 Protein sequence

Gene name: ESTs
 Unigene number: Hs.293102
 Probeset Accession #: AI951118, AW170035, AL044891, AI908272
 Protein Accession #: none found
 Signal sequence: none
 Transmembrane domains: none
 Cellular Localization: nuclear

1 11 21 31 41 51
 QKEIDKINGK LEESPNDNGF LKAPCRMVVS IPTKALELMD MQTFKAEPPE KPSAFEPALB 60
 MQKGVFNEAL ELKNEQTLEA DQMFPSESKQ KKVEENSWSB ESLRETVBSQK DVCVFKATHQ 120
 KEMDKISGKL EDSTSLSKIL DTVHSCERTR ELQKDPDPR SGK

Breast**A19 DNA SEQUENCE**

Gene name: TMPS93a
 Unigene number: Hs.298241
 Probeset Accession #: AI538613
 Nucleic Acid Accession #: AB038157
 Coding sequence: 202-1566 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 ACCGGGCACC GGACGGCTCG GGTACTTTCT TCTTAATTA GGTGATGCCG GTGTGAGCCA 60
 GGAAAGGSGT GTGTTTATGS GAAGCCAGTA ACACGTGAGC CTACTATCTC TTCCGTGGTG 120
 CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCGGA GCGGATGTC 180
 AGAGGTCTTG AATAGTACAC CATGGGGGAA AATGATCCGC CTGCTGTGA AGCCGCCCTC 240
 TCATTCGAT CGCTTTTGG CCTTGATGAT TTGAAATTA GTCTGTGTC ACCAGATGCA 300
 GATGCTGTG CTGCACAGAT CCTGTCACTG CTGCCATGTA AGTTTCTTC AATCATCGTC 360
 ATTGGGATCA TTGCATGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC 420
 TCAGGGAGST ACAGATGTCG CTCATCCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480
 GGAGTCTCGG ATTGCAAGA CGGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGTGAG 540
 AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCCTGGAAGA CCATGTGCTC CGATGACTGC 600
 AAGGTCACT ACACAAATGT TGCTGTGCC CAACCTGGGT TCCCAAGCTA TGTGAGTTCA 660
 GATAACCTCA GAGTGAAGTC GCTGGAGGGG CAGTTCGGG AGGAGTTTGT GTTCATCGAT 720
 CAOCTCTTGC CAGATGACAA GGTGACTGCA TTACACACT CAGTATATGT GAGGGAGGGA 780
 TGTGCTCTG GCCACGTGGT TACCTTGCAG TGACACAGCT GTGTCATAG AAGGGGCTAC 840
 AGCTCACGCA TCGTGGGTGG AAACATGTCC TTGCTCTGCG AGTGGCCCTG GCAGGCTGAC 900
 CTTCAGTTCC AGGGCTACCA CCTGTGCGGG GGCTCTGTCA TCAGGCCCTC GTGGATCATC 960
 ACTGCTGCAC ACTGTGTTTA TGACTGTGAC CTCCCAGAT CATGACCAT CCAAGTGGGT 1020
 CTAGTTTCCC TGTGAGACAA TCCAGCCCA TCCCACCTGG TGGAGAGAT TGTCTACAC 1080
 AGCAGTACA AGCCAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GGCAGGCGCA 1140
 CTCACBTTC ATCAAGATAT CCAGCCTGTG TGCCTGCCCA ACTCTGAGA GAACCTTCCC 1200
 GATGGAAAG TGTGCTGGAC GTACAGATGG GGGGCCACAG AGGATGAGAC AGGTGACGCC 1260
 TCCCTGTCC TGAACACAGC GGCCGTCCCT TGTATTCCA ACAAGATCTG CAACACAGC 1320
 GACGTGTAGG GTGGCATCAT CTCGCCCTCC ATGCTCTGCG GGGCTACTCT GACGGGTGGC 1380

5
10
15
20

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GTGGACAGCT GCCAGGCGGA CAGCGGGGG CCCTGGTGT GTCAAGAGAG GAGGCTGTGG 1440
AAGTTAGTGG GAGCGACCAG CTTTGGCATC GGCTGCGCAG AGGTGACAA GCCTGGGGTG 1500
TACACCGGTG TCACCTCCCTT CCTGGACTGG ATCCACGAGC AGATGGAGAG AGACCTAAAA 1560
ACCTGAAGAG GAAGGGGACA AGTAGCCACC TGAGTTCTTG AGGTGATGAA GACAGCCCGA 1620
TCCTCCCGTG GACTCCCGTG TAGGAACCTG CACACGAGCA GACACCCCTG GAGCTCTGAG 1680
TTCCGGCACC AGTAGCAGGC CCGAAAGAGG CACCTTCCA TCTGATTCCA GCACAACTTT 1740
CAAGCTGCTT TTTGTTTTTT GTTTTTTTGA GGTGGAGTCT CGCTCTGTG CCCAGGCTGG 1800
AGTGCAGTGG CGAAATCCCT GCTCACTGCA GCCTCGGCTT CCCTGGTTCA AGCGATTCTC 1860
TTGCCTCAGC TTCCCCAGTA GCTGGGACCA CAGGTGCCCG CCACCACACC CAACTAATTT 1920
TTGTATTTTT AGTAGAGACA GGGTTTCACC ATGTTGGCCA GGCTGCTCTC AAACCCCTGA 1980
CCTCAAATGA TGTGCTGCTT TCAGCCTCCC ACAGTGTCTG GATTACAGGC ATGGGCCACC 2040
ACGCTTAGCC TCACGCTCCT TTCTGATCTT CACTAAGAAC AAAAGAAGCA GCAACTTGCA 2100
AGGGCGGCGT TTCCCACTGG TCCATCTGGT TTTCTCTCCA GGGTCTTGC AAAATTCCTG 2160
ACGAGATAAG CAGTTATGTG ACCTCACGTG CAAAGCCACC AACAGCCACT CAGAAAAGAC 2220
GCACCAGCCC AGAAGTGCAG AACTGCAGTC ACTGCACGTT TTCATCTCTA GGGACCAGAA 2280
CCAAACCCAC CTTTCTTACT TCACAGACTT ATTTTCACAT GTGGGGAGGT TAATCTAGGA 2340
ATGACTCGTT TAAGGCCTAT TTTTCATGAT TCTTTGTAGC ATTTGGTGCT TGACGTATTA 2400
TTGTCTTGTG ATTCCAAATA ATATGTTTCC TTCCTCATA AAAAAAATA AAAAAAATA 2460
AAAAAATA

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A20 Protein sequence:

25
30

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Gene name: TMPRSS3a
Unigene number: Es.298241
Probeset Accession #: AI538613
Protein Accession #: BAB20077
Signal sequence: none found
Transmembrane domains: 43-65, 239-261
Tryp_SPC domain: 216-444
Cellular Localization: not determined

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35
40

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1 11 21 31 41 51
| | | | |
MGENDPPAVE APFSERSLFG LDDLKISFVA FDADAVAAQI LSLLEPLKFFP IIVIGIILALI 60
LALAIGLGIH FDCSGKRYCR SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVLOVF 120
TAASWKTMCSS DDWKGHYANV ACAQLGFPSY VSSDNLRVSS LEQQFREEFV SIDHLLPDDK 180
VTALHSHSVY REGCASGEVV TLQCTACGER RGYSSRIVGG NMBLLSQWPW QASLQFQYH 240
LOGGSHVITPL WIITTAHCVY DLYLPSKWTI QVGLVSLLDN PAPSRLVEKI VYHSKYKPKR 300
LGNLIALMKL AGPLTFNEMI QVCLPNSKE NFPDGKVCWT SGWGATEDGA GDASFVLNHA 360
AVPLISNKIC NHRDVGIIII SP6MLCAGYL TGGVDSQQGD SGGPLVCQER RLWLVLGATS 420
FGIGCAZVWK PGVYTRVTSF LDWIEHQMER DLKT

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A21 DNA SEQUENCE

45
50

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Gene name: ESTs; opposite strand to TRPS1
Unigene number: none
Probeset Accession #: AA428090
Nucleic Acid Accession #: AA428090
Coding sequence: 1-558 (underlined sequences correspond to start and stop codons)

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55
60
65
70
75
80

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1 11 21 31 41 51
| | | | |
ATGAAGCCCA GTTTGAACA CTGGGCTGAT ATAAAAATGT TTTCTGAAT AGACCAAAGS 60
CAGTTGTGTG GAGAAGAAT TCATCTACAA GTAGTATCTG TATCTTATCT TGTAGAAAC 120
TTTTACACA CAGATGATCT TATGTCATA GTGGAGGAAT CAGACAGCTG CTACAACTGT 180
GATTTCTGTG GGCCTCTCGG TAGAGCTGGA GACAGACTGC AACCCAAGAC AAAACCCAGA 240
GGAAAAACAA CTAACTCTAG CCRNTTGCCC AATTTCCACC TTGCTAGITA TCAGAGITCA 300
CTATTGTTTA AGCTCCAGGG GTCATACTAT GGCAATCTAC TGGTGGAAAT TATTCTGAGC 360
AAGTGTTTTG TTCAGCTTGC AGTATTAATA CAAAAAATAC ATTGCCTCCA GCTGCAAAAGC 420
AAGGGCATTS CCATTATGAA AGCCCTCTCA AGACTCTCTG CTATTTTCAA AACATGGAAA 480
AAAAAAGGGA AAAAAAGAAA AAAAAATAATA ATTAGAAGGA TTTGTTCTCT AATTTGGGCT 540
CCCAAAATG AGAAATGAAG ATTGTATAAT GAGGGGAGAT ACTAATTATT TTAACTCTC 600
CAAGCAATC TTCTGAAGCA ATCAATTATT TATATACTTT ATGTTCTGTC TTTTGTGATT 660
TTTCTCTCTG GTTAAAAACA TGCAGGTGAG TCTTGCCAAC GTCCCTTCTT ATCTGGATCT 720
GTTCTGCTTC ATTTCTCTTT CAAAGTCATC TTTGAGGGA CTTCGCTTGA TTAATTGAT 780
TTTAACCAA CAAATAAGAT ATTGTATATA TTAATTAAAA CTTTGTGAGA TGATTGATTA 840
GGAAATGCAT CATGTTCACA TGAGTATACC GAATTCAAAG TTAACCTTCA TAAGCAGGAG 900
TTTTTACACA TGTAAACATA ATCAATTACC AATACTGAC ACTCAATATT TGATACTCAA 960
CTGAATGTTT TTGAATAAAA CACATTTTFA TGTATCTCT CTGGAGAAAG TAGTATATAT 1020
CTTTTACAT AAAATATATC AGTGAGAGAG TGTGTGTTTA AGAAAAAAA TCAAAGCACA 1080
ACAAGTTGAG AGAGTCCAGG CTTTATCAAT ATAAGTAATA ATTTTITAGA ATGGTGATTT 1140
GATTTCACA TTTCAATTA TATATATATA TATATATATA TATATATATA TATATATATA 1200
TATATATATA TATATATATA TATATTACAA TGATCTGTAT TTCCTATTGC TAGAAGGATG 1260
AAGTGAATC CATATAAACC ATACCAAGCC CGTTATGTGT AACTGTTGTT AAAACTTTAT 1320
TATTCAGTT TAGATGTAA AGACATCTTT GCTGCTGAA GATTGTTTGC ATAAGAATA 1380
CACCAGAAGC ATGTTTGTGA GTAGAAATGA ACATGCACTA TGAACACAAA ATAAATATAA 1440
ACGAAAAAAT TFCATGTGTT GTAGAACAG AACATATTATA GCCAATCTC TAGTATTCAA 1500
ATCAGGACTA CAAATTGAAT TCTTTTCTT AGCAACATGA AATCATTTCA TATGAAAGAC 1560
ATTTCTGCT GGTGAATATT GCTGTAAAGT AAATTTTACA TTGGCATTTT GAGATGTTCC 1620
CCCTCTATGC CTCGCCAAAA GTTTTCCATG TGGTTGTCAA ATAGTCCG

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A22 Protein sequence:

Gene name: ESTs; opposite strand to TRPS1
 Unigene number: none
 Probeset Accession #: AA428090
 Protein Accession #: none found
 Signal sequence: none found
 Transmembrane domains: 113-129
 Cellular Localization: not determined

1 11 21 31 41 51
 MKPSLKHQWAD IKMFSEIDQR QVVGEEIHLQ VVSVSYLVEN FSDTDDLMSI VEESDSCYNR 60
 DSVGLPGRAG DRLPKTKPR KGTNNLSHLP NFHLASYQSS ILFKLQGSYY GNLLVEPILS 120
 KCFVQLAVLK QKRKHLQLQS KGIAIMKAPQ RLSAIFKTKW ERGKKEKKII IRRITCSLIWA 180
 PKNEK

A23 DNA SEQUENCE

Gene name: ESTs
 Unigene number: Hs.29383
 Probeset Accession #: AW207206
 Nucleic Acid Accession #: AL133619
 Coding sequence: 1-2070 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 ATGAGCGGTG CCGGGGTGGC GGCTGGGACG CGGCCCCCA GCTCGCCGAC CCGGGCTCT 60
 CGGCGCCGCG GCCAGCGCCC CTCTGTGGGC GTCCAGTCCT TGAGGCCGCA GAGCCCGCAG 120
 CTCAGGCAGA GCGACCCGCA GAAACGGAA CTTGGACCTG AGAAAAGCCT GCAGTTCCTG 180
 CAGCAGCAGC ACTCGGAGAT GCTGGCCAA GCTCATGAGG AGATCGAGCA TCTGAAGCGG 240
 GAAACAAGG GTGAGCCGGC GCGGGGCCCT AGGCCCGGCC TGCTCCCA GGCACACTCA 300
 ACACGTGCGG TCCCGCAGCA CAGAAACACA GCCATCAACT CCAGCACAGC CTTGGGCTCA 360
 GGGGGAACAC AGGAGCGGGA GCCCTCCAG ACTGTCTTG CCCACCTGCG TGCACTGGCC 420
 CCTGTATGCC AACCCAGTGG GTACAGGTC TGGGGGACCT GGACAGATGC CGCTACCTCT 480
 AGCCGTGGCT GAGCGATGTT ATGCAGCCAA GCACAGCAGG TGCTGCTCTC GGGAAAGCCCA 540
 GGGCCTGAGG TCATTGCAAG GCGGCAGGTG GCCACAGGGT GCTCCCGAGA CCTCCCTCCT 600
 CCAAGTAGAG CTGAAATGGG AAGGAACCTT TGGGACAGCC CTTGCCCTGC TAGATCTTTG 660
 CCTCAGATTG CTGCTGTGGC CAGGCCAGG ATTTCCAGCC CTATGGCTCT GAGTCTTCAC 720
 ATGCTGGGGG CCCAGGGGAT ATGGACACAC TCCATCCAGG GATCCCTTCC TGCCATCTGG 780
 GCAGCAACCA TGGGGACAAA GGGAGGAAGC AGAGTCTGTG TTCTTGGCCA CTGTGCCAAG 840
 GCACCTCCCC ATCTGACAGC CGGCCCCAC CACAGCCAGG ATCCTGGGCT GTGGTCTCAA 900
 GCTCACTCC CATATCTTT GGGCTGGGG CTGACATCAG GAGGACATCT GACTGGTGG 960
 TGGAGCCAGC CTGGGAACAT CGCAGCTGGG GCAGTGCTTA GGGCTCTGCC TTCCAGGGA 1020
 GACATGGAGA AGGGGTTGA GGGAGGGGCC TTCCCTAGCG GCTGTGGCAA CTCCAGTAG 1080
 CTGTCTGGG CAAAGTCTGG CCAAGTCTGG CAGCCCGAGC CTTGCACTGC TGGGGACGCT 1140
 GACAGGACAC GGGAGAGGCG CATGCTTTCC CTGCGGACCT GCTGTTCAT GTGTCCAG 1200
 CCTCTCTCT TTCCAGATCT CCGCTCAGGA AACCACTTT CCAGGGCCTC TGCTCCCTTG 1260
 GGGCTCGCT GGGTCTGCAT CAACGGAGTG TGGGTAGAGC CCGGAGGACC CAGCCCTGCC 1320
 AGGCTGAGAG AGGGCTCTCT ACAGACACAC AGGCCAGGAG CGAAGCGTGG GCGTCTTGG 1380
 GGGGTAGGG CCGGCGGGGC CGGACATGTT GCGCTCTCTT GCAGACAGCC TCTCCATGTC AAGCTTCCAG 1440
 TCTGTCAAGT CCACTCTCAA TTCAGCCAA TCTCAAGGCA AGGCCAGGCC CCAGCCCGGC 1500
 TCCCTCAACA AGCAAGATG AAAAGCTGAC GTCTCCAGA AGGGGACAT GGAAGAGGAG 1560
 CCGCTACTTC ACAACAGCAA GCTGGACAAA GTTCTCTGGG TACAAGGGCA GGCCGAAG 1620
 GAGAAAGCAG AGGCTCTCAA TGCCAGAGCT GCCTGTATGG GGAACAGCCA GCACCAAGGC 1680
 AGGCAGATGG GGGCGGGGGC ACACCCCGCA ATGATCCTGC CCGTTCCTCT GCGAAGGCC 1740
 ACCACACTTA GGCAGTGCBA AGTGCTCATC CGCGAGCTGT GGAATACCAA CCTCTGCAG 1800
 ACCCAAGGC TGCAGCATCT CAGTCCCTC CTGGAAGGGA GGCAGAGGCC CAGGCAGGCC 1860
 CCGAGGGAAG CTAGCTTTCC CAGGGACCAA GAAGCCAGC ATTTCCCAA GGTCTCCACC 1920
 AAGAGCCTCT CCAAGAAATG CCTGAGCCCA CCTGTGGCG AGCGTGCCAT CTGCGCGCA 1980
 CTGAAGCAGA CCCGAAGAA CAACTTTGCC GAGAGGCAGA AGAGGCTGCA GGCATGTCAG 2040
 AAACGCGGCC TGCTCGCTC AGTGCCTTGA

A24 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.29383
 Probeset Accession #: AW207206
 Protein Accession #: T43457
 Signal sequence: none found
 Transmembrane domains: 303-322
 Cellular Localization: not determined

1 11 21 31 41 51
 MSGAGVAAGT RPPSSPTPGS RRRQRPSVG VQSLRFQSPQ LRQSDPQKRN LDLEKSLQFL 60
 QQHSEFMALX LHSEIEHLKR ENKGEFARGP RPAFPQAHG TLPLPQERN AINSSTRLQS 120
 GGTODGEPLQ TVLRLAALA FVQPSGYRF WGTWDAATS SRGNTMLCSQ AQHVLSSGP 180
 GPEVIAGRQV ATGCSFDLFP PSRAEMGRNP WDSFPCPARSL PQIAAVARPR ISSFMALSPH 240
 MLGAQGINTH SIQGSPLPAIW AATNGITKGG RVLPFCILSK ALPHPDGSPH PAQDPGLWSQ 300
 AHFFLSLGLG LITSGGLTGG WSQPGNLAAG AVPRALPSQG DMEKGVGGP FPSRCGNSSE 360
 LFWAKCGPSR QPQFCSAGDA DRTEERAMLS LGTCCSMCEK PSCFFDQPSG NELSASAPL 420
 GARWVCINVR WEPGGPSPA BLKEGSSRTH RFGGKRGLLA GGSADTVRSP ADSLMSSEFQ 480
 SVKSISNSAN SQGKARPOFG SFNRQDSKAD VSQKADLEE PLLANSKLDK VPGVQQAARK 540

EKAASNAGA ACMGNSQBQ RQMGAAGHP MILPLPLRKP TLLRQCEVLI RELWNTNLLQ 600
 TOELRLHLSL LBSQRPAQA PEASPPRDQ EATHEPKVST KSLSKKCLSP PVAERAILPA 660
 LKQTFKNMFA ERQKRLQAMQ KRRLHRSVL

A25 DNA SEQUENCE

Gene name: ESTs; prolactin receptor
 Unigene number: Hs.25252
 Probeset Accession #: AA057193
 Nucleic Acid Accession #: NM_000949
 Coding sequence: 285-2153 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 15 GAGGCTGAA ATCCCCAGAC GCGGTTTTC TGGCTGGGC TTCTGCTTA CTCACCTCTT 60
 CTCCCTCTTT CTGGATTITA CCGACCGTTC GCGAACACAGC TTCCACACA ATGGAGCTTC 120
 ATGTCTCTGT GCAGGAAGTA CTGATGAGCAG ACITGCTCTC CTGACAAAC 180
 TAAAGAAGCT TCCTATTTCAT GAGGCGGAGC ACITGAGGATG CTCTCCACAT GAAACCTGAA 240
 GTGAAGCTTC GATACATTTT CTGCAGCAAG AGAAGGCAGC CAACATGAAG GAAATATGTG 300
 20 CATCTGCAAC CGTTTTCAC TGTCTACTTT TTCTCAACAC CTGCTTCTG AATGGACAGT 360
 TACCTCTGTG AAAACCTGAG ATCTTTAAAT GTGCTTCTCC CAATAAGGMA ACATTACCT 420
 GCTGCTGGAG GCCTGGGACA GATGGAGGAC TTCTACCAA TTATTCAGT ACTTACCACA 480
 GGGAGGAGA GACACTCATG CATGAATGTC CAGACTACAT AACCGGTGGC COCAACTCTC 540
 GGCACCTTGG CAAGCAGTAC ACCTCCATGT GGAGGACATA CATCATGATG GTCAATGCCA 600
 25 CTAACAGAT GGGAGCAGT TTCTCGGATG AACTTTATGT GACGTGACT TACATAGTTC 660
 AGCCAGACCC TCCTTTGAGG CTGCTGTGAG AAGTAAACCA GCCAGAAGAC AGAAAACCTC 720
 ACTGTGGAT TTAATGTGCT CCACCTACCC TGATTGACTT AAAAAGTGGT TGGTTCACGC 780
 TCCTGTATGA AATTCGATTA AAACCCGAGA AAGCAGCTGA GTGGGAGATC CATTTTGTCT 840
 GGCAGCAAC AGAGTTTAAG ATTCTCAGCC TACATCCAGG ACAGAAATAC CTGTCCAGG 900
 30 TTGCTGCAAA ACCAGACCAT GATACCTGGA GTGCTGGAG TCCAGCGACC TTCATTGAGA 960
 TACCTAGTGA CTTCACCATG AATGATACAA CGGTGTGGAT CTCTGTGCT GTCTTTCTG 1020
 CTGTCTCTGT TTGATTATTT GTCTGGGACG TGGCTTGAAG GGGCTATAGC ATGGTACCT 1080
 GCATCTTCC GCCAGTTCTT GGGCCAAAAG TAAAGGATT TGATGCTCAT CTGTTGAGA 1140
 35 AGGCAAGTC TGAAGAACCTA CTGAGTGCCT TGGGATGCCA AGACTTCTC CCCACTCTG 1200
 ACTATGAGGA CTGCTGTGTC GAGTATTTAG AAGTAGATGA TAGTGGGAC CAGCATCTAA 1260
 GTTCAGTCCA TTCAAAGAA CACCCAGATC AAGGTATGAA ACCACATAC CTGGATCCTG 1320
 ACATGACTC AGCCCGGGG AGCTGTGACA GCOCTTCCCT TTGTCTGAA AAGTGTGAGG 1380
 AACCCAGGC CAATCCCTCC ACATCTCATG ATCTGTAGGT CATGAGAGG CCAGAGATC 1440
 40 CTGAACAAC CACACCTGG GACCCCAAGT GCATAAGCAT GGAAGGCAAA ATCCCCATT 1500
 TTCATGCTG TGGATCCAAA TGTTCACAT GGCCTTACC ACAGCCAGC CAGCACACC 1560
 CCGATCTCT TTACCAAAAT ATTACTGATG TGTGTGAGCT GGTGTGGGC CCTGCAGGTG 1620
 CACCCGCTAC CTCTGTGAT GAGCAGGTA AAGATGCTTT AAAATCCTCT CAACACATTA 1680
 AGTCTAGAGA AGAGGGAAG GCAACCCAGC AGAGGGAGGT AGAAGCTTC CATCTGAGA 1740
 45 CTGACAGGA TACGCCCTGG CTGCTGCCCC AGGAGAAAC CCCCCTTGGC TCCGCTAAC 1800
 CCTGTGATTA TGTGAGATT CACAAGTCA ACAAGATGG TGCMTTATCA TTGCTACCA 1860
 AACAGAGAG GACAGCGGC AAGCCAGGA AGCCCGGAC TCCTGAGAAC AATAAGGAGT 1920
 ATGCCAAGGT GTCCGGGGTC ATGGATAACA ACATCTGCT GTTGGTGCCA GATCCACATG 1980
 CTAACAACT GCTTGTCTTT GAAAGATCAG CCAAGAGGC CCCACCATCA CTGGAACAGA 2040
 50 ATCAAGCTGA GAAAGCCCTG GCCAACTTCA CTGCAACATC AAGCAAGTGA AGGCTCCAGC 2100
 TGGGTGGTT GATATACCTG GATCCCGCAT GTTTTACACA CTCTTTTAC TGATAGCTTG 2160
 ACTAATGGA TGAATGGTTA AATGTGATTT TTCTTCAGG TAACACTACA GAGTACGTGA 2220
 AATGCTCAAG AATGTAGTCA GACTGACACT ACTAAGCTC CCAGCTCTCT TCACTGCCA 2280
 TTTTAAACCA CTGCTCTCTT TCTCCAGCAG CTGATTCAG AACAAATCAT TATGTTTCTT 2340
 55 AACGTGAGT TACGATTTTA CTTTGTCTG TTAGTTATAA AACTATGAT TCAATGAAAT 2400
 AAAGCACAC TGCTTAGTAT TCTTGAGGGA CAATGCCAAT AGGTATATCC TCTGGAAAG 2460
 GCCTTCATGA TTTGGCATGG GACAGACGGA AATGAAATTT TCAAAATGTT TTACCATAGA 2520
 AAGATGACAA AAGAAATTT TCCACATAGG AAAATGCCAT GAATATGCT TTTGAAAC 2580
 AACTGCATAA CCTTTACACT CCGTCCCAT TTTATTAGGA TTACCCAAAT ATAACCAATT 2640
 60 AAAGAAAGAA TGCATTCCAG AACAAATGTT TTACATAAGT TCCEATACCT TACTGACACA 2700
 TTGCTGATAT GCAAGTAAAG AAT

A26 Protein sequence:

Gene name: ESTs; prolactin receptor
 Unigene number: Hs.25252
 Probeset Accession #: AA057193
 Protein Accession #: NP_000940
 Signal sequence: 1-23
 Transmembrane domains: 237-253
 70 FN3 domains: 28-112, 127-215
 Cellular Localization: plasma membrane

75 1 11 21 31 41 51
 MKENVASATV FTLLFLNTC LLNGQLPPGK FEIPKCRSPN KETFTCWNP GTDGLPTNY 60
 SLTYHRSGET LMHECPDYIT GGPNSCHFGK QYTSMWRTYI MMVATNQMG SSFSDLYVD 120
 80 VTYIQPDPP LELAVSVKQP EDRKPYLWIK NSPFLIDLK TGNFTLLYEI RLKPKKAAEW 180
 EIHFAQQTE FTILSLHPGQ KYLVQVRCKP DHGWSANSP ATFIQIPSDF TMDTITVWIS 240
 VAVLSAVICL IIVWAVALKG YSMVTCIFPP VPGPKIKGFD AHLEKQKSE ELLSALGQD 300
 FEFTSDYEDL LVEYLEWDDH EDQHLMSVHS KEHPSQMKP TYLDPTDQ9 RGSCDPSLL 360
 SEKCEEPQAN PSTFYDPEVI EKPENPETTH TWDQCISME GKIPYFHAGG SKCSTWPLPQ 420

PSQENPRSSY HNTITDVCELA VGPAGAPATL LNEAGKDALK SSQTIKSREE GKATQOREVE 480
 SFHSEIDQDT PWLLPQEKTP PGSAPLDDYV EIEKVNKQGA LSLLPKQREN SGKPKKPGTP 540
 ENNKEYAKVS GVMNNILVL VEDPEAKNVA CFESAKEAP PSLEQNQAEK ALANFTATSS 600
 KRLQLGLD YLDPACFTHS FH

A27 DNA SEQUENCE

Gene name: Human neuropeptide Y receptor Y1 (NPYY1)
 Unigene number: Hs.169266
 Probeset Accession #: L07615
 Nucleic Acid Accession #: NM_000909.1
 Coding sequence: 209-1363 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 | | | | |
 CATCCACC CTCTCTCT TAATAAGCAG GAGCGAAAA GACAAATTC AAAGAGGATT 60
 GTTCAGTTCA AGGGAATGAA GAATTCAGAA TAATTTTGGT AAATGGATT CAATATCGGG 120
 AATAAGATA AGCTGAACAG TTGACCTGCT TTGAAGAAAC ATACTGTCCA TTGTCTATAA 180
 ATATCTATA ACAACCAAA CAATCAAAAT GAATTCACAA TTATTTTCCC AGGTGAAAAA 240
 TCATTCTAGT CACTCTAAAT TCTCAGAGAA GAATGCCAGG CTCTGCGCTT TTGAAATGA 300
 TGATTGTGCT CTGCCCTTGG CCATGATATT TACCTTAGCT CTTCCTTAGT GAGCTGTGAT 360
 CATCTCTGGT GTCTCTGGAA ACCTGGCCTT GATCATAATC ATCTTGAAAC AAAAGGAGAT 420
 GAGAAATGTT ACCACATATC TGATTGTGAA CCTTTCCTTC TCAGACTTGC TTGTTGCCAT 480
 CATGTGTCTC CCTTTTACAT TTGTCTACAC ACTTATGGAC CACTGGGTCT TTGGTGAGGC 540
 GATGTGTAAG TTGAATCCCT TTGTGCAATG TGTTCCTAAT ACTGTGTCCA TTTTCTCTCT 600
 GGTTCTCATT GCTGTGCAAC GACATCAGCT GATAATCAAC CCTCGAGGGT GGAGACCAAA 660
 TAATAGACAT GCTTATGTAG GTATTGCTGT GATTGGGTC CTGCTGTGAG CTCTCTCTTT 720
 GCCTTTCCTG ATCTACCAAG TAATGACTGA TGAGCCGTTT CAAAATGTAA CACTTGTATG 780
 GTACAAAGAC AAATAGCTGT GCTTTGATCA ATTTCCATCG GACTCTCATA GGTGTCTCTA 840
 TACCCTCTC CTCTTGTGTC TGCAATATTG TGGTCCACTT TGTTTTATAT TTATTGTCTA 900
 CTTCAAGATA TATATACGCC TAAAAAGGAG AAACAACATG ATGGACAAGA TGAGAGACAA 960
 TAAGTACAGG TCCAGTGAAA CAAAAGAAAT CAATATCATG CTGCTCTCCA TTGTGGTAGC 1020
 ATTTGCAATC TGTCTGCTCC CTCTTACCAT CTTTACACT GTGTTTGATT GGAATCATCA 1080
 GATCATGCTC ACCTGCAACC ACAATCTGTT ATCTCTGCTC TGCCACCTCA CAGCAATGAT 1140
 ATCCACTTGT GTCAACCCCA TATTTTATGG GTTCTGTAAC AAAAATCTCC AGAGAGACTT 1200
 GCAGTCTCTC TTCAACTTTT GTGATTTCCG GTCTCGGATG GATGATTATG AAACAATAGC 1260
 CATGTCCACG ATGCACACAG ATGTTTCCAA AACTTCTTTG AAGCAAGCAA GCCCAGTCGC 1320
 ATTTAAAAAA ATCAACAACA ATGATGATAA TAAAAAATC TGAACACTAT TATAGCCTAT 1380
 GGTCCCGGAT GACATCTGTT TAAAAACAAG CACRACCTGC AACATACCTT GATTACCTGT 1440
 TCTCCCAAGG AATGGGGTGG AAATCATTTG AAAATGACTA AGATTTTCTT GTCTTGCTTT 1500
 TACTGCTTTT TGTGTAGTGT GTCATTAATA CATTGGAAC AAAAGGTGTG GGCTTGGGG 1560
 TCTTCTGAAA ATAGTTTGA CCAGACATCT TTGAAGTGT TTTTGTGAAT TTATGCATAT 1620
 AATATAAGA CTTTATATCT GTACTTATG GAATGAATTT TCTTTAAAGT ATTACGATGC 1680
 GCTGACTTCA GAAGTACCTG CCATCCATA CGGTCAATAG ATTGGGTCAT CTGTATTAGA 1740
 TTAGATTAGA TTAGATTGTC AACAGATTGG GCCATCTTA CTTTATGATA GGCATCATTT 1800
 TAGTGTGTTA CATAGTAAAC AGTATGCAAA AGCAGCATTC AGGAGCCGAA AGATAGTCTT 1860
 GAAGTCATTC AGAAGTGTGT TCAGGTTTCT GTTTTGTGTT GGTTTTGTGT TGTTTTGT 1920
 TTTTTCACG TTAAGGGAGG CTTTCATTC CTCGCACTG ATTGTCACTT AAATCAAAAT 1980
 TTAATAATGA ATAAAAAGAC ATACTTCTCA GCTGCAATA TTATGGAGAA TGGGGCACCC 2040
 ACAGGAATGA AGAGAGAAAG CAGCTCCCCA ACTTCAAAAC CATTTTGGTA CTGACACAA 2100
 AGAGCATTTT AGAGTAATTA ATTTAATAAA GTAAATTAGT ATTGCTGCAA ATAGCTAAAT 2160
 TATATTTATT TGAATGTATG GTCAAGAGAT TTCCATTTT TTTTACAGAC TGTTCAGGT 2220
 TGTCAAGCT TCTGGTCTAA TAGTACTCG AAAGACTTTC CGCTTAACTT TTGTAGAAAC 2280
 ACAAAATCG TTTTCCATAC AGCAGTGCCT ATATAGTGAC TGATTTTAAC TTTCAATGTC 2340
 CATCTTTCAA AGGAAGTAAC ACCAAGGTAC AATGTTAAAG GAATATTCAC TTACCTTAGC 2400
 AGGAAATAAT ACACAAAAAC TGCAGATACT TCATATAGCC CATTTTAACT TGTATAAAT 2460
 GTGTGACTTG TGGCGTCTTA TAAATAATGC ACTGTAAAGA TTAATGAATA GTTGTGTCAT 2520
 GTTAATGTTC CTAATTTTAT GTATCTTGTG ATCATGATTG AGCCTCAGAA TCATTGGAG 2580
 AAATATATT TTAAGAACA AGACATACCT CAATGTATTA TACAGATAAA GTATTACATG 2640
 TGTTTGATT TAAAGGGCG GACATTTTAT TAAATCAAT ATTTTGTG CTTTTCTGA 2700
 GGAGCTCTCT TCAGTTTCAT TTTTCTCAT CCCATGACTT CCTTCGATG GT

A28 Protein sequence:

Gene name: Human neuropeptide Y receptor Y1 (NPYY1) mRNA, exon 2-3 and complete cds
 Unigene number: Hs.169266
 Probeset Accession #: L07615
 Protein Accession #: NP_000900.1
 Signal sequence: none found
 Pfam domains: 7tm_1 [57-91]
 Transmembrane domains: 39-61, 77-99, 118-139, 157-179, 212-234, 264-286, 300-322
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 | | | | |
 MNSTLFSQVE NRSVSNFSFE KNAQLLAFEN DDCHLPLAMI FTLALAYGAV IILGVSGNLA 60
 LIIILKQKE MRNVNIIIV NLFSDDLVA IMCLPFTFVY TIMDHWVFG AMCKLNPFVQ 120
 CVSITVSIYS LVLLAVERHQ LIINPRGWRP NERHAYVGLA VIWVLAVASS LPFLIYQVMT 180
 DRPFDVTLID AYKDKYVCPD QPPSDSHRLS YTTLLVLQY GPPLCFIFIC YPKIYIRLKR 240
 RNNMMDKMDK NKYSSETER INTMLLSIVV AFAVCWLELT IFNTVFDWNH QIIATCQHNL 300
 LFLLCSLTAM ISTCVNPIFY GFLNKNFQRD LQFFNFPCDF RSRDDYETI AMSTMHTDVS 360

KTSLSKQASPV AFKKINNDD NKKI

A29 DNA SEQUENCE

Gene name: Homo sapiens G protein-coupled receptor (HOT7T175)

Unigene number: Hs.208229

Probeset Accession #: AI819198

Nucleic Acid Accession #: NM_032551.1

Coding sequence: 1-1197 (underlined sequences correspond to start and stop codons)

10 1 11 21 31 41 51
 | | | | |
 ATGCACACCG TGGCTACGTC CGGACCCAAC GGGTCTCTGG GGGCACCCGG CAAAGCCCTCC 60
 GGCTGCCCGG GCTGTGGCGC CAAAGCCCTCG GACGGCCAG TCCCTTCGCC GCGGGCCGTG 120
 15 GACGCCTGGC TCGTCCCGCT CTTCTTCGGG GCGCTGATGC TGCTGGGCCT GGTGGGAAC 180
 TCGCTGGTCA TCTACGTCAT CTGCGGCCAC AAGCCGATGC GGACCGTGAC CAACTTCTAC 240
 ATGCCCAACC TGGCGGCCAC GGACGTGACC TTCTCTCTGT GCTGGCTCCC CTTCAAGGCC 300
 CTGCTGTACC CCGTCCCGCG CTGGGTGCTG GCGGACTTCA TGTGCAAGTT GGTCAACTAC 360
 ATCCAGCAGG TCTCGGTGCA GGCACGTTGT GCCACTCTGA CCGCCATGAG TGTGGACCGC 420
 20 TGGTACGTGA CCGTGTTCCT GTTGGCGGCC CTGACCGGCC GCACGCCCGC CCGTGGCGCTG 480
 GCTGTGAGCC TCAGCATCTG GGTAGGCTCT GCGCGGTTGT CTGCGCCGCT GCTCGCCCTG 540
 CACCGCTCTG CACCGCGGCC GCGCGCTTAC TGCACTGAGG CTTTCCCGAG CCGCGCCCTG 600
 GAGCGCGCCT TCGCACTGTA CAACTTGTGT GCGCTGTACC TGTGCGCGCT GCTCGCCACC 660
 TCGCGCTGCT ATCGCGCTGA GCTCGGCCAC CTGGCGCCGG TCGCGCTGCG CCGCGCCCGC 720
 25 CCGCATAGCG CCGTGCAGCG GCAGGTGCTG GCAGAGCGCG CAGCGCGCGT GCGGGCCAG 780
 GTCTCGCGCG TGGTGGCGCG CCGTGTCTCT CTCTTCGCGG CTTGCTGGGG CCGCATCTAC 840
 CTCTTCTCTG TCGTGCAGCG GCTGGCGGCC GCGGCTCTCT GGCACCCAGC CAGCTACGCC 900
 GCCTACGCGC TTAAGACCTG GGTCTCACTG ATGTCTCTAC GCAACTCGCG GCTGAACCCG 960
 CTGCTCTACG CTTCTCTGGG CTGCACTTCC CGACAGGCGT TCGCGCGCGT CTGCGCTGCG 1020
 30 GCGCGCGCGC GCGCGCGCGC CCGCGCGCGC CCGCGACCGT CCGACCCCGC AGCCCGCAC 1080
 GCGGAGCTGC ACCGCTCGGG GTCCACCCCG GCGCGCGCGC GCGCGCGCGC GCTCAAGGAG 1140
 AGTGGGCTCG CCGCGCGCGG GCTGTGCTTC CTGGGGGAGG ACAACGCCCC TCTCTGA

A30 Protein sequence

Gene name: Homo sapiens G protein-coupled receptor (HOT7T175), mRNA

Unigene number: Hs.208229

Protein Accession #: AI819198

Signal sequence: none found

Pfam domains: 7tm_1 [59-323]

40 Transmembrane domains: 43-65, 86-108, 122-144, 159-181, 203-225, 260-282
 Cellular Localization: plasma membrane

45 1 11 21 31 41 51
 | | | | |
 METVATSGPN ASWGAAPANAS GCPGCGANAS DGFVPSRAV DAWLVPLPFA ALMLLGLVGN 60
 SLVIYVICRH KPMRTVTNFX IANLAATDVT FLCCVPFPTA LLYPLPGWVL GDFNCKFVNY 120
 IQQVSVQATC ATLTAMSVDR WYVTVEPLRA LHRRTPLRAL AVSLSIWVGS AAVSAFVLAL 180
 50 HRLSPGFRAY CSEAPPSRAL ERAPALYNLL ALYLLPLLAT CACYAAMLRH LGRVAVRPAP 240
 ADSALQGVQL AERAGAVRAK VSRLLVAAVVL LFAACNGPIQ LFLVLQALGP AGSHMPSRYA 300
 AYALKTNARC MYSYNSALNP LLYAFLGSHF RQAFRRVPCPC AFRPRPRPRP PGPSPDPAAPH 360
 AELHRLGSHF AFARAGKPGS SGLAARGLCV LGEDNAPL

A31 DNA SEQUENCE

Gene name: CH22_FGENES.706; cadherin, EGF LAG seven-pass G-type receptor 1, flamingo (Drosophila) homolog (CELSR1)

Unigene number: Hs.252387

Probeset Accession #: NM_014246

Nucleic Acid Accession #: NM_014246

Coding sequence: 1-9045 (underlined sequences correspond to start and stop codons)

65 1 11 21 31 41 51
 | | | | |
 ATGGCGCGCG CCGCGCGCGC CGTGTGCGCC GTGCTGCTGC TCGTGGCGCG CCGCGCGCGC 60
 CTGCGCGCGA TGGGGCTGCG AGCGCGCGCC TGGGAGCGCG GCGTACCCCG CCGGACCCGC 120
 GCCTTGGCCC TCGCGCGCGC CTGTACTTAC GCGGTGGGCG CCGCTTGACG GCGCGCGCGC 180
 CCGCGCGGAG TCGTGGAGCT GCGCGCGGAT GCGCGGCTGG CAGGAGCTGG GCGCGTCTCG 240
 70 GCGCGCGGCG GCGCGCTGCC GCTGCAAGTC CCGTGTGGTG CCGCGCACTG CCGCGCGCGC 300
 CTGAGCGCGC GCGTGGCGCG GCGCGCGCAC CTTCGCGGCT GCGGAGCCCG TCGCGCGCTC 360
 TCGGGAACCG GTACCGCGCT CTGCGCGCGC CTCTGCTTCC CCGTCCCGCG CCGCTGCGCG 420
 GCGCGCGGAG ATTGCGCGCT CCGCGCTCGG ACCACTTAC CCGCGCTCGC CTGCGCGCGC 480
 CCGCGCGGCG CCGCTGCTGC CCGCGCTTCC ATCTGCTTGC GCGCGCGCGC CTGCGTCCCG 540
 75 CTGCGCTTGC TGTGCGCGCT GCGCGCGCGC GCTGCGCGCG TCGCGGTGGG ACTGCGCGCT 600
 GAGGCGCGCA CCGCGCGGAC GCGCTCGCGC TCGCATCCCG CATGCGCGCC CTGCGCGCGC 660
 AACTTGGCGG AAGCCCGGCG GCGCGCGCGC CCGCGCGCGC GCGCGCGCAC GAGCGCGAGA 720
 GGGAGCTTGA AGTTTCCGAT GCGCAACTAC CAGGTGGCGT TGTITGAGAA CGAACCGCGC 780
 GGCACCTTCA TCGTCCAGCT GCACGCGCAC TACACCATCG AGGGCGAGGA GAGCGCGCTG 840
 80 AGCTATTACA TGGAGGGGCT GTTCGACGAG CGCTCCCGGG GCTACTTCCG AATCGACTCT 900
 GCCACCGGCG CCGTGAGCAC GCACAGCGTA CTGGACCGCG AGACCAAGGA GAGCGCGCTC 960
 CTCAGGGTGA AAGCCGTGGA CTACAGTACG CCGCGCGCGT CCGCGCACAC CTACATCACT 1020
 GTCTTGTGTA AAGACACCAA CGACCAACAG CCGGTCTTCG AGCAGTCCGA GTACCGCGAG 1080
 CGCGTGGCGG AGAACCTTGA GGTGGGCTAC GAGGTGCTGA CCATCCCGCG CAGCGACCGC 1140

843

	GGCGGCATCT	GGTGGCCACA	GACCAAGTTC	GGGCAGCCGG	CTGCGGTGDC	ATGCCCTAAG	6240
	GGATCCCGTTG	GAATGCGGT	CCGACACTGC	AGCGGGGAGA	AGGGCTGGCT	GCCCCAGAG	6300
	CTCTTTAACT	GTACCACCAT	CTCCTTCGTG	GACCTCAGGG	CCATGAAATGA	GAAGCTGAGC	6360
5	CGCAATGAGA	CGCAGGTGGA	CGGCGCCAGG	CGCCTGCAGC	TGGTGAGGGC	GCTGCGCAGT	6420
	GCTACACAGC	ACACGGGCAC	GCTCTTTGGC	AATGACGTGC	GCACCGGCTA	CCAGCTGCTG	6480
	GGCCACBTCC	TTCAGCAAGA	GAGCTGGCAG	CAGGGCTTCG	ACCTGGCAGC	CACGACAGAC	6540
	GGCGACTTTC	ACGAGGACGT	CATCCACTCG	GGCAGCGCCC	TCCTGGCCTC	AGCCACCAAG	6600
	GCGGCGTGGG	AGCAGATCCA	GCGGAGCGAG	GGCGGCAAGG	CACAGCTGCT	CCGCGCCCTC	6660
	GAAGGCTACT	CCAGCAACGT	GGCAGCGAAC	GTGCGGCGGA	CGTACCTGCG	GCCCTTCGTC	6720
10	ATCGTCAACG	CCACACATGAT	TCCTGCTGTC	GACATCTTTG	ACAAGTTCAA	CTTTACGGGA	6780
	GCCAGGGTCC	CGGATTTGGA	CACCATCCAT	GAAGAGTTCC	CCAGGGAGCT	GGAGTCTTCC	6840
	GTCTCCTCTC	CAGCGGACCT	CTTCAGACCA	CCTGAAGAAA	AAGAAGGCCG	CCTGCTGAGG	6900
	CCGCTTGGCC	GGAGGACACC	CCCGCAGACC	ACGCGCCCGG	GGCTTGGCAC	CGAGAGGGAG	6960
15	GCCCCGATCA	GCAGGCGGAG	GGGACACCTT	GATGACGCTG	GCCAGTTCGC	CGTCTCTCTG	7020
	GTCACTATT	ACCGCACCTT	GGGCGAGCTC	CTGCGCGAGC	GCTACGACCC	CGACCGTCCG	7080
	AGCCTCCGGT	TGCTCTCAGG	GGCCATCAT	AATACCCCGA	TGGTGAGCAC	GCTGGTGTAC	7140
	AGCGAGGGGG	CTCCGCTCCC	GAGACCCCTG	GAGAGGCCCG	TCCTGGTGGG	GTTCGCCCCG	7200
	CTGGAGGTGG	AGGAGCGAAC	CAAGCTCTTC	TGCGTGTCT	GGAACCACTC	CCTGGCCGTT	7260
20	GGTGGGAGCG	GAGGGTGGTC	TGCCCGGGGC	TGCGAGCTCC	TGTCCAGGAA	CCGACACAT	7320
	GTCCCTTCCG	AGTGCAAGCA	CACAGCCAGC	TTTGCGGTGC	TCATGATAT	CTCCAGGGGT	7380
	GAGAACGGGG	AGGTCTCTGC	TCTGAAGATT	GTCACTCTATG	CCGCTGTGTC	CTTGTCACTG	7440
	GCACCCCTGC	TGGTGGCCTT	CGTCTCTCTG	AGCCTGGTCC	GCATGCTGCT	CTCCAACTCT	7500
	CACAGCATTC	ACAGGACCTT	CCCGTGGCG	CTCTCTCTCT	CTCAGCTGGT	GTTCGTGATT	7560
25	GGGATCAACC	AGACCGAAAA	CCCGTTTCTG	TGCACAGTGG	TTGCCATCTT	CCTCACTTAC	7620
	ATCTACATGA	GCACCTTTTC	CTGACCCCTC	GTGGAGAGCC	TGCATGCTTA	CCGATGCTGT	7680
	ACCGAGGTGC	GCACATCTGA	CACGGGGCCG	ATGCGGTTC	ACTACGTCTG	GGGCTGGGGC	7740
	ATCCCGGGCC	TTGTTCACAG	ACTGGCGGTC	GGCTTGAACC	CCAGGGCTTA	CGGGAATCCG	7800
	GACTTCTGCT	GGCTGTGCTT	TCAGACACCC	CTGATTTGGA	GCTTTGCGGG	GCCCATCGGA	7860
30	GCTGTTATAA	TCATCAACAC	AGTCATCTCT	GTCTATCTG	CAAAGGTTTC	CTGCCAAGA	7920
	AAGACCATTT	ATTATGGGAA	AAAAGGGATC	GTCTCCCTGC	TGAGGACCCG	ATTCTCTCTG	7980
	CTGCTGTCTA	TCAGCGCCAC	CTGGCTGTCT	GGGCTGTCTG	CTGTGAACCG	CGATGCACTG	8040
	AGCTTTCACT	ACCTCTTCCG	CATCTTCAGC	GGCTTACAGG	GCCCTTCTGT	CCTCTCTTTC	8100
	CACCTGCTGC	TCACACAGGA	GGTCCGGAAG	CACTGAAGG	GGTGTCTTGG	CGGAGGGAAG	8160
35	CTGCACCTGG	AGGACTCCGC	CACCAACAGG	GGCACCCTGC	TGACGCGCTC	CCTCACTTGC	8220
	AACACCACTT	TCGGTGACGG	GGCTGACATG	CTGGCGACAC	ACTTGGGGGA	GTCCACCGCC	8280
	TGGCTGGACA	GCATCTGTCA	GGATGAAGGG	ATCCAGAAAG	TCGGCGTCTC	CTCTGGGCTG	8340
	GTGAGGGGCA	GCCACGGAGA	GCCAGACCGG	TCCCTCATGC	CCAGGAGCTG	CAAGGATCCG	8400
	CCTGGCCACG	ATTCGCACTC	AGATAGCGAG	CTGTCCCTGG	ATGAGCAGAG	CAGCTCTTAC	8460
40	GCTCTCTCAC	ACTCTCTCAG	CAGCGAGGAC	GATGGGGTGG	GAGCTGAGGA	AAATGGGAC	8520
	CGGCGCAGGG	GCGCCGTCCA	CAGCACCCCC	AAAGGGGAGC	CTGTGGCCAA	CCACGTTCCG	8580
	GCGCGCTGCG	CGACCCAGAG	CCTGGCTGAG	AGTGACAGTG	AGGACCCCGG	CGGCAAGCCC	8640
	CGCCTGAAGG	TGGAGACCAA	GGTCAAGCTG	GAGCTGCAAC	GCGAGGAGCA	GGGCACTCAC	8700
	CGTGAGAGGT	ACGCCCGGGA	CCAGGAGAGC	GGGGCGCGAG	CCAGGCTTGC	TAGCAGCCAG	8760
45	CCGCCAGAGC	AGAGGAAAGG	CATCTTGAAA	AATAAGTCA	CCTACCCGCG	GGCGCTGAGC	8820
	CTGACGGAGC	AGACGCTGAA	GGGCGGGCTC	CGGGAGAAAG	TGGCGGACTG	TGAGCAGAGC	8880
	CCCACATCTT	CGGCGACGTC	TTCTCTGGGC	TCTGGCGGCC	CCGACTGGGC	CATCAGAGTC	8940
	AAGAGCCCTG	GGAGGGGAGC	GGGGCGTGAC	CACCTCAACG	GGGTGGCCAT	GAATGTGCGC	9000
	ACTGGGAGCG	CCCAGGCGGA	TGGCTCTCAC	TCTGAGAAAC	CGTGAGGCAA	GCCCGTCAAC	9060
50	CCACACAGGC	TGCGGCATCA	CCCTCAGACC	TTGAGGCCCA	AGGGGCCACT	GCCCTTGAGG	9120
	TGGAGTGGGC	CCAGAGTGTG	GGGCTCCCA	TGGTGGCAGC	CCCGGACTG	ATCATCCAGG	9180
	CACAAAGGTC	TTGGTTCTCC	CAGGAGCTCA	GGGCCCTGCA	GACCTTGCTA	CAAAGTCCAA	9240
	AGGCCACAGG	CTGAGGAGAG	GGTGGGAGCA	CTGGGCCAGC	ACCGCTGAGT	CCTAAGACTG	9300
	CAGTCAAAAG	CAGAACTGAG	AGGGGACCCC	AGACTGGGCG	CAGAGGCTGG	CCAGAGTTCA	9360
55	GGAAAGCCCG	GCACAGACCA	AGAACCGCGG	TCCAGCCCGG	CCCAAGCGGG	CATCTCATGG	9420
	CAGTGGCGAC	CCGTGGCTGG	CAGCCCGGGC	AGTCTTTTGC	AAAGGCAACC	CTGTCTTAA	9480
	AATCACTCTG	CTATGTGGGA	AAGGTGGAGA	TACTTTTATA	TATTTGTATG	GAAGTCTGAG	9540
	GAGGTGCAAC	CTGTATATAT	ATGTGATTCG	TGCTGACTTT	GTATCCCGGA	GAGATCCATG	9600
	CAATGATCTC	TGCTGTCTCT	CTCTGTCAAG	ATTGCACAGT	TGTACTTGAA	CTTGGCATGT	9660
60	GTTGACGAAA	CTGGTGCCCC	AGCAGATCAA	AGGTGGGAAA	TACCTCAGCA	GTGGGGCTAA	9720
	AACCAAGCGG	CTAGAAAGCC	TACAGCTGCC	TTCGGCCAGG	AAGTGAGGAT	GGTGTGGGCC	9780
	CTCCCGCCCG	GCCGCCCTGG	TCCCGAGTGT	TCCCTGTGTG	TGCGTTTGTG	CTCTGCTGCC	9840
	ATCTGCCCCG	GCTGTGTGAA	TTCAAGACAG	GGCAGTGCA	CATAGGCGAG	GTGTGAGGAG	9900
	CCCTGCTGAG	GTCACTGTGG	GGCACGGTTG	CCACACGGCT	GTCAATTTTC	ACCTGGTCAT	9960
65	TCTGTAGCCA	CCACCCCTTC	CTCCAGGTG	GCCCGGGAGC	TGCAGGTGGG	10020	
	GATGGCTTTG	TCTTTTGTCT	CTGCTCCCGG	TGGGACCTGG	GACCTTAAAG	CGTTGCAGGT	10080
	TCTGTATTTG	GACAGAGGTG	TGGGGCTTTC	CAGGCGGTTA	CATACCTCTG	GCCATTTCTC	10140
	TAACTCTCTG	AGACTGCGAG	GATCTCCAGG	CAGGGTCTTC	CCCTCTGGAG	TCTGACCAAT	10200
	TACTTCAATT	TGCTTCAAA	GGCCAAATGT	GACAGGGGAC	AAAGCCACAG	CCACACTCTT	10260
70	CAAGGTTAC	CAAACTGTTT	TTGGAATTC	ACACCAAGGT	CGGGCCCACT	GCAGGCGACT	10320
	GGCAGAGGCT	GGCCCGAGGG	GCTGTGGAAC	GGGTCCCGGA	ACTGTGAGAC	ATGTTTGATT	10380
	TTAGCGTTTC	CTTTGTTCCT	CAAAATCAGGT	GCCCAATAAA	GTGATCAGCA	CAGCTGCTTC	10440
	CAAAATAGAG	AAACCATAAA	ATAGAGTAA	AATGCAAGAA	TGTCCACACT	TGTCCACACT	10500
	GTTTTAAACT	TGACCCGTAT	GAATATGTGA	GCATGTTAG	CAGATGCCCTA	TGGGAGAGGA	10560
75	AAAGCGTATC	TGAAAATGGT	CCAGGACAGG	AGGATGAAAT	GAGATCCAGG	AGTCTCACA	10620
	CCTGAATGAA	TTATACATGT	GCCTTACCAG	GTGAGTGGTC	TTTCGAAAGT	AAAAAACTCT	10680
	AGTCCCTTTA	AACGTTTGCC	CTGTGGCTTT	CCTAAGTACG	AAAAGGTTTT	TAAAGTCTTC	10740
	AACAGTCTCC	TTTCAATGAT	TTAACAGGAT	TCTGCCCTCT	GAGGTGTAAAT	TTTTTTGTTC	10800
	TATTTTCTTC	CAGGTACTCT	ACAGCCCAACA	TACAGAGGTG	TAAATTTTAA	TTTGATCAGA	10860
80	ACTGTACCA	AAAAACAAT	GTCAATTTTA	TTGAGATGGG	AAAAATGTAA	ACCTAATTTT	10920
	ATTACTTAAG	ACTTTATGGG	AGAGATTAGA	CAGTGGAGGT	TTTTAACAGA	AGGTGTATTT	10980
	ATTAAATGTC	AAAAACACTG	AATTACAAAT	GAGAAGATTC	TACATAAAT	TAAAGTTTTT	11040
	GAATTTGTAC	TTCTGCGGTG	CTGGTCTTTC	TCCACAAACA	CCCCCGCCCC	TCOCATGCCC	11100
	CAGGGTGGCC	GTGGAGGGGA	CGGTTTACGG	ACGTGACAGT	GAGCTGTCCG	TGTCCCATGC	11160
	TCCCTCAGCC	AGTGAACGCT	GCCGGAACCT	TTTGCCCAT	CCCTAGTAGG	CCTGCCACAG	11220

CCTAGATGGG CAGTTTTTGT CTTTCACCAA ATTGAGGAC TTTTTTTTTT TGCCATTATT 11280
 TCTTCAGTTT TCTTTTCTTG CACTGATCTT TCTCCTCTCC TTCTGTGACT CCAGTGACTC 11340
 AGACGTTAGA CCTCTTGATG TTTTCCCACT GGTCCCTGAG GCTCTGTTT

5

A32 Protein Sequence

Gene name:

CH22_FGENES.706; cadherin, EGF LAG seven-pass G-type receptor 1, flamingo
 (Drosophila) homolog (CELSR1),
 Hs.252387

Unigene number:

NP_055061

10

Protein Accession #:

Signal sequence:

1-20

Cadherin domains:

250-344, 358-449, 464-556, 570-678, 692-780, 794-883, 897-990, 1004-1092,
 1110-1199

Pfam domains:

Laminin_EGF [2003-2048], 7tm_2 [2465-2708]

15

Letrophilin/GPS domains:

2407-2460

Transmembrane domains:

1219-1238, 2473-2492, 2507-2522, 2529-2547, 2616-2634, 2659-2675, 2687-2704

Cellular Localization:

plasma membrane

20 1 11 21 31 41 51
 MAPPPPPVLP VLLLLAAAA LPAMGLRAAA WEPRVPGGTR AFALRPGCTY AVGAACFPRA 60
 PRELLDVGRD GRLAGRRRVG GAGRELPLOV RLVARSAFTA LSRRRLKARTH LPGCGARARL 120
 CGTGARLCSA LCFPPVPGGCA AAQHSALAAP TTLPAACRCP RPRPRCPGRP ICLPPGGSVR 180
 25 LRLCALRAA AGAVRVGLAL EAATAGTSPA SPSPSPPLFP NLPEARAGPA RRAREGTSGR 240
 GSKKFPMPNY QVALVENEPA GTLLQLLHAH YTIEGEEKV SYVMEGLFDE RSRGYFRIDS 300
 ATGAVSTDSV LDRETKEHV LRKAVDYST PERSATTYIT VLKEDTNDHS PVFEQSEYRE 360
 RVRENLEVRG EVLTTRASDR DSPINANLRY KVLGGANDVF QLNSSSGVVS TRAVLDREEA 420
 ASYQLLVEMN DQGRNEGPLS ATATVYIEVE DEMDNYPQFS EQNYVVQVPE DVGLMTAVLR 480
 VQATDRDQGG NAATHYSILS GNVAGQFTIH SLSGILDVIN PLDFEDVQKY SLSTKAQDGG 540
 30 RPPLINSSGV VSVQVLVDVD NEPIFVSSPF QATVLENVPL GYPVVEIQAV DADSGENARL 600
 HYRLVDTAET FLGGGSAGPK NEAPTDFDFF QIENSSGWIT VCABLEREEV RHYSFGVEAV 660
 DHGSPMSSS TSVSITVLIV MNDPVPFTQP TYELRLNEDA AVGSSVLTLO ARDRDANSVI 720
 TYQLTGGNTR NRFALESQRG GGLITLALFL DYKQEQQYVL AVTASDSTHS RTAHVLIINV 780
 DANTRFPVQ SSHYIVSVBE DRPVGTSIAT LSANDRTGE NARITYVIQD PVPQFRIDPD 840
 35 SGTMYTMMLL DYENQVATIL TIMAQDNGIP QKSDTTILBI LILDANDNAP QFLMDFYQGS 900
 IFEDAPPSTS ILQVATDRD SQPNRGLLYT FQGGDGDGDG FYIEPTSGVI RTQRRLDREN 960
 VAVYNLMALA VDRGSFTPLS ASVEIQVTL DINDNAPMFE KDELELFVEE NNPVGSVVAK 1020
 IRANDEDEGE NAQIMYQIVE GDMRBEFQID LLNGDLRAMV ELDFEVRERY VLVVQATSAP 1080
 40 LVSRATVHIL LVDQDNDFV LPDFQILFNN YVTNKNSFP TGVIQCIAPH DEDVSDSLNY 1140
 TFVQGNELRL LLLDPATGEL QLSRDLDNNR PLBALMEVSV EDGIHSTVAF CTLRVTIITD 1200
 IMILTNSITVR LBNMFSQKFL SPFLALFVEG VAAVLSTTKD DVVFVNVQND TDVSSNINLV 1260
 TFALALEGGV RQGFPTPLS QEQIYLNRTL LTTISTQRLV PFDDNICLRE PCENYMECVS 1320
 VLFDFBSAPF LSSTTVLFRF IHPINGLRCL CPFGTGDYVC ETEIDLCYSO PCJANGRCRS 1380
 45 REGGYTCECF EDFTGHECEV DARSGRCANG VCKNGGTCVN LLIGGFHCVC PPGYERPYC 1440
 EVTRSEPPQ SFVTFRGLRQ RFHFTISLTP ATQERNGLLL YNGRFNEKED FIALEIVDEQ 1500
 VQLTFBAGET TTTVAPKVP SVDGGRHWSV QVQYINKPNI GHLGLFEGPS GEKMAVTVVD 1560
 DCDTMAVRF KQDIGNVSCA AQGTQTGSKK SLDLTGFLLL GGVPNLPEDF FVBNKQFVGC 1620
 MRNLSDGKN VDMAGFIANN GTREGCAER NFDGGRQCN GGTVCVRNMM YLCBCLRF 1680
 50 GKNCQAMPH PQLFSGESVV SWSDLNIIIS VPWYLGMPF TRKEDSVLME ATSGGPTSPR 1740
 LQILNNYLP EVSHGSPDVE SVMLSGLRVT DGBWHLLIE LKNVKEDESE KHLVTMTLDY 1800
 GMDQNKADIG GMLPGLTVRS VVVGASGSDK VSVRRGRFC MQGVRNGGTP TNVATLNMN 1860
 ALKRVKMDG DVDDPCTSSP CPFNRSCHDA WEDYSCVCDK GYLGINCVDA CELNFCENMG 1920
 ACVRSPGSPQ GYVCEGSPSH YGFCENKLD LDCPRGMWGN FVCGPCECAV SKGDFDPCNK 1980
 55 TNGQCCCKEN YKLLAQDTL LFCDCPFHGS HSRTCDMATG QCACKPGVIG RQCNRCNPF 2040
 AEVTLGCEV IYNGCPKAF AGIHWPTKE GPAAVECPK GSVGNVREHC SGEKWLFP 2100
 LYNCTTISFV DLRAMNEKLS RMTQVQDAR ALQVRLARS ATQSTGTLEF NDVRTAYQLL 2160
 GEVLQHSBG IQKLGVSGL ADPHEDVLHS GSALLAPATR AAWEQIQRSE GDTQLLEEL 2220
 EGYFSNVARN VRTYLRPFV IVTANMILAV DIFDKPFTG ARVPRDTTH HEPFRELESS 2280
 VSPADFPFP PEEKGFLLR PAGRRTTPTQ TRPQPGTERE APISRRRRHF DDAGQFAVAL 2340
 60 VIYRTLQQL LPRYDFDRR SLRLPHRP11 NTPMVSTLVY SEGAPLPRFL RRFVLVEFAL 2400
 LEVEERTKPV CVFVNSLAV GGTGWSARG CELLSRNRTE VACQCSHTAS FAVLMDISRR 2460
 ENGEVLPLKI VTYAANVLSL AALLVAFVLL SLVRMLRSNL HSLHKLAVA LFLSQLVFI 2520
 GINQNTENFL CTVAALLHY IYMTFAWTL VESLHVYRML TEVRNIDTGP MRFYVVVGW 2580
 65 IPAIVTGLAV GLDPQGYGNT DFCNLSLQDT LIWSFAGPIG AVIINTVTS VLSAKVSCIR 2640
 KHHYKKGKI VSLRTAFLL LLLISATWLL GLLAVNRDAL SFHYLFAIPS GLQGFVLLF 2700
 HCVLNQVRK HLKGLVGRK LHLKDSATTR ATLLTRSLNC NTTFGDPDM LRIDLGESTA 2760
 SLDSIVRDEG IQKLGVSGL VRGSGEPDA SLMPRSCKDP PGHDSDSSE LSLDRQSSSY 2820
 ASSHSDSDSD DGVGAEKWD PARGAVHSTP KGDVAVNHVP AGWPDQSLAS SDSDDPGKP 2880
 70 RLKVEIKVSV ELHREEQGSH RGEYFDQES GGAARLASSQ PPEQRKGILK NKVTYPPPLT 2940
 LTBQTLKRL REKLADCEQS PTSSRTSLG SGGEDCAITV KSPGRPGRD HINGVAMVR 3000
 TGAQADGSD SEKP

75

A33 DNA SEQUENCE

Gene name: CXCR3 (G protein-coupled receptor 9); chemokine (C-X-C) receptor 3

Unigene number:

Hs.198252

Probeset Accession #:

X95876

Nucleic Acid Accession #:

X95876

80

Coding sequence: 69-1175 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 CCAACCAAA GCACCAAGC AGAGGGGCG AGAGCACACC ACCCAGCAGC CAGAGCAACA 60
 GCCCAGCCAT GGTCTTGTAG GTGAGTGACC ACCAAGTGCT AAATGACGCC GAGGTTGCCG 120

5	CCCTCCTGGA	GAACCTTCAGC	TCTTCCTATG	ACTATGGAGA	AAACGAGAGT	GACTCGTGCT	180
	GTACCTCCCC	GCCTTGCCCA	CAGGACTTCA	GCCTGAACCT	CGACCGGGCC	TTCTGCCCAG	240
	CCCTCTACAG	CTCTCTCTTT	CTGCTGGGGE	TGCTGGGGCA	CGCGCGGGTG	GCAGCCGTGC	300
	TGCTGAGCCG	GCGGACAGCC	CTGAGCAGCA	CCGACACCTT	CCTGCTCCAC	CTAGCTGTAG	360
	CAGACAGSCT	GCTGGTGCTG	ACACTGCCGC	TCTGGGCAGT	GGACGCTGCC	GTCCAGTGGG	420
	TCITTTGGCTC	TGGCCTCTGC	AAAGTGGCAG	GTGCCCCCTT	CAACATCAAC	TTCTACGCAG	480
	GAGCCCTCCT	GCTGGCCTGC	ATCAGCTTTG	ACCGCTACCT	GAACATAGTT	CATGCCAACC	540
	AGCTCTACCG	CCGGGGGCCC	CCGGCCCCGC	TGACCTCTAC	CTGCTGGCTC	GTCTGGGGGC	600
10	TCITGCCCTGT	TTTCGCCCTC	CCAGACTTCA	TCTTCCTGTC	GGCCCAACAC	GACGAGCGCC	660
	TCACAGCCAC	CCACTGCCAA	TACAACTTCC	CACAGGTGGG	CCGCAOCCGT	CTGCGGGTGC	720
	TGCAGCTGGT	GGCTGGCTTT	CTGCTGGCCC	TGCTGGTCAT	GGCTACTGTC	TATGCCACCA	780
	TCCTGGCCGT	GCTGGCTGGT	TCCAGGGGCC	AGCGGGCCCT	GCGGGCCATG	CGGCTGGTGG	840
	TGCTGGTGGT	GGTGGCTTTT	GCCCTCTGCT	GGACCCCTTA	TCACCTGGTG	GTGCTGGTGG	900
15	ACATCCTCAT	GGACCTGGGC	GCTTTGGCCC	GCAACTGTGG	CCGAGAAAGC	AGGGTAGACG	960
	TGGCCAAGTC	GGTCACTTCA	GGCCTGGGCT	ACATGCAGTG	CTGCCCTAAC	CGGCTGCTCT	1020
	ATGCTTTTGT	AGGGGTCAAG	TTCCGGGAGC	GGATGTGGAT	GCTGCTCTTG	CGGCTGGGCT	1080
	GCCCAACCA	GAGAGCCAGC	CATCGTCTTC	CCGCCGGGAT	TCACTCTGGT	TCATCTGGT	1140
	CTGAGACCTC	AGAGGGCTCC	TACTCGGGCT	TGTGAGGCCG	GAATCCGGGC	TCCCTTTTGG	1200
20	CCACAGTCT	GACTTCCCGG	CATTCCAGGC	TCTCTCCCTC	CTCTGCCCGC	TCCTGGCTCTC	1260
	CCCATATATCC	TGCTCTCCCG	GACTCACTGG	CAGCCCCAGC	ACCACCCAGT	CTCCCGGGAA	1320
	GCCACCTTCC	CAGCTCTGAG	GACTGCACCA	TTGCTGTCTC	TTAGCTGCCA	AGCCCCATCC	1380
	TGCGGCGCGT	GCTGGCTGGC	TGGAGCCCCA	CTGCCCTTCT	CATTTGGAAG	CTAAAACTTC	1440
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25	CAGCCAGGCC	CTCCAGCTCA	GCACTGACTG	TGGCCATGGT	CCCAAGAGCC	TCTATATTTC	1560
	CTCTTTTATT	TTTATGTCTA	AAATCTGTCT	TAAAACTTTT	CAATAAACAA	GATCGTCAGG	1620
	ACCAAAAAAA	AAAAAAATAA	AAAAAAATAA	AAAAAAATAA	AAAAAAATAA	BHCLITERAT	1680
	UREBHCBLAS	TFEBHCBLAS	LOGUESMOUS	ECXCRMVLEV	SERQVLDASD	PAPLLENSTIS	1740
	PYDXGENESD	FSDSPPCPDQ	FSLNFDRTFL	PALYSLLFLL	GLLNGAVAA	VLLSOTALS	1800
30	STDTFLHLHL	VADVLLVLT	PLMAVDAAVQ	WVFGPLCKV	AGALFNINFX	AGAPILLACTIS	1860
	FDRYLSIVHA	TQIYRRDPV	RVALTCIVVW	GLCLLFPALPD	FTYLSANYDQ	RLNATHCQYN	1920
	FPQVGRTRALR	VLQVAVGFL	PLVVMAYCYA	HILAVLVSR	GQRRFRAMRL	VVVVVAFAV	1980
	CNTFYHLVVL	VDILMDVGV	AENCRESRE	DVAKSVTSGM	GYMHCLNPL	LYAFVGVKFR	2040
	BQMMLFTRL	GRSDQGRFQR	QPSRRRESS	NSETTEASYL	GL		
35	A34 Protein sequence						
	Gene name:			CXCR3 (G protein-coupled receptor 9); chemokine (C-X-C) receptor 3			
	Unigene number:			Hs.198252			
40	Protein Accession #:			P49682			
	Signal sequence:			none found			
	Pfam domains:			7tm 1 [70-318]			
	Transmembrane domains:			57-78, 92-113, 129-147, 169-190, 222-243, 257-275, 307-323			
	DRY box:			148-149			
45	Cellular Localization:			plasma membrane			
50	1	11	21	31	41	51	
	MLLEVSDREQV	INDAEVAALL	ENFSSSYDYG	ENESDSCCTS	PPCPDQFSLN	FDRAFLPALY	60
	SLLFLGLGLG	NGAVAAVLLS	RRTALSSTDT	FLHLAVADT	LLVLTLPLMA	VDAAVQWVEG	120
	SGLCKVAGAL	FWINIFYAGAL	LLACTSFDRY	LNIVHATQLY	RRGPPARVTL	TCLAVHGLCL	180
	LFALPDPYFL	SABHDERLINA	THCQYNFPQV	GRTALRLVLQ	VAGELFLPLV	MAYCAEILLA	240
	VLLVSRGQRR	LRAMRLVVVV	VVAFALCWT	YHLVVLVDIL	MDLGLALBNC	GRESRVDAK	300
55	SVTGLGLYME	CCLAPLLYAF	VGKFRFRMW	MLLLRLGCEN	QRGLQRQFSS	SRRDSWSSET	360
	SEASYGL						
60	A35 DNA SEQUENCE						
	Gene name:			Differentially expressed C016 gene (clone MGC:5257)			
	Unigene number:			Hs.69517			
	Probeset Accession #:			AA447522			
	Nucleic Acid Accession #:			BC001291			
	Coding sequence:			44-541 (start and stop codons are underlined)			
65	1	11	21	31	41	51	
	GGGGGCGCGG	CGCGCTGACC	CTCCCTGGGC	ACCGCTGGGG	ACGATGGCGC	TGCTCGCCTT	60
	GCTGCTGGTC	GTGGCCCTAC	CGCGGGTGTG	GACAGACGCT	AACCTGACTG	CGAGACAACG	120
70	AGATCCAGAG	GACTCCACAG	GAAACGGACG	GGGTGACAAT	AGAGTGTGGT	GTCTATTTTG	180
	TGAGAGAGAA	AACACTTTGG	AGTGCCAGAA	CCCAAGGAGG	TGCAATGGGA	CAGAGCCATA	240
	CTGCTTTATA	GCGGCCGTGA	AAATATTTCT	ACGTTTCTTC	ATGGTTGCGA	AGCAGTGTCT	300
	CGCTGGTTGT	GCAGCGATGG	AGAGACCCAA	GCCAGAGGAG	AAGCGTTTTC	TCTTGGGAAG	360
	GCCCATGCCC	TTCTTTTACC	TCAAGTGTGG	TAAATTTGCG	TACTGCAATT	TAGAGGGGCG	420
75	ACCTATCAAC	TCACTAGTGT	TCAAGAATA	TGCTGGGAGC	ATGGGTGAGA	GCTGTGGTGG	480
	GCTGTGGCTG	GCCATCTCTC	TGCTGCTGGC	CTCCATTGCA	GCGGGCTTCA	GCTGTGCTTG	540
	AGCCACGGGA	CTGCCACAGA	CTGAGCCTTC	CGAGCATGGG	ACTGCTTCCA	GACCGTTGTC	600
	ACCTGTTGCA	TTAAACTTGT	TTTCTGTGTA	TTACCTCTTG	GTTTGACTTC	CCAGGTCTCT	660
	GGGATGGGAG	AGTGGGATGC	AGGTGCAGTT	GGCTCTTAAC	CCTCAAGGGT	TCTTTAATCT	720
80	ACATTCAGAG	GAACTCCAGA	TCTCTGAGT	AGTGATTTTG	GTGACAGTT	TTTCTCTTTG	780
	AAATCAAAAC	TTGTAATCTA	TTTATTGCTG	ATGGCCACTC	TTTTCCTTGA	CTCCCTCTCT	840
	CCTCTGAGGG	CTTCACTATT	GATGGGGAGG	GAGGCCCTAG	TACCACTCAT	GGAGAGTATG	900
	TGCTGAGATG	CTTCCGACCT	TTCAAGTGAC	GCAGGAACAC	TGGGGGAGTC	TGAATGATTG	960
	GGGTGAAGAC	ATCCCTGGAG	TGAAGGACTC	CTCAGCATGG	GGGGCAGTGG	GGCACAOGTT	1020
	AGGGCTGCCC	CCATTCCAGT	GGTGGAGGCG	CTGTGGATGG	CTGCTTTTCC	TCAACCTTTC	1080

5 CTACCAGATT CCAGGAGGCA GAAGATAACT AATTGTGTG AAGAACTTA GACTTCACCC 1140
 ACCAGCTGGC ACAGGTGCAC AGATTCTATA ATTCCACAC GTGTGTGTTC AACATCTGAA 1200
 ACTTAGGCCA AGTAGAGAGC ATCAGGTGTA ATGGCGTTCA TTCTCTGTG AAGATGAGC 1260
 CATCAATGGG GAGCTGAGAA ATCAGACTCA AAGTTCCACC AAAAAAAAT ACAAGGGGAC 1320
 TTCAAAGTT CACGAAAAAA AAAAAAAATA AAAAAAAATA AAAAAAAATA AAA

A36 Protein sequence:

10 Gene name: Differentially expressed CO16 gene (clone M3C:5257)
 Unigene number: Hs.69517
 ProbeSet Accession #: AA447522
 Protein Accession #: AAH01291
 Signal sequence: 1-17 (first underlined sequence)
 Transmembrane domain: 146 - 162
 Cellular localization: plasma membrane

20 1 11 21 31 41 51
 MALLALLLVV ALPRVWTDAN LTARQEDFED SQRTDESDNR VMCHVCEREN TFEQNPRRC 60
 KWTEPYCVIA AVKIPRPFPM VAKQCSAGCA AMERPKPEEK RFLLEPMFMY FYLKCKKIRY 120
 CNLEGPPIINS SVEKEYAGSM GESCGGLWLA ILLELLASIAA GLSLLS

A37 DNA SEQUENCE

25 Gene name: ESTs
 Unigene number: Hs.293616
 ProbeSet Accession #: AW043782
 Nucleic Acid Accession #: none found
 Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

35 1 11 21 31 41 51
 AGCAACGACG CCGGBCAGCG GGAGCGGCGG CCGGCGCCATG TGGCTGCTGG GGCCTGCTGG 60
 CCTGCTGCTG AGCAGCGCCG CGGAGAGCCA GCTGCTCCTC GGAACAACT TCACCAATGA 120
 GTGCAACATA CCAGGCAACT TCATGTGACG CAATGGAGCG TGCATCCCGG GCGCTGCGCA 180
 GTGTGACGGG CTGCTGACT GCTTCGACAA GAGTGATGAG AAGGAGTGCC CCAAGGCTAA 240
 GTCGAAATGT GGCCTCAACT TCTTCCCTTG TGCCAGCGCG ATCCATTGCA TCATTGGTCG 300
 CTTCGCGTGC AATGGGTTTG AGGACTGTCC CGATGGCAGC GATGAGAGAG ACTGCACAGC 360
 AAACCCCTCG CTTGTCTCCA CGCCCGCTA CCACTGCAAG AACGGCTCT GTATTGACAA 420
 GAGCTTCATC TGGATGGGAC AGAATAACTG TCAGACAAC AGTGATGAGG AAAGCTGTGA 480
 AAGTTCCTCA GAACCCCGCA GTGGGCAAGT GTTTGTGACT TCAGAGAAC AACCTGTGTA 540
 TTAACCCAGC ATCACCCTAT CCATCATCGG CAGCTCCGTC ATTTTGTGTC TGGTGTGGC 600
 CCTGCTGACA CTGCTCTTGC ACCACCAAGG GAAGCGGAAC AACCTCATGA CGCTGCCCGT 660
 GCACCGGCTG CAGCACCCTG TGTGCTGTGC CGCGCTGGTG GTCCCTGAGC ACCCCACACA 720
 CTGCAACGTC ACCTACAAGG TCAATAATGG CATCCAGTAT GTGGCCAGCC AGCGGAGCA 780
 GAATGCGTGC GAATGAGGCT CCCCACCCCT CTACTCCGAG GCCTTGTCTG ACCAGAGGCC 840
 TGGTGTGATG GACCTTCTTC CACCGCCCTA CTCTCTGAC ACGGAATCTC TGAACCAAGC 900
 CGACCTGCCC CCTTACCGCT CCGGCTCCGG GAGTGCCAC AGTGCCAGCT CCCAGSCAGC 960
 CAGCAGCCTC CTGAGCGTGG AAGACACCAG CCACAGCCCG GGGCAGCCTG GCCCCAGGA 1020
 GGGCACTGCT GAGCCACAGG ACTCTGAGCC CAGCCAGGGC ACTGAGAGAG TATAAGTCCC 1080
 AGTATTCTCA AAGTCCATAT GGGTAAATCT GCTCTGACTT GTTGCCATTG TAACTATTG 1140
 TGCTCTGAGG AAGCTCTTTA AGCACCIGTA AAGATGTCTC AAGTTACAGT TTGGGATATT 1200
 AACTATCTCT GCATTCCTCT CCTCCCCAGC ACTTCAGAGA TGTTTTCTG GGTCTCTAGT 1260
 TGACATGATC TGTGTGTGGT CTTTCTGTGC AGGTCACTCT TCCCTTGGGA CCCAGATCA 1320
 CACCCCTATT TTTCACATTA TTCTGTCTCT GTTGGAGAGA CAGCATATAA AACAGTATTG 1380
 AAATAGGCTG GAGAGAGACA ATGTTTCTGT GCTATATTGG ATGCTCAGAA GTGAGGAGA 1440
 CGCTGGACCG AATTCTCTCT GCTGGGTAGT TACCTTATAG CATTTGGGGA TTTGGGTTAG 1500
 ATGATCTAAC CAGGAGGCCA TCACTGGATG GTCAACCCCG CAAAAAAT CCATTGTAGC 1560
 ATCAAAACCT GCTTTGCACA ATCCTATTGG ATGCCCCAG TTACAGAGAG TCAGTGGCCA 1620
 AAGAAACTT TGAAGGTGAG TAACAACCTT CAGCAGTGGC AACGTATATT TGGTTTGTG 1680
 AAGGACTCTG AAGCTATCTA CCTGTATATA ATCTGCGCT TAGAAATTG CCCAAGATG 1740
 CTATTCTGA GAGCTTCTCT CAGCAGCATA TATCATCAGC CTCATCTTAA AATAGGCAGG 1800
 GAGCCCTCC CATGAGTTTA TCCAAGTTCT CAGCTCTTAA AATGACGGCT GCCAGACCC 1860
 TACACCTGCG CTGGCTTAC AGCCACTTAC CTGGTTCTG GACTGTCACT CTCCAGCTG 1920
 ACCTGCCCGT AGCCAGGGA TGAGGACCTA ACTTGAGTTG GCCCAAAGTC TGAACCTGGC 1980
 GTATGTCCCT GTGGCCACCA CCCAGCCTGT CTGTGCTATT CATGACGGCT CAACACTGGC 2040
 CTCCAAAGTT CCTTAAACAC TTGCAAGTTC CTTTTACCT GTGCAATTGG ACTTGAGGAC 2100
 ACTGTTTCT ATCAGAGTG AGAGCCATGT TCAATACCTC CAGCAAGCTC TCGTGGCTCC 2160
 CTGCACTGTG CAGCTCTCTC TTCCCAAGT CCCAATACCA GCACCTCTAG TTAGAGTTAG 2220
 GGTCAAGGTC AGGCTCTCC CAACATCCA GTAGTTTCTC CTCTGAGACA CATGGCAAG 2280
 AGACAATTG GAGTCAAGAT TTTCATTG GTATCTATTT AAATCTTTTA GAAATGCAAT 2340
 TGAACACTG TGTGTTTCTT TTCCCTTCTA GTTAAGGAGC TATTTATATG TGTATAGGAA 2400
 AGCTGTCTCT TTTTGTGTTT TTCCCTTAAAC AAGGTCCAAA GAAAGATGCA AAGGAGATC 2460
 ACACCCCTGC CCGCTGAGC CCGGTGATAA CAAGTCACTC CAGACTAACC TGTGTGCCAG 2520
 ACATTGTGTC ATTGTGTCAC TTGAGGTTA TTATTATCA AGTTCGTGAA GGAAGCAGAA 2580
 AGAGGAGACT CTCTCTCCCT CCGTGTATAG TCTCTATGTT TGTGCTAGTT TTTCTTTT 2640
 TTCTCTGTGT CAGCTCAGCC ACAGGCCCCG OCTCCCTGCA GGAATAAGGG GTAAAACTT 2700
 AGGTGTTGTT TGGCAGAGAA CCACACTGAC TGATGAGGGG TAAATGGGAA CCAGGTAGAG 2760
 CCACCTCGGG CAGCTGTAC CCACTCAGAA CTCTCTTCCB CAGCTGAAGA ATGTTCAGT 2820
 AACCTGTGTT ACGCTAATTA AAACAGAGCC TGCAGGAAGT GGGGCTAAGG TGGCATTAG 2880
 TGATCTGTT CTGTAGACTT TTCTTTCTTT TTTTAAACCA ATCCAAGGA TGTATCAGAA 2940
 AAGCTAGCCA CTGTATTTT GTTTTGTTTA AAAAAAATAA GAAAGAAAGA AAGAAAGAAA 3000

AACGGAAAGG AACCTAGCTG CCTGTATCTT TCATTTTTAA AATAGCACTT GAGTTATTTT 3060
 CTGAGTAATC CAATAAAGAA CTTTGTATGA CAGCCAGAAT GTGTTAGAAC TCTGGCTGAA 3120
 CATTTCATCT CCTGTGAGTC AGAAGGGCTT TAITTTCTCC TTGTATGGGG CCCCTTCTTC 3180
 TTTCTGGTGC TCTGGAAGTT GTTTAGAGGA AAGAATTCTA ATTTTAAATTA ATTGCGCAGT 3240
 GAGTTAATCT CACTCGCTTT TCTGCTTCCA GGCATCTTAG GAAAAACAAA TGGTTTATGT 3300
 AGATAAGGGA TGCCTACTAA TGCTTTTITA AAACAAACAG GGACATTTT ATTATAGATT 3360
 TGATTTTITT AATGAATGTT TTTAAAAATA TATAAATAGG ACACCAAAGC GGCAGGGTTT 3420
 TTTTGGGGG GAGGGGGTTT GTTTTCCAAC TCAAGATGGC ACATTAGTGG CCAGCAATAT 3480
 TTTTAACTC ATTCCAACCA GGAAGCTTTT TTATACATTG CCTAAATCTA CGCCAACCCAG 3540
 AAAATAGTCT CATCTCTTTT TTTCTCAAT GAGATCCGTG TTTTATTTTA GCATTAATTT 3600
 AGTTACACAG TGATGACTGG CCTATTACCT GACTCAGCTC CCTCTACCTT GAAATGACA 3660
 TTTTAAAAA ATGCAACTAA GTGGTTAATA GTGTGTGACG CTCAAAGTTA ATGTAAACTG 3720
 GAAAGGTTGT GTGTGTTGTC TTTTGTGTT TGTGTTAGGC TTGGTTTGT TTTTAAATTT 3780
 TTATACTTT TAATAAATTT GCAGTTTCAT TCTTCTGTTT TGTGCAAAWG GNMCTAMARM 3840
 AAMMAAAAC ANYNITGGGG GGCCTTGGGC CTCGAAAAA GTTTTAAACA CCACCTCGGG 3900
 TGGGGCGGGG GGGCCACGTT AGGTACGGCG ACCACGGCGG CCCAAACGGG ACCCCAGAGG 3960
 GAAACCTCTG CCAAGAAAAA GGTGGCGAGA ATTCTCCACA CCAAGAAAAA ACSCGCGGG 4020
 GGAACCCGCA GAGTGTGCG TAAACCAAC CCGAAGAGAG AACTCAGAG CACACAAGCG 4080
 GGACTCAAC AGGAGGACCC AAGGGAACCC GATAGAGTAC G

A38 Protein sequence:

Gene name: ESTs
 Unigene number: Hs.293616
 Probeset Accession #: AN043782
 Protein Accession #: none found
 Signal sequence: 1-17
 Transmembrane domains: 169-191
 LDL domains: 28-66, 70-108, 112-149
 Cellular localization: plasma membrane

1 11 21 31 41 51
 MLLGLFLCLL LSSAAESQLL PGNFTNECN IPGNFMCNNG RCIPGAWQCD GLPDCFDKSD 60
 EKECPKAKSK CGPTFPFPCAS GIHCIIGRFR CNGFEDCPDG SDEENCTAMP ILCSTARYHC 120
 KNGLCIDKSF ICDGQNNQD NSDRESCSS QEPGSGQVVF TSENQLVYYP SITTAIIGSS 180
 VLPVIVVALL ALVLHQRKR NNLMTLPVHR LQHPVLLSRL VVLDEPHCN VTYNVNNGIQ 240
 YVASQAEQNA SEVSGPPSYS EALLDQREAW YDLPPPPYS DTESLNQADL PPYRSRSGSA 300
 NSASSQAABS LLSVELTSHS PQPQPGQEGT AEPDSEPSQ GTREV

A39 DNA sequence

Gene name: ESTs
 Unigene number: Hs.128899
 Probeset Accession #: AA983251
 Nucleic Acid Accession #: AA983251
 Coding sequence: 1-1749 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 ATGCTGCTCTG GCTTCTTGAT GAGTCCCACT ACCCAGCACA GAGCAGTA CACTCCCGGA 60
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 GACCGGAGCA GGGAGAGCCG SCGGAGGCTT GCGGGGCTCC TGTGGGACCG CGCTGCGAGC 180
 GGGGAGGCGG AGAAGGGGAA CCGGGGCGAG CCGCCCGCTT GGAATCCGCG CCAGCAGCAG 240
 CCGGGGCGCG CGCCAGCTGG GCAGGCTCCG GGGACTGCGG CTGGGGGCGC GCAGGACCTT 300
 CGCCTGCGTC CTGAGGCTTC CCGGGGAGG GTCCGCTTGC CAGTGAACCT TCAGAGGCT 360
 TCCGAGCAGC AGCCCGGGGG GCCTTCTGAC TGATCCCGGA GATTTCATC AGCGAGTGCA 420
 ACTCATAGG CAGTCCCTAA GGGGACCGGG CCACCGGCTG AGGACGGGGA TGGCTTAGGA 480
 GCTCTGGGAC CTAGGGCCCG CGGTCTGTCG CTCTGGGGCG TCAGGCGAGA GGGAGTGGC 540
 CCGGCGGAAA AGCGCCCGCG GACAGTCACT GACGAGGCCC GGGGGTCCGC GGGGCCACGA 600
 CTTCTCGGAG ACCGCTCTGC GCTCTCTGGA GACGCGCTGT CCGCGCCAG GGTGGTCCA 660
 TGTGGGGCGC TCGCGCTCG TCCGTCTCCT CATCTCGAAA CCGCGCTCG CTCTGCGAGC 720
 TGCTGCTGGC TGGCTGCTG GCGGCGGGGG CGAGGCGCCA GCGGCGAGTA CTGCCAGCGC 780
 TGGCTGGAGC CGCAGGGGCT CTGGCGCATC GGTTCAGT GTCCGAGCG CTTCGACGCG 840
 GGGGACGCA CCACTCTGCT GCGCAGCTGC GCGFTGCGCT ACTGCTGCTC CAGCGCGAG 900
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 CAGACTCTG TGCCCATGAC AGCTGTGCCA CCTTTCATGG ACAGGCTGCA GCTTGGCTAC 1680
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 GATTCTCGAG GTCCAGTCC GCACATGTCG GTGTATTATA TGGCACGATT CCTTGGATG 1860
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 CATCCAGGTT ATCATTGATT TATGATGAA AACCGCCTC AGCTGGAGAT GACGTGATG 1980
 TTGCTGATGG GTGTATAACA AATGCTTAG TCCGAGTGC CCTGAGATA TGGTTGACGA 2040
 AAGAATTTTA TAAACTGATA AATTAAGGAT TTTTATTATG TTGTTATTAT TATTCTTTT 2100

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 15
 20
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TTGTTGTTGA CTGCACAGGA TCAAAATGCC TGTTATCTCC CTFTTACTGG GACTTTTTTT 2160
TTTTTTTTTT TCGGCTCACT GCAACTTCAG CCTCCTGGAT TCAGGCCAAC CTCTGCCTC 2220
TGGTGCATC TCGGCTCACT GCAACTTCAG CCTCCTGGAT TCAGGCCAAC CTCTGCCTC 2280
AGCCTCCAC GTGGCTGGGA TTACAGGTGC CTGCCCCCAT GGCTAATTTT TTGTAATTTT 2340
TGTAGAGATG GGGTTTCACC ATGTTGGCTG GGCTGGTCTC ACTCTCTGTA CCTCAAGCAA 2400
TCGGCTGTC TCAGCCTCCG AAAGTGCCTG GATTACAGGC GTGAGCCACC GCCCCAGCC 2460
TGAGCCTTTT TTTTCTTCTA ATGCATCCAA GGTAAAGGGG AAGACGCAAA TAACAGGACT 2520
ATTCTAAAAG GAAACCTGTT TGAACCTCTG GAGATCAGTC ATCAGTCTCA GTATTCACCA 2580
GGCACACCTT AATTTCAATG TAAAAAGATA TATATATTTT GTCTATTTTT GTGCTTTTGG 2640
GGGCTATTTT TGTGCTTTTT TACCTTATGT AGAGATCTTA TTACAAAGTG ATTTCTTACA 2700
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TAGCTCCTCA GCCATAACTT GAGACTTGGG ATGAAATTTA AACCAGATAC GATTACTTTT 3180
GCAGATCATA AGGCTTTTTA TACTCTTGT ATCAAAATGG CTATTTTTT AGGCACTAAG 3240
GATTGTTAAG AGAAAAGCTT TTCACGAAG GATTGCTTTT CTCTCCAC ACTGTCTCTG 3300
ATTTCTCTC TCCTTCAGGC CTCACAGGC ACTGTATCTA TTGCCAATGT TCCAAATAT 3360
CAAAATCAG TGAATTTTAT TGTTGTTTCT TTACTTATAT AAAAAAGAT AACTTTAAG 3420
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GTATGTTATG GTCTTCTACA CATTTATGTC TATAGATATC TATCGATCAT CTTCTATTTC 3540
TGTTCATGA CTGAATAATG TAAAACAGT GTTGGCAATT GGTATCATCA ATGATACTCA 3600
TTTTTAATA ACCAAAGGCA GGGGAAATC ATTTTACTTA TTAATAAATA TTTTATGATG 3660
TGAAAAAAA AAAAAAAA AAAAAAAA
  
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30
 35

A40 Protein sequence
 Gene name: ESTs
 Unigene number: Hs.128899
 Protein Accession #: none found
 Signal sequence: 1-11
 Transmembrane domains: 402-424
 Cellular localization: not determined

40
 45
 50

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1 11 21 31 41 51
| | | | |
MLSGFLMSPS TORRAYTTPG GKLLPWEAST GAHTSRGRGS DRERESRPEA AGLLWDRAAA 60
GEAEKNGRGE PPWIRAOQQ PRPPAGQAP GTAAGGAQDP RLPRGRSRGR VRLPVKPEA 120
SGRQPRGFSO CIPRFPASAS TEKAVPKGTG PPAEDCGDLG APGFRARRRR LLGVAAEGSG 180
PRGRRRGTVS DEARGSPGPR LLGDRPALSG DALSAFVRVP OGALAARPEP HPGTFLRSCS 240
CCWLRCWRRG RGPSEGYCHS WLDAGVWRI GFQCPERFDG GDATICGSGC ALRYCCSSAE 300
ARLDQGGCDN DRQGGAGBPS RADKDGPRRL GRASCLRGQT GDGEGAPPPV RAWQRCSPEB 360
SPKCRQLLRA FPGLLFRARR RGFSSSPRGG PSPLQRPALP IYVFFLIVGS VFAVFIILGS 420
LVAACCCRCI RPKQDPQQR APGGNRLMET IPMIFSASTS RGSSSRQSSST AASSSSSANS 480
GARAPPTRSQ TNCLPEGIN NNVYVAMPIN FSVLNCQQAT QIVPRHQQYL HPPYVGYTVQ 540
HDSVPMTAVP PFMDGLQPGY RQIQSFFPHY NSBQKMPAV TV
  
```

55

A41 DNA SEQUENCE:
 Gene name: ESTs, Weakly similar to JB0350 Anterior gradient-2 [H.sapiens]
 Unigene number: Hs.100686
 Probeset Accession #: AA487468
 Nucleic Acid Accession #: AA487468
 Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

60
 65
 70
 75

```

1 11 21 31 41 51
| | | | |
CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTCTGAGAG AGTCTCTAGA AGACATBATG 60
CTACACTCAG CTTTGGGTCT CTGCTCTTCA CTGCTCACAG TTCTCTCCAA CCTTGCCATT 120
GCAATAAAAA AGGAAAAGAG GCTCTCTCAG ACACCTCTCA GAGGATGGGG AGATGACATC 180
ACTTGGGTAC AAACCTTATG AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240
ATGGTTATTC ATCACCCTGA GATTGTGCAA TACTCTCAAG CACTAAAGAA AGTATTGGCC 300
CAAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTICA TCATGCTAAA CCTTATGCAT 360
GAAACCACTG ATAAGAATTT ATCACTGAT GGGCAATATG TGCTAGAAAT CATGTTGTA 420
GACCTTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA 480
TATGAGCCTC GGGATTACT CCTATTGATA GAAAACATGA AGAAAGCATT AAGACTTATT 540
CAGTCAGAGC TATAAGAGAT GATAGAAAAA AGCCTTCACT TCAAAGAGT CAAATTTTAT 600
GAAGAAACCC TCTGGCACAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTATA 660
TTACTATTTA GTTTTTTAA TGTGTTGCA ATAGTCTTAT TAAATAAAT GTTTTTTAA 720
TCTGAAAAA AAAAAAAA AAAAAAAA
  
```

80

A42 Protein sequence:
 Gene name: ESTs, Weakly similar to JB0350 Anterior gradient-2 [H.sapiens]
 Unigene number: Hs.100686
 Probeset Accession #: AA487468
 Protein Accession #: none found
 Signal sequence: 1-23
 Transmembrane domains: none found
 Cellular localization: secreted

1 11 21 31 41 51
 5 MMLHSAIGLC LLLVTVSSNL AIAIKKCKRP PQTLSRGWGD DITWVQTYEE GLFYAQKSKK 60
 FLMVHHELED CQYSQALKKV PAQNSEIQEM AQNKFMIMNL MRETTDKNLS PDGQYVPRIM 120
 FVDPSLTVRA DIAGRYSNRL YTYEPRDLPL LIENMKKALR LIQSEL

A43 DNA SEQUENCE

Gene name: ATPase, Ca++ transporting, type 2C, member 1
 Unigene number: Rs.106778
 Probeset Accession #: N51919
 Nucleic Acid Accession #: AF189723
 Coding sequence: 1-2712 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 20 ATGATTCCTG TATTGACATC AAAAAAGCA AGTGAATTAC CAGTCAGTGA AGTTGCAAGC 60
 ATTCTCCAAG CTGATCTTCA GAATGGICTA AACAAATGTG AAGTTAGTCA TAGGCGAGCC 120
 TTTCATGGCT GGAATGAGTT TGATATTAGT GAAGATGAGC CACTGTGGAA GAAGTATATT 180
 TCTCAGTTTA AAAATCCCCT TATTATGCTG CTTCTGGCCT CTGCAGTCAT CAGTGTTTTA 240
 25 ATGCATCAGT TTGATGATGC CPTCAGTATC ACTGTGGCAA TACTTATCGT TGTACAGTT 300
 GCCTTTGTTC AGGAATATCG TTCAGAAAAA TCTCTTGAAG AATTGAGTAA ACITGTGCCA 360
 CCAGAAATGCC ATTTGTGTGC TGAAGGAAAA TTGAGCATA CACTTGCCTG AGACTTGTT 420
 CCAGGTGATA CAGTTTGCCT TCTGTGTGGG GATAGAGTTC CTGTGACTT ACGCTTGTT 480
 GAGGCTGTGG ATCTTTCCAT TGATGAGTCC AGCTTGACAG GTGAGACAAC GCCTTGTTCT 540
 AAGGTGACAG CTCCTCAGCC AGCTGCAACT AATGGAGATC TTGCATCGAG AAGTAACATT 600
 30 GCCTTTATGG GAACACTGCT CAGATGTGGC AAAGCAAAGG GTGTGTGCAT TGGAACAGGA 660
 GAAATTTCTG AATTTGGGGA GGTTTTAAAT ATGATGCAAG CAGAAGAGGC ACCAAAAACC 720
 CCTCTGCAGA AGAGCATGGA CCTCTTAGGA AAACAACCTT CCTTTACTC CTTGGGTATA 780
 ATAGGAATCA TCATGTGTGT TGGCTGGTTA CTGGGAAAAG ATATCCTGGA AATGTTTACT 840
 35 ATTAGTGTAA GTTGTGCTGT AGCAGCAATT CCTGAAGGTC TCCCATTTGT GGTACAGTGT 900
 ACGCTAGCTC TTGCTTTAT GAGAATGGTG AAGAAAAGGG CCATTGTGAA AAAGCTGCCT 960
 ATTTGTTGAA CTCTGGGCTG CTGTAATGTG ATTTGTTGAG ATAAAACTGG AACACTGACG 1020
 AAGAAATGAA TGACTGTTAC TCACATATTT ACTTCAGATG GTCTGCATGC TGAGGTTACT 1080
 GGAGTTGGCT ATAATCAATT TGGGGAAGTG ATTTGTTGAT GTGATGTTGT TCATGGATTCT 1140
 40 TATAACCCAG CTGTTAGCAG AATTGTTGAG GCGGGCTGTG TGTGCAATGA TGCTGTAATT 1200
 AGAARCAATA CTCCTAATGG GAAGCCAACA GAAGGGGCTT TAATTGCTCT TGCAATGAAG 1260
 ATGGGTCTTG ATGGACTTCA ACAAGACTAC ATCAGAAAAG CTGAATACCC TTTTAGCTCT 1320
 GAGCAAAAGT GGAATGCTGT TAAGTGTGTA CACCGAACAC AGCAGGACAG ACCAGAGATT 1380
 TGTTTTATGA AAGGTGCTTA CGAACAGTA ATTAAGTACT GTACTACATA CCAGAGCAAA 1440
 45 GGGCAGACCT TGACACTTAC TCAGCAGCAG AGAGATGTGT ACCAACAAGA GAAGGCACGC 1500
 ATGGGCTCAG CCGGACTCAG AGTTCTTGCT TTGGCTTCTG GTCTGAACT GGGACAGCTG 1560
 ACATTTCTTG GCTTGGTGGG AATCATTGAT CCACCTAGAA CTGGTGTGAA AGAAGCTGTT 1620
 ACAACACTCA TGACCTCAGG AGTATCAATA AAAATGATTA CTGGAGATTCT ACAGAGACTC 1680
 GCAGTTGCAA TGCCAGCTCG TCTGGGATTG TATTCCAAAA CTTCOCAGTC AGTCTCAGGA 1740
 50 GAAGAAATAG ATGCAATGGA TGTTTCAGCAG CTTTCACAAA TAGTACCAAA GGTTCAGTA 1800
 TTTTCAGAG CTAGCCCAAG GCACAAGATG AAAATTATTA AGTCGCTACA GAAGAACGGT 1860
 TCAGTTGTAG CCATGACAGG AGATGGAGTA AATGATGCAG TTGCTCTGAA GGCTGCAGAC 1920
 ATGGAGTTG CGATGGGCCA GACTGGTACA GATGTTTGA AAGAGGCAGC AGCATGATC 1980
 CTAGTGCATG ATATTTTCA AACCAATATG TCTGCARTCG AAGAGGGTAA AGGGATTAT 2040
 55 AATAACATTA AAAATTTCTG TAGATTCCAG CTGAGCAGCA GTATAGCAGC ATTAACITTA 2100
 ATCTCATTGG CTACATTAT GAACCTTCTC AATCCTCTCA ATGCCATGCA GATTTTGTG 2160
 ATCAATATTA TTATGGATGG ACCCCCACTC CAGAGCCTTG GAGTGAACCC AGTGGATATA 2220
 GATGTCATTC GTAAACCTCC TCGCAACTGG AAAGACAGCA TTTTACTATA AAACITGATA 2280
 CTTAAATATC TTGTTTCATC AATAATCAAT GTTTGTGGGA CTTTGTGTTGT CTTCTGGGCT 2340
 60 GAGCTACGAG ACAATGTGAT TACACCTCGA GACACAACAA TGACCTTCAC ATGCTTTGTG 2400
 TTTTGTGACA TGTTCAATGC ACTAAGTTCC AGATCCGAGA CCAAGCTCTG GTTTGAGATT 2460
 GGACTCTGCA GTAAATAGAA GTTTTGCTAT GCAGTTCTTG GATCCATCAT GGGACAAATTA 2520
 CTAGTTATTT ACTTTCCTCC GCTACAGAA GTTTTTCAGA CTGAGAGCCT AAGCATACTG 2580
 65 GATCTGTGT TTCTTTTGGG TCTCACCTCA TCAGTGTGCA TAGTGGCAGA AATTATTAAG 2640
 AAGGTTGAAA GGAGCAGGGA AAAGATCCAG AAGCATGTGA GTTCGACATC ATCATCTTTT 2700
 CTTGAAGTAT GA

A44 Protein sequence:

Gene name: ATPase, Ca++ transporting, type 2C, member 1
 Unigene number: Rs.106778
 Probeset Accession #: N51919
 Protein Accession #: AAF27813
 Signal sequence: none found
 Transmembrane domains: 60-82, 86-108, 252-274, 282-304, 757-779, 827-849, 856-878
 Pfam domains: Cation ATPase N [6-83], E1-E2 ATPase [89-324], Hydrolase [328-649], Cation ATPase C [744-889]
 Cellular Localization: not determined

1 11 21 31 41 51
 80 MIPVLTSKKA SELPVSEVAS ILQADLQNL NKCEVSHRA FRGWNEFDIS EDEPLWKKYI 60
 SQFKNPLIML LLASAVISVL MEQFDDAVSI TVAILIVTV AVVQHYRSEK SLEELSKLVP 120
 PECHCVREBK LEHILARDLV PGDTVCLSVG DRVFDLRLF EAVDLSDIES SLTGETTPCS 180
 KVTAPQPAAT NGDILASRNTI AFMGTLVRCG KRGVVIGTG ENSFGEVFK MNQAEAPKT 240
 PLQKSMOLLG KQLSPYSPGI IGIIMLVGWL LGRDILEMPT ISVSLAVAAI PEGLLPIVVTV 300

5	TLALGVMRMV	KKRAIVKKLP	IVETLGCCNV	ICSDKTGTLT	KNEMTVTHIF	TSDGLHAEVT	360
	GVGYNQFGEV	IVDGDVHGF	YNPAVSRIVE	AGCVCNDAVI	RNNTLMGKPT	EGALIALAMK	420
	MGLDGLQQDY	IRKAEYFFSS	EQKWMHVKCV	HRTQQDRPEI	CFMKGAYBQV	IKYCTTYQSK	480
	GQTLTLTQQQ	RDVYQQEKAR	MGSAGLRVLA	LASGPGLGQL	TFLGLVGIID	PPRTGVKEAV	540
	TTLLASGVSI	KMITGDSQET	AVAIASRLGL	YKTSQSQSVG	EEIDAMDVQQ	LSQIVPKVAV	600
	FYRASPRHKM	KIKSLQKNG	SVVAMTGDGV	NDAVALKAAD	IGVAMSGTGT	DVCKEADMT	660
	LVDDDFQTIM	SAIEEGKGIY	NNIKNFVRPQ	LSTSIALLTL	ISLATLMNFP	NPLNAMQLW	720
	INIIMDGPPA	QSLGVEPVDK	DVIRKPPROW	KDSILTKNLI	LKILVSSIII	VCGLTFVFWR	780
10	ELRDNVITFR	DTIMFTCFV	FFDMFNALSS	RSQTKSVFEI	GLCENRMFCY	AVLGSIMGQL	840
	LVYFFPLQK	VQTESLSIL	DLLPILGLTS	SVCIVAEIHK	KVEREREKIQ	KEVSTSSSP	900
	LEV						

A45 DNA sequence

15	Gene name:	ESTs
	Unigene number:	Hs.157601
	Probeset Accession #:	W07459
	Nucleic Acid Accession #:	AC005383
20	Coding Sequence:	328-2751 (underlined sequences correspond to start and stop codons)

	1	11	21	31	41	51	
	GACAGTGTTC	GCGGCTGCAC	CGCTCGGAGG	CTGGGTGACC	CGCGTAGAAG	TGAAGTACTT	60
25	TTTTATTTCG	AGACCTGGGC	CGATGCGGCT	TTAAAAACG	CGAGGGGCTC	TATGCACTTC	120
	CCTGGCGGTA	GTTCTCTCGA	CCTCAGCCGG	GTCGGGTCTG	GCCGCGCTCT	CCCAGGAGAG	180
	ACAAACAGGT	GTCACACGTG	GCAGCCCGGC	CCCGCGCGCC	CCTCCTGTGA	TCCCGTAGCG	240
	CCCCCTGGCC	CGAGCCCGGC	CGGGTCTGT	GAGTAGAGCC	GCCCGGGCAC	CGAGCGCTGG	300
	TGCGCGCTCT	CCTTCGGTGA	TATCAACATG	CCCCCTTTCC	TGTTGCTGGA	GGCGCTCTGT	360
30	GTTTTCCTGT	TTTCCAGAGT	GCCCCATCT	CTCCCTCTCC	AGGAAGTCCA	TGTAAGCMAA	420
	GAADACATCG	GGAAGATTTT	AGCTGCCAGC	AAAATGATGT	GGTGTCTGGC	TGCAGTGGAC	480
	ATCATGTTTC	TGTTAGATCG	GTCTAACAGC	GTCCGGAAAG	GGAGCTTTGA	AAGGTCCAGG	540
	CACCTTGCCA	TCACAGCTCG	TGACGGTCTG	GACATCAGCC	CCGAGAGGGT	CAGAGTGGGA	600
	GCATTCAGT	TCAGTTCCAC	TCCTCATCTG	GAATTCCTCT	TGGATTCAAT	TTCAACCCAA	660
35	CAGGAAGTGA	AGGCAAGAAT	CAAGAGGATG	GTTTTCAAG	GAGGGCGCAC	GGAGACGGAA	720
	CTTGCTCTGA	AATACCTTCT	GCACAGAGGG	TTGCCCTGAG	GCAGAAATGC	TTCTGTGCCC	780
	CAGATCCTCA	TCATCGTCAC	TGATGGGAAG	TCCCAGGGGG	ATGTGSCACT	GCCATCCAGG	840
	CAGCTGAAGG	AAAGGGGTGT	CACCTGTGTT	GCTGTGGGGG	TCAGGTTTCC	CAGGTGGGAG	900
	GAGCTGCATG	CATGCGCCAG	CGAGCCTAGA	GGGCAGCAGC	TGCTGTGTGG	TGAGCAGGTC	960
40	GAGGATGCCA	CCAAACGCTT	CPTCAGCACC	CTCAGCAGCT	CGCCCATCTG	CTCCAGCGCC	1020
	ACGCCAGACT	GCAGGGTCGA	GGCTCACCCC	TGTGAGCACA	GGAGCTGTGA	GATGGTCCGG	1080
	GAGTTGCTCG	GCAATGCCCC	ATGCTGGAGA	GGATCGCGGC	GGAGCTTTGC	GGTGTCTGGT	1140
	GCACACTGTC	CCCTTCTACG	GTGGAGAGAG	GTGTTCTTAA	CCACACCTGC	CACCTGTCTC	1200
	AGGACCACTT	GCCGAGGCCC	CTGTGACTCG	CAGCCCTGCC	AGATGAGAGG	CACATGTGTT	1260
45	CAGGAAGTGA	TGAGCGGCTA	CCAGTGCCCT	TGCCCGCTGG	CCCTTGGAGG	GGAGGCTAAC	1320
	TGTGCGCTGA	AGCTGAGCCT	GGAATGCAGG	GTGCACTTCC	TCTTCTGTCT	GGACAGCTCT	1380
	GCGGGCACCA	CTCGGAGCGC	CTTCCGTGGG	GCCAAAGTCT	TGTTGAAGCG	GTTTGTGCGG	1440
	GCCTGTCTGA	GCGAGGAGCT	TGCGGCCCGA	GTGGGTGTGG	CCACATACAG	CAGGGAGCTG	1500
50	CTGTGTGGGG	TGCTGTGGGG	GGAGTACCCG	GATGTGCTCG	ACCTGTGTCTG	GAGCCTCGAT	1560
	GGCATTCCTT	TCCGTGGTGG	CCCCACCTTG	ACGGGCGAGT	CCCTTGGGCA	GGCGCGCAGG	1620
	CGTGGCTTCG	GGAGCGCCAC	CAGGACAGGC	CAGGACCGGC	CACGTAGAGT	GGTGGTTTGT	1680
	CTCAGTGAAT	CACACTCCGA	GGATGAGGTT	GCGGGCCCGG	CGCTTACCTG	AAGGGCGCGA	1740
	GAGCTGCTCC	TGCTGGGTGT	AGGCAGTGAG	GCTGTGGGGG	CAGAGCTGGA	GGAGATCACA	1800
55	GGCAGGCCAA	AGCATGTGAT	GGTCTACTCG	GATCCTCAGG	ATCTGTTCAA	CCAAATCCCT	1860
	GAGCTGCAGG	GGAGCTGTGT	CAGCCGCGAG	CGGCCAGGGT	GCCGGACACA	AGCCCTGGAC	1920
	CTCGCTTCA	TGTTGACAC	CTCTGCTCA	GTAGGGCCCG	AGAATTTTGC	TCAGATGCAG	1980
	AGCTTTGTGA	GAAGCTGTGC	CCTCCAGTTT	GAGGTGAACC	CTGAGCTGAC	ACAGGTCCGC	2040
	CTGTGTGTGT	ATGCGAGCCA	GGTGCAGACT	GCCTTGGGGC	TGGACACCAA	ACCCACCCCG	2100
60	GCTGCGATGC	TGCGGGCCAT	TAGCCAGGCC	CCCTACCTAG	GTGGGGTGGG	CTCAGCCGGC	2160
	ACCGCTCTGC	TGCACATCTA	TGACAAAGTG	ATGACCGTCC	AGAGGGGTGC	CCGCGCTGGT	2220
	GTCGCCAAGG	CTGTGTGTGT	GCTCACAGGC	GGGAGAGGGC	CAGAGGATGC	AGCCGTTTCT	2280
	GCCCGAAGC	TGAGGAACAA	TGGCATCTCT	GTCTTGGTGG	TGGGCGTGGG	GCCTGTCTTA	2340
	AGTGAGGATC	TGCGAGGCTT	TGCAGGTCCC	CGGATTCCTC	TGATCCACGT	GGCAGCTTAC	2400
65	GCCGACCTGC	GGTACCAACA	GGAGGTGCTC	ATTGAGTGGC	TGTGTGAGGA	AGCCAGCGAG	2460
	CCAGTCAACG	TCTGCAAAAC	CAGCCGCTGC	ATGAATGAGG	GCAGCTGGGT	CCTGCAGAAAT	2520
	GGGAGCTACC	GCTGCAAGTG	TGCGGATGGC	TGGGAGGGCC	CCCACTGCGA	GAACTGTGAG	2580
	TGGAGCTCTT	GCCTGTATG	TGTGAGCCAG	GGATGGATTC	TTGAGACGCC	CCTGAGGCAC	2640
	ATGCTCTCCG	TGCAGGAGGG	CAGCAGCCGT	ACCCCTCCCA	GCAACTACAG	AGAGGGCCCT	2700
70	GGCACTGAAA	TGCTGCTTAC	CTTCTGGAAT	GTCTGTGCCC	CAGGTCTCTA	GAATGTCTGC	2760
	TTCCCGCCGT	GGCCAGGACC	ACTATTTCTA	CTGAGGGAGG	AGGATGTCCC	AACTGCAGCC	2820
	ATGCTGCTTA	GAGACAAGAA	AGCAGCTGAT	GTCAACCCACA	AACGATGTTG	TTGAAAAGTT	2880
	TGATGTGTGA	AGTAAATACC	CACCTTCTGT	ACCTGCTGTG	CCTTGTGTAG	GCTATGTGAT	2940
	CTGCCACCTT	TCCCTTGAGG	ATAAACAGGG	GGTCTGGAAG	ACTTAAATTT	AGCGGCTTGA	3000
75	CGTTCCTTTG	CACACAATCA	ATGCTGCGCA	GAATGTGTTT	GACACAGTAA	TGCCAGCAGG	3060
	AGGCTTTTAC	TGAGGATCTC	TTTGAGCGGC	GAAGGCCACG	GCCTTTCAAG	ATGGAAGACA	3120
	GCAGCTTTTC	CACCTTCCCA	GAGACATCTT	GGATGCATTT	GCATTTGAGT	TGAAAGGGGG	3180
	CTTGAGGGAC	GTTTGTGACT	TCTTGGCGAC	TGCCCTTTTGT	GTGTGGAAGA	GACTTTGAAA	3240
	GGTCTCAGAC	TGAATGTGAC	CAATTAACCA	GCTTGGTTGA	TGATGGGGCA	GGGGCTGAGT	3300
80	TGTTCATGGG	CCAGGTCTGT	GAGGGCCACG	TAAATCGTTT	CTGAGTCTGT	AGCAGTGTCC	3360
	ACCTTGAAGG	TCTTCT					

A45 Protein sequence

Gene name: ESTs

Unigene number: Hs.157601
 Protein Accession #: none found
 Signal sequence: 1-17
 Transmembrane domains: none found
 VGN domains: 49-223; 341-518; 529-706
 EGF domains: 298-333; 715-748
 Cellular Localization: secreted

```

10 1      11      21      31      41      51
    |      |      |      |      |      |
MPPFLLEAV CVFLFSEVPF SLPLQSEVHS KETIGKISAA SKMMWCSAAV DIMFLDGSN 60
SVGKGSFERS KHEAITVCDG LDISPERVRV GAFQFSSTPH LEFPLDSFST QQEVKARIKR 120
MVFKGGRTST ELALKYLLHR GLPGGRNASV PQILIIIVTDG KSGQDVALPS RQLKERGVTV 180
15 FAVGVPRPRW EELEALASEP RGQHVLLAEQ VEDAINGLFS TLSSSAICSS ATPDCRVEAH 240
PCRHRTLEMV RFPAGNAPCH RGSRRTLAVL AAHCPPFYSWK RVFLTHPATC VRTTCPGPCD 300
SQPCQNGGTC VPEGLDGYQC LCPLAFGBEA NCALKLSLEC RVDLLFLDLS SAGITLDGFL 360
RAKVFVRFV RAVLSEDSRA RVGVATYSRE LLVAVPVGEY QDVPLVWSL DGIPFRGPT 420
20 LTGSALROAA ERGFGSATRT GQDRPRRVV LLTSHSEDE VAGPARHARA RELLLLGVS 480
EAVRAELEBI TGSPKHVMVY SDPQDLFNQI PELQGLCSR QRPGRCTQAL DLVFMLOTS 540
SVGFENFAQM QSFVRSCALQ FEVNPDTQV GLVVGSGVQV TAFGLDTKET RAAMLRAISQ 600
APYLGGVGSA GTALLHIYDK VMTVQRGARP GVPEKVVVLT GSGAEDAAV PAQKLNNNGI 660
SVLVVGVGPF LSEGLRLLAG PRDSLIVAA YADLYEYQDV LIEMLCGEAK QFVNLCKPSP 720
CMNBSGCVLQ NGSYRCKCRD GWEGPHCENR EWSSCSVCVS QGWILEYPLR HMAFVQEGSS 780
25 RTPPSNYREG LGTEMVPTFW NVCAPGP

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COLON

30 A47 DNA SEQUENCE:
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
 Unigene number: Hs.100686
 Probeset Accession #: AA487468
 Nucleic Acid Accession #: AA487468
 35 Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

```

40 1      11      21      31      41      51
    |      |      |      |      |      |
CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTCTGAGAG AGTCTCTAGA AGACATGATG 60
CTACACTCAG CTTTGGGTCT CTGCTCTTCT CTCTCACAG TTTCTTCCAA CCTTGGCATT 120
GCAATAAAAA AGCAAAAGAG GCCTCCTCAG ACACCTCTCA GAGGATGGGG AGATGACATC 180
ACTTGGGTAC AAACCTTATG AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240
45 ATGGTTATTC ATCAGCTGGA GGATTGTCTA TACTCTCAAG CACTAAAGAA AGTATTGGCC 300
CAAAATGAAG AAATACRAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360
GAAACCACTG ATAAGAAATT ATCACTGATG GGGCAATATG TGCTAGAAAT CATGTTTGT 420
GACCTTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGTACACA 480
TATGAGGCTC GGGATTATCC CCTATTGATA GAAAACATGA AGAAAGCATT AAGACTTATT 540
50 CAGTCAGAGC TATAAGAGAT GATAGAAAAA AGCCTTCACT TCAGAGAGT CAAATTTTAT 600
GAAGAAACC 1CTGGCACAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTATA 660
TTACTATTTA GTTTTITTA TGTGTTTGCA ATAGTCTTAT TAAATAAAT GTTTTITTA 720
TCTGAAAAAA AAAAAAATA AAAAAAATA

```

55 A48 Protein sequence:
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
 Unigene number: Hs.100686
 Probeset Accession #: AA487468
 Protein Accession #: none found
 60 Signal sequence: 1-23
 Transmembrane domains: none found
 Cellular Localization: secreted

```

65 1      11      21      31      41      51
    |      |      |      |      |      |
MMLHSAALGLC LLVTVSSNL AIAIKGEKRP PQLSRGWD DITWVQTYEB GLFYAQSKK 60
PLWVIHLED CQYSQALKKV PAQNEEIQEM AQNKFIMNL MHTTIDKNLS PDGQYVPRIM 120
70 FVDPSLVRA DIAGRYSNRL YTYERDLFL LIENMKALR LIQSEL

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75 A49 DNA SEQUENCE
 Gene name: G protein-coupled receptor 56
 Unigene number: Hs.6527
 Probeset Accession #: AA478599
 Nucleic Acid Accession #: NM_005682
 Coding sequence: 163-2244 (underlined sequences correspond to start and stop codons)

```

80 1      11      21      31      41      51
    |      |      |      |      |      |
CGGCAGCAGG GTCTCGCTCT GTACACAGG CTGGAGTGCA GTGGTGATG CTTGGCTCAT 60
CGTAACCTCC ACCTCCGGG TCAAGTGAT TCTCATGCT CAGCTCCCG AGTAGCTGG 120
ATTACAGGTG GTGACTTCA AGATGACTC GTCGGAGGA AAATGACTCC CCAGTCTGCTG 180

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	CTGCAGACGA	DACTGTTCT	GCTGAGTCTG	CTCTTCTCTG	TCCAAGGTGC	CCACGGCAGG	240
	GGCCACAGGG	AAGACTTTGG	CTTCTGCAGC	CAGCGGAACC	AGACACACAG	GAGCAGCTTC	300
	CACTACAAAC	CCACACACGA	CCTGCGCATC	TCCATCGAGA	ACTCCGAAGA	GGCCCTCACA	360
5	GTCCATGCCC	CTTTCCCTGC	AGCCCAACCT	GCTTCCCGAT	CCTTCCCTGA	CCCCAGGGGC	420
	CTCTACCACT	TCTGCTCTTA	CTGGAACCGA	CATGCTGGGA	GATTACATCT	TCTCTATGGC	480
	AAGCGTGACT	TCTTGCTGAG	TGACAAAGCC	TCTAGCTTCC	TCTGCTTCCA	GCACCAAGAG	540
	GAGAGCTGG	CTCAGGGGCC	CCCGCTGTTA	GCCACTTCTG	TCACTTCTTG	GTGGAGCCCT	600
	CAGAACATCA	GCTGCCCCAG	TGCCCCCAGC	TTCACCTTCT	CCTTCCACAG	TCTTCCCCAC	660
10	ACGGCCGCTC	ACAATGCCCTC	GGTGGACATG	TGCGAGCTCA	AAAGGGACCT	CCAGCTGCTC	720
	AGCCAGTTCC	TGGAAGCATCC	CCAGAAGGCC	TCAAGGAGGC	CCTGGCTGCG	CCCCGCCAGC	780
	CAGCAGTTCC	AGAGGCTCGA	GTCGAAACCT	ACCTCTGTGA	GATTCAATGG	GGACATGGTG	840
	TCCTTCGAGG	AGGACCGGAT	CAACGCCACG	GTATGGAAGC	TCCAGCCAC	AGCCGGCTTC	900
	CAGGACCTGC	ACATCCACTC	CCGGCAGGAG	GAGGAGCAGA	BCAGATCAT	GGAGTACTCG	960
	GTGCTGCTGC	CTCGAACACT	CTTCCAGAGG	ACGAAAGGCC	GGAGCGGGGA	GGCTGAGAAG	1020
15	AGACTCTTCC	TGCTGCTCTT	CAGCAGCCAA	GCCCTGTTC	AGGACAAGAA	TTCAGCCCAA	1080
	GTCTGGGTG	AGAAGGTCTT	GGGATTGTGT	GTACAGAAAC	CCAAAGTAGC	CAACCTCACG	1140
	GAGCCCGTGG	GTGCTCACTT	CCAGCACCA	CTACAGCCGA	AGAATGTGAC	TCTGCAATGT	1200
	GTGTTCTGGG	TGGAAGACCC	CACATTGAGC	AGCCCGGGGC	ATTGGAGCAG	TGCTGGGTGT	1260
20	GAGACCGTCA	GGAGAGAAGC	CCAAACATCC	TGCTTCTGCA	ACCATTGAC	CTACTTTGCA	1320
	GTGCTGATGG	TCTCTCTGGT	GGAGGTGGAC	GCGGTGCACA	AGCACTACCT	GAGCTCTCTC	1380
	TCTTACGTGG	GCTGTGTGCT	CTCTGCCCTG	GCCCTGCTTG	TCAACATTGC	CGCTTACCTC	1440
	TGCTCCAGGG	GTGCTGCTCC	GTGCAAGGAG	AAACCTCGGG	ACTACACCAT	CAGGTGTCAC	1500
	ATGAACCTGC	TGCTGGCCGT	CTTCTGCTG	GACACGAGCT	TCTGCTCTAG	CGAGCCGGTG	1560
25	GCCTTGACAG	GCTCTGAGGC	TGCTGCGGCA	GCCAGTGCCA	TCTTCTTGCA	CTTCTCTCTG	1620
	CTCACTCTGC	TTTCTGTGAT	GGGCTCGAG	GGGTACAACC	TCTACCGACT	CGTGTGGGAT	1680
	GTCTTTGGCA	CTATGTCTCC	TGGCTACCTA	CTCAAGCTGA	GCGCCATGGG	CTGGGGCTTC	1740
	CCCATCTTTC	TGGTGAAGCT	GGTGGCCCTG	GTGGATGTGG	ACAACATATG	CCCATCATC	1800
	TTGCTGTGTC	ATAGGACTCC	AGAGGGCGTC	ATCTACCTTT	CCATGTGCTG	GATCGGGGAC	1860
30	TCCTTGCTCA	GCTACATCAC	CAACCTGGGC	CTCTTCAGCC	TGGTGTCTCT	GTTCACATGT	1920
	GCCATGCTAG	CCACCATGGT	GGTGCAATGC	CTGGGCTGCG	GCCCCACAC	CCAAAAGTGG	1980
	TCACATGTGC	TGACACTGCT	GGGCTCAGC	CTGTCTCTTG	GCTTGGCTTG	GGCTTGTATC	2040
	TTCTTCTCTT	TGCTTCTGG	CACCTTCCAG	CTTGTCTGCT	TCTACCTTTT	CAGCATCATC	2100
	ACCTCTCTTC	AAGGCTTCT	CATCTTCATC	TGCTACTGGT	CCATGCGGCT	GCAGGCCCGG	2160
35	GGTGGCCCTT	CCCTCTGAA	GAGCAACTCA	GACTGCGCCA	GGCTTCCCAT	CAGCTCGGGC	2220
	AGCACTCTGT	CCAGCCGAT	CTAGGCTTCC	AGCCCACTCG	CCCATGTGAT	GAAGCAGAGA	2280
	TGGGCGCTCG	TGCAACACTG	CCTGTGGGCC	CCGAGCCAGG	CCAGGCCCA	GGCCAGTCAG	2340
	CCGCAACTTT	TGGAAGCCG	AAAGACCAAG	GAGAGATGGG	CGTTTGGCAT	GGTGGACGGA	2400
	CTCCCGGGGC	TGGGCTTTT	GAATGGGCT	TGGGACTTAC	TGGGCTTCTA	CTCAGCTCCC	2460
40	ACGGGACTCA	GAAGTGGCGC	GCAATGCTGC	CTAGGGTACT	GTCCCAACAT	CTGTCTCAAC	2520
	CCAGCTGGAG	GCGCTGTCTC	TCCTTACAAC	CCCTGGGCCC	AGCTCATATG	CTGGGGGCCA	2580
	GGCTTGGAT	CTTGAAGGTC	TGGCACATCC	TAAATCTGT	GCCCCCTGCT	GGGACAGAAA	2640
	TGTTGGCTCA	GTGCTCTCT	CTCTGTGCT	CACCTTGGG	GCACTCTGCA	TCTCTGTCA	2700
	TTTAACTCTC	AGGTGGCACC	CAGGCGCAAT	GGGGCCAGG	GCAAGCTTTC	AGGGCCAGAG	2760
45	CCCTGGCGGA	GGAGAGGCC	TTTGCCAGGA	GCACAGCAGC	AGCTGCGCTA	CCTCTGAGCC	2820

A50 Protein sequence

50	Gene name:	G protein-coupled receptor 56
	Unigene number:	Hs.6527
	Protein Accession #:	NM_005682.1
	Signal sequence:	1-26
	GPS domain:	342-394
55	Pfam domain:	7tm_2[400-665]
	Transmembrane domains:	410-432, 446-468, 482-504, 517-539, 575-597, 608-630, 638-659
	Cellular localization:	plasma membrane

60	1	11	21	31	41	51	
	MTPTQLLQTT	LFLLSLLPLV	QGAHGRGHR	DFRCSQRNQ	THRSSLYKPK	TPDLRISIEH	60
	SSEALTVHAP	FPAHPASRS	FPDPRGLYHF	CLYWNRRAGR	LHLLYGRDF	LLSDKASSLL	120
	CFQDEESLA	QGPPELLTST	TSWSPQNTS	LPSAASFTFS	FHSPPHTAAH	NASVDMCEBK	180
65	RDLQLLSQFL	KHPQKASRR	SAAPASQQLQ	SLESKLTSVR	FMGDMVSPFE	DRINATVWKL	240
	QPTAGLQDLH	IHSRQREBQS	HIMBYSVLLP	RTLPORTKGR	SGEAKRLLLL	VDFSSQALFQ	300
	DKNSSQVLGE	KVLGIUVQNT	KVANLTSPVV	LTFQEQQLQPK	NVTLCQVFWV	EDPTLSSPGE	360
	WSSAGCTFVR	RETQTSCEFN	HLTYFAVLNV	SSVEVDAVHK	HYLSLLSYVG	CVVSALACLIV	420
	TIAAYLCGRV	PLPCRRKPRD	YTIKVRMNL	LAVFLLDTEF	LLSEFVALTG	SEAGCRASAI	480
70	FLHPSLLTCL	SHMGLGYNL	YRLVVEVFGT	YVPGYLLKLS	AMGWGFPIFL	VTLVALVDVD	540
	NYGPILLAVE	RTPEGVIYPS	MCWIRDSLVS	YITNLGLFSL	VFLNMAMLA	TMVVQILRLR	600
	PHTQKWSHVL	TLLGLSLVLG	LPWALIFFSF	ASGTFQLVVL	YLFSLIITSFQ	GFLIFIWYNS	660
	MRLQARGGPS	PLKMSDCAR	LPISGGSTSS	SHI			

A51 DNA SEQUENCE

75	Gene name:	Hypothetical protein FLJ20063
	Unigene number:	Hs.5940
	Probeset Accession #:	AA053660
	Nucleic Acid Accession #:	AA053660
80	Coding sequence:	218-1360 (underlined sequences correspond to start and stop codons)

1	11	21	31	41	51	
CCCCATGAC	TTTGATACAGC	TACTTCACTG	CTTCCCCCA	ATTAGTACAC	ATAGTCTCTC	60

5	CACAAATTCCT	ACACCTGCTC	CCCCATAAT	CAGTACACAT	AGTTCTCTCA	CAATTCCTAT	120
	ACCTACTGCT	GCAGACAGTG	AGTCAACAC	AAATGTAAAT	TCATTAGCTA	CCTCTGACAT	180
	AATCACCGCT	TCATCTCCAA	ATGATGGATT	AATCACAAATG	GTTCCTTCTG	AAACACMAAG	240
	TAACAATGAA	ATGTCCCCCA	CCACAGAAGA	CAATCAATCA	TCAGGGCCCT	CCACTGGCAC	300
	CGCTTTATTG	GAGACCCAGCA	COCTAAACAG	CACAGGTCCC	AGCAATCCTT	GCCAAAGATGA	360
	TCCCTGTGCA	GATAATTCGT	TATGTGTAA	GCTGCATAAT	ACAAGTTTTT	GCTGTGTATT	420
	AGAAGGGTAT	TACTACAAC	CTTCTACATG	TAAGAAAGGA	AAGGTATTC	CTGGGAAGAT	480
	TTGATGACA	GTATCAGAAA	CATTTGACCC	AGAAGAGAAA	CATTCCATGG	CCTATCAAGA	540
10	CTTGATAGT	GAAATTACTA	GCTTGTTTAA	AGATGTATTT	GGCAGATCTG	TTTATGGACA	600
	GACTGTAAAT	CTTACTGTAA	GCACATCTCT	GTCAACAGGA	TCTGAAATGC	GTGCTGATGA	660
	CAAGTTTGT	GATGTAAACRA	TAGTAACAAT	TTTGGCAGAA	ACCACAAATG	ACAATGAGAA	720
	GACTGTGACT	CAGAAATTA	ATAAAGCAAT	TAGAAGTAGC	TCAAGCAACT	TTCTAAACTA	780
	TGATTTGACC	CTTCGGGTGG	ATTATATATG	CTGTAACCAAG	ACTGCGGATG	ACTGCCTCAA	840
15	TGGTTTACGA	TGCAATTGCA	AATCTGACCT	GCAAAGGCCT	AACCCACAGA	GCCCTTTCTG	900
	CGTTGCTTCC	AGTCTCAAGT	GTCTGATGTC	CTGCAACGCA	CAGCACAGGC	AATGCTTAAT	960
	AAAGAAGAGT	GGTGGGGCCC	CTGAGTGTGC	GTGCGTGCCC	GGCTACCCAG	AAGATGCTAA	1020
	TGGGAACCTG	CAGAAAGTGC	CATTGGGCTA	CAGTGGACTC	GACTGTAAAG	ACAAATTTCA	1080
	GCTGATCCTC	ACTATTGTGG	GCACCATCGC	TGGCATTGTC	ATTCTCAGCA	TGATAATTGC	1140
20	ATTGATTGTC	ACAGCAAGAT	CAAATAACRA	AACGAAGCAT	ATTGAAGAAG	AGAATCTGAT	1200
	TGACCAAGAC	TTTCAAAATC	TAAAACTGCG	GTGACAGGCG	TTCAACCAATC	TTGGAGCAGA	1260
	AGGGAGCGTC	TTTCTTAAGG	TCAGGATAAC	GGCCTCCAGA	GACAGCCAGA	TGCAAAATCC	1320
	CTATTTCAAG	CACAGCAGCA	TGCCCCGCC	TGACTATTAG	AATCATAAGA	ATGTGGAACC	1380
	CGCCATGGCC	CCCAACCAAT	GTACAAGCTA	TTATTTAGAG	TGTTTAGAAA	GACTGATGGA	1440
25	GAAGTGAGCA	CCAGTAAGGA	TCGGGCTCC	GGGGTTTTTC	TTCCATCTGA	CATCTGCCAG	1500
	CCTCTCTGAA	TGGAAGTTGT	GAATGTTTGC	AACGAATCCA	GCTCACTTGC	TAAATAAGAA	1560
	TCTATGACAT	TAAATGTAGT	AGATGCTATT	AGCGCTTGTG	AGAGAGGTGG	TTTCTTCAA	1620
	TCAGTACAAA	CTAGTAGAC	AATGGTTAGG	GTGTTTTTCT	TAAATCTTTT	CCTGGTAGGG	1680
	CAACAAGAAC	CATTTCCAAT	CTAGAGGAAA	GCTCCCCAGC	ATTGCTTGCT	CCTGGGCAAA	1740
30	CATTGCTCTT	GAGTTAAGTG	ACCTAATTCC	CCTGGGAGAC	ATAAGCATCA	ACTGTGGAGG	1800
	TCCGAGGGGA	TGAGAAGGGA	TACCCACCAT	CTTCAAGGG	TCACAAGCTC	ACTCTCTGAC	1860
	AAGTCAGAA	AGGGACACTG	CTTCTATCCC	TCCATGGAG	AGATTCTGGC	AACCTTTGAA	1920
	CAGCCACAG	CTTGCAACCT	AGCCTCAACC	AAGAAGACTG	GAAAGAGACA	TATCTCTCAG	1980
	CTTTTTCAGG	AGGCGTCCCT	GGGAATCCAG	GAACTTTTTG	ATGCTAATTA	GAAGGCTCTG	2040
35	ACTTAAATATG	TCCACTATGG	GGTGCACTCT	ACAGTTTTTG	AAATGCTTAGG	AGGCAGAGG	2100
	GGCAGAGAGT	AAAAACATC	ACCTGGTAGA	AGGAAGAGAG	GCAAGGAAA	CTGGGTGGGG	2160
	AGGATCAATT	AGAGAGGAGG	CACCTGGGAT	CCACCTCTTT	CCTTAGGTCC	CCTCCTCCAT	2220
	CAGCAAGGGA	GCACCTCTCT	AATCATGCCC	TCCCGAAGAC	TGGCTGGGAG	AAGGTTTAAA	2280
	AACAAAAAAT	CCAGGAGTAA	GAGCCTTAGG	TCAGTTTGAA	ATTGGAGACA	AATGTCTCTG	2340
40	CAAAGGGTGC	GAGAGGGAGC	TGTGCTCAG	GAGTCCAGCC	GTCCAGCCTC	GGGGTGTAGG	2400
	TTTCTGAGGT	GTGCCATTGG	GGCCTCAGCC	TTCTCTGGTG	ACAGAGGCTC	AGCTGTGGCC	2460
	ACCAACACAC	AACCAACAC	ACACAACAC	ACACAACAA	GGGGGCAACC	ACATCCAGTA	2520
	CAGCTTTTAT	CAAATGTTAT	TAGTGCTCTT	TTTATTTTCT	AATGCCCTGT	CCTCTTAAAA	2580
45	GTATTTTAT	TTGTTATTAT	TATTTGTTCT	TGACTGTAA	TTGTGAATGG	TAAATCAATA	2640
	AAGTGCCCTT	GTATAGTGT	GAATAAAAA	AAAAAATAAA	AAAAAATAAA	A	

A52 Protein sequence:

50	Gene name:	Hypothetical protein FLJ20063
	Unigene number:	Hs.5940
	Probeset Accession #:	AA053660
	Protein Accession #:	none found
	Signal sequence:	none found
55	Transmembrane domains:	289-311
	EGF domain:	45-74
	SEA domain:	80-196
	Cellular Localization:	plasma membrane

60	1	11	21	31	41	51	
	MVPSETQSMN	EMSPITTEDNQ	SSGPPTGTAL	LETSTLNSTG	PENPCQDDPC	ADNSLCVKLH	60
	NTSFCLCLEG	YYNNSSTCKK	GKVPFGKISV	TVSETTDPES	KHSMAYQDLR	SRITSLFKDV	120
	FGTSVYGQTV	ILTVSTSLSP	RSEMRADDKF	VDVTIVTILA	ETTSNDEKTV	TEKINKAIRS	180
65	SSSNFLNYDL	TLRCQVYGCN	QTADDCLNGL	ACDCKSDLQR	ENFQSPFCVA	SSLKCPDACH	240
	AQHKQCLIKK	SGGAPEACV	PQYQEDANGN	CQKCAFQYSG	LDCCKDFQLI	LTIVGTIAGI	300
	VILSNIIALI	VTARSMNKTK	HIEKENLIDE	DFQNLKLRST	GETNLGAREG	VFFKVRITAS	360
	RDSQMNPYS	RHSMPRPDY					

A53 DNA SEQUENCE

70	Gene name:	TMPS83a
	Unigene number:	Hs.298241
	Probeset Accession #:	AI538613
	Nucleic Acid Accession #:	AB038157
75	Coding sequence:	202-1566 (underlined sequences correspond to start and stop codons)

80	1	11	21	31	41	51	
	ACCGGGCACC	GGACGGCTCG	GCTACTTTCG	TTCTTAATTA	GGTCATGCC	GTGTGAGCCA	60
	GGAAAGGGCT	GTGTTTATGG	GAAGCCAGTA	ACACTGTGGC	CTACTATCTC	TTCCGTGGTG	120
	CCATCTACAT	TTTTGGGACT	CGGGAATTAT	GAGGTAGAGG	TGGAGCGGGA	GCCGGATGTC	180
	AGAGGTCTCG	AAATAGTCAC	CATGGGGGAA	AATGATCCGC	CTGCTGTGTA	AGCCCCCTTC	240

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TCATTCGGAT CGCTTTTGG CCTTGATGAT TTGAAAATAA GTCCCTGTTGC ACCAGATGCA 300
GATGCTGTTG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTTCC AATCATCGTC 360
ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTCGACTGC 420
TCAGGGAAAGT ACAGATGTGC CTTATCCCTT AAGTGATATG AGCTGATAGC TCGATGTGAC 480
GGAGTCTCGG ATTGCAAGA CGGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540
AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGAAGA CCATGTGCTC CGATGACTGG 600
AAGGGTCACT ACGCAAAATG TGCCTGTGCC CAACTGGGTT TCCCAAGCTA TGTGAGTTCA 660
GATAACCTCA GAGTGAGCTC GCTGGAGGGG CAGTTCCGGG AGGAGTTTGT GTCCATCGAT 720
CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780
TGTGCCCTCG GCCACGTGGT TACCTTGCAG TGCACAGCCT GTGTCATAG AAGGGGCTAC 840
AGCTACGCA TCGTGGGTGG AACATGTGCC TTGCTCTGCG AGTGGCCCTG GCAGGCCAGC 900
CTTCAGTTCC AGGGCTACCA CCTGTGCGGG GGCTCTGTCA TCACGCCCTT GTGGATCATC 960
ACTGTGTCAC ACTGTGTTTA TGACTTGTAC CTCCCAAGT CATGGACCAT CCAGGTGGGT 1020
CTAGTTTCCC TGTGGACAA TCCAGCCCCA TCCCACTTGG TGGAGAAGAT TGTCTACCAC 1080
AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GGCAGGGCCA 1140
CTCAAGTTCA ATGAATGAT CCAGCCTGTG TGCTTCCCCA ACTCTGAAGA GAATCTCCCC 1200
GATGGAAGA TGTGCTGGAC GTCAAGATGG GGGGCCACAG AGGATGGAGC AGGTGAAGCC 1260
TCOCCGTGCC TGAAGCACGC GGCCTGCTCT TTGATTTCCA ACAAGATCTG CAACCCAGAG 1320
GACGTGTACG GTGGCATCAT CTCCCTCTCC ATGCTCTGGG CGGGCTACCT GACGGGTGGC 1380
GTGGACAGCT GCCAGGGGGA CAGCGGGGGG CCGCTGGTGT GTCAAGAGAG GAGGCTGTGG 1440
AAGTTAGTGG GAGCGACGAG CTTTGGCATC GGCTGCGCAG AGGTGAACAA GCCTGGGGTG 1500
TACACCCGTG TCACCTCTCT CCTGGACTGG ATCCACGAGC AGATGGAGAG AGACCTAAAA 1560
ACCTGAAGAG GAAGGGGACA AGTATGCCAC TGAGTTCTCG AGGTGATGAA GACAGCCCGA 1620
TCCTCCCTCG GACTCCCTGG TAGGAACCTB CACACGAGCA GACACCCCTG GAGCTCTGAG 1680
TTCCGGCACC AGTAGCAGGC CGAAGAGAG CACCCCTCCA TCTGATTTCCA GCACAACCTT 1740
CAAGCTGCTT TTGTGTTTTT GTTTTTTTGA GGTGGAGTCT CGCTCTGTTG CCCAGGCTGG 1800
AGTGCAGTGG CGAATCCCTT GCTCACTGCA GCCTCCGCTT CCCTGGTTCA AGCGATTCTC 1860
TTGCCCTCAG TTCCCCAGTA GCTGGGACCA CAGGTGCCCG CCACCAACAC CAACTAATT 1920
TTGTATTTTT AGTAGAGACA GGGTTTCACC ATGTTGGCCA GCTGCTCTC AAACCCCTGA 1980
CCTCAAATGA TGTGCTGCTC TCAGCCTCCC ACAGTGTCTG GATTACAGGC ATGGGCCACC 2040
AGCCTAGGCC TCACGCTCCT TTCTGATCTT CACTAAGAAC AAAAGAAGCA GCAACTTGCA 2100
AGGGCCGCCCT TTCCCACTGG TCCATCTGGT TTTCTCTCCA GGGGTCTTGC AAAATTCCTG 2160
ACBAGATAAG CAGTATGTGT ACCTCACGTC CAAAGCCACC AACAGCCACT CAGAAAAGAC 2220
GCACCAAGCC AGAAGTGACG AACTGACGTC ACTGCAAGT TTCTCTCTA GGGACCAAG 2280
CCAAAACCCAC CCTTTCTACT TCCAAGACTT ATTTTCACAT GTGGGGAGGT TAATCTAGGA 2340
ATGACTCGTT TAAGGCTTAT TTTCATGATT TCTTTGTAGC ATTTGGTGCT TGACGTATTA 2400
TGTGCTTTG ATTCCAAATA ATATGTTTCC TTCCCTCAAA AAAAAAATAA AAAAAAATAA 2460
AAAAAAA

A54 Protein sequence:

Gene name: TMFRSS3a
Unigene number: Hs.298241
Probeset Accession #: AI538613
Protein Accession #: BAB20077
Signal sequence: none found
Transmembrane domains: 43-65, 239-261
Tryp_SPC domain: 216-444
Cellular Localization: plasma membrane

50
55
60

1 11 21 31 41 51
MGENDPPAVE APFSFRSLFG LDDLKISFVA PDADAVAAQI LSLLPLKFFP IIVIGIIALI 60
LALAIGLGIH FDCGKYRCR SSFKCIELIA RCDGVSDCED GEDEYRCVRV GGNNAVILQVF 120
TAASWXTMCS DDWKGHYANV ACAQLGFPSY VSSDNLKRVSS LBGQFREEFV SIDHLLPDK 180
VTALHHSVIV REGCASHGVV TLQCTACBHR RGYSSRIVGG NMSLLSQWFW QASLQFQGYH 240
LCGGSVITPL WIITAARCVY DLYLPEKSWTI QVGLVSDLDN PAPSHLVEKI VYHSRYKPKR 300
LGNDLALMKL AGPLTFNEMI QPVCLFNSBE MFPGDKVCWT SGWGATEDGA GDASFVLEHA 360
AVPLISNKKC MERDVYGGII SPSSMLCAGYL TGGVDSQGD SGGPLVCQER RLWXLVWATS 420
PGIGCAEVNK PGVTRVTSF LDWHEQMER DLRT

A55 DNA SEQUENCE

Gene name: Putative G protein-coupled receptor GPCR150
Unigene number: Hs.97101
Probeset Accession #: AA215333
Nucleic Acid Accession #: NM_014373
Coding sequence: 322-1338 (underlined sequences correspond to start and stop codons)

70
75
80

1 11 21 31 41 51
GTGGCTCGA GGTGGTGGCA GGGCCGCCCC CTGCACTCCB GAGACGAACG CACGGACCGG 60
GCCTCCGGAG GCGAGTTCGG CTGGAAGGAA CCGCTCTCCG TTGCTCTTAC ACTTGCACAA 120
ATGTCCTCGA GCTTACTCAC ATAGCATATT GGTATATCAA AATGAAATGC AAGGAACCAA 180
AAATAACATA ATTGAAGGCA GTAAAAGTGA AATTAATAG GAAGATCATC AGTCAAGGAA 240
GACCACTGG AGAGGACAGA AATGAAGCA GTGTTTATC ATGTGTATT TTTTCAAGT 300
TCTTGAAAT TAACTAATAA TATGACTGCT CTCTCTTAC AGAAGTCTC TTTTCACTAC 360
CAGTACGTC AAACAAACCA GCGCTTAGAC GTTAACATC TGCTATTCTT GATCATACTT 420
GGGAAATAT TATTAAATAT CCTTACACTA GGAATGAGAA GAAAAACAC CTGTCAAAAT 480
TTATGGAAT ATTTTTCAT TTCACTAGTA TTGTTGATC TTTTACTTTT GGTAAACATT 540
TCCATTATAT TGTATTTCAG GGATTTGTA CTTTAAAGCA TTAGGTTTAC TAAATACCAC 600
ATCTGCCAT TTAACCAAT TATTTCCCTT ACTTATGGCT TTTTGCATTA TCCAGTTTTC 660
CTGACAGCTT GTATAGATTA TTGCTGAAT TTCTCAAAA CAACCAAGCT TTTATTAAAG 720
TGTCAAAAT TATTTATTT CTTTACAGTA ATTTTAAATT GGATTTCACT CTTTCTTATT 780

5 GTTTTGGGAG ACCCAGCCAT CTACCAAGGC CTGAAGGCAC AGAATGCITA TTCTCGTCAC 840
 TGTCTTTTCT ATGTACGCAT TCAGAGTTAC TGGCTGTCTAT TTTTCATGGT GATGATTTTA 900
 TTGTAGCTTT TCATAACCTG TTGGGAAGAA GTTACTACTT TGGTACAGGC TATCAGGATA 960
 ACTTCCTATA TGAATGAAC TATCTTATAT TTTCTTTTTC CATCCCACTC CAGTTATACT 1020
 GTGAGATCTA AAAAATATAT CTATCCCAAG CTCATTGTCT GTTTTCTCAG TACCTGGTTA 1080
 CCTATTGTAC TACTTCAGGT AATCATTGTT TTAATTAAAG TTCAGATTCC AGCATATATT 1140
 GAGATGAATA TTCCCTGGTT ATACTTTGTC AATAGTTTTC TCATTGCTAC AGTGTATTGG 1200
 TTTAATTGTC ACAAGCTTAA TTTAAAGAC ATTGGATTAC CTTTGGATCC ATTTGTCAAC 1260
 TGGAAAGTCT GCTTCATTCC ACTTACAAAT CCAATCTTTC AGCAAATTGA AAAGCCTATA 1320
 10 TCATAATGA TTTGTAAATA TTATTAATTA AAAGTTACAG CTGTCAATAG ATCATAATTT 1380
 TATGAACAGA AAGAACTCAG GACATATTAA AAAATAAACT GAACTAAAAC AACTTTTGCC 1440
 CCCTGACTGA TAGCATTTC GAATGTGTCT TTTGAAGGGC TATACCAGTT ATTAAATAGT 1500
 GTTTTATTTT AAAACAAAA TAATTCCAAAG AAGTTTTTAT AGTTATTCAG GCACACTATA 1560
 TTACAAATAT TACTTTGTTA TTAACACAAA AAGTCAATAG AGTTAACATT TGGCTATATA 1620
 15 GATGTTTGTG TTACTCAAAA AAACACTGAG ATGCAAACTG TTATGTAAAT CTGAGATTTC 1680
 ACRGACAACT TTAAGATATC AACCTAAACA TTTTATTAA ATGTTCAAT GTAAACAGA 1740
 AAAAAAAA

20 A56 Protein sequence
 Gene name: Putative G protein-coupled receptor GPCR150
 Unigene number: Hs.97101
 Protein Accession #: NP_055188
 Signal sequence: none found
 25 Transmembrane domains: 23-45, 59-81, 97-119, 138-160, 184-206, 241-263, 276-297
 Cellular Localization: plasma membrane

30 1 11 21 31 41 51
 | | | | |
 MTALESSENC FQYQLRQTNQ PLDVNYLLFL IILGKYLNI LTLGMRKNT CQNFMEYFCI 60
 SLAFVDLLL VMSIILYFR DFVLLSIRFT KYHICLPQI ISFTYGLFHY PVFLTACIDY 120
 CLNPSKTKL SPKCKQLFYF FTVILINISV LAVVLGDPAL YQSLKAQNAV SRKCFYVSI 180
 QSYWLSFMV MILEVAFITC WEEVTLVQA IRITSYNNET ILYPFRSSSE SYTVRSKKIF 240
 35 LSKLIVCFIS TWLPPVLLQV IIVLLKVGIP AYIEMNIPWL YFVNSPLIAT VYWFNCHRLN 300
 LKDIGLPLDP FVNKKCCFIP LTIPLNEQIE KPISIMIC

40 A57 DNA SEQUENCE
 Gene name: ESTs, Weakly similar to CGH07L collagen alpha 1(III) chain precursor [H.sapiens]
 Unigene number: Hs.19322
 Probeset Accession #: AA088458
 Nucleic Acid Accession #: AA088458
 Coding sequence: 862-1995 (underlined sequences correspond to start and stop codons)

45 1 11 21 31 41 51
 | | | | |
 GCCCTTGGAC ACTGACATGG ACTGAAGGAG TAGAATGGAG CAGGAGGACA CTGACATGGA 60
 CTGAAGAAAA AGGAGCTTGA GCAGGAGAG GAGGTGCTGC TGCAGGTTT GGAGATGATG 120
 50 GCGCGGGGCC GCGACTGGTA CCAGCAGCAG CTGCAACGAG TGCAGGAGCG CCAGCGCCGC 180
 CTGGGCCAGA GCAGAGCCAG CCGCCACTTT GGGGCTGCAG GAGGCCCCCG CTTACTGGGG 240
 CGGCTACTGC CCAAGGTACA AGAGGTGGCC CGGTGCTTGG GGGAGCTGCT GGCTGCAGCC 300
 TGTGCCAGCC GGGCCCTGCC CCGTCTCTCC TCGGGGCCCG CTTGCCCTGC CTTGACCTCC 360
 55 ACCTCACCCC CGGTCTGGCA GCAGCAGACC ATCTCATGCT TGAAGGAGCA GAACGAGCTC 420
 CTCACCCAGG AGGTGACCGA GAAGAGTGAG CGCATCAAGC AGCTGGAGCA GGAGAAAGTC 480
 GCGCTCATTA AGCAGCTGTT TGAGGCCCGC GCGCTGAGCC AGCAGGACGG GGGACCTCTG 540
 GATTCCACCT TCATCTAGTC CTGTGGGGCC GGTGGGGCCC CAGGGGCCAG CTTGGCACTC 600
 AGCCCTTCGA GGGTGGGCGC CCATCGGCAC CCACCCCTCTC TGGCTGGAGA CCCCCGGCAG 660
 60 GCCCAGGCAC AGTCCCGGAG TGGGCGCCTT CTTGCCGCCC TTGCCAGATG GGCYCCCCAG 720
 GCGTCTCCCG GGTGCTGCCC CGCACCAGAG GCTTGACTCC GTTTGGCTC CTGGTTGTTG 780
 ACATGGGCTG GGGGCTCTCT TGAGTCCGCA TAGTCCGCG CTACTACTGG CCGCTGTGAG 840
 TGGACAGTGG GGTACCCCTC CATGAGTTAG GGTCCCGCCG TTTCCAGCGG TGCCGCCCCTG 900
 GGTCCCATCT TCAGGGAAG GCATGCCCCA CGCCAGGCTG CACTTCCAC AACCGGCAGC 960
 65 AGAGGCGCGG GGGCGGCTCC GAOCGCGGTC CAGGGGCAGC TTCCCGCTCA ACCAGGGCAC 1020
 CAGGACGAGG TGGCTGTAGC TCGGACGGAC GGAAGTAGAT GGAGGGGGTG GGGAGGGCCT 1080
 GTAAAGCGGG GGTGCTGCCC TGGCTGGGGA GCGCCAGGGA TAGCGGTGCG ACTTCAGGTT 1140
 CTGGCCAGAG CTGAGGAGCC CTGGCTGCAG CGGATCGGCA GCGCCGGGTG GCGAGAGCTT 1200
 GGCCTGCATG TGCTCTCCAC AGACCCCTGG GTGATGGCTT TCCCTCTCTT GGCCTGGGAG 1260
 70 TTGGCCCAAG TTGAGTCCCA CACAACATCC TGTGAGCTTG GCTCCCCAGG AGGGCCCCCA 1320
 GACAGCTCCC AGGCACGTCA TAGGCAAGGC CTGTTTCCCC CGACTCAGGA TTTCCAAGGC 1380
 CTGGGGTCTT GCTCACCCCC CTTTGCTCTC AGGCCCGGCC TGTCCCCAGG TTTCACTGCT 1440
 GAGAGGCCAC CTCCCTCAGC CAGGAAACAG GAGAAACCCC AGGGTACAGG AGGAGGCTGG 1500
 GGCAGGTCCC CTGGGTGCTC ACTCCCTCAG CCGCTGCCCA GGCCTACTCC CGCTGGTCTC 1560
 75 GGAGTACGCA CTGGTGGGGG GGCCCTGCTC AGCCCAACCT GGAGGGTCCC AGTGTACCA 1620
 GAACCAAGGG CACGGCAACA GCATCGATGG GTTCTGCAGC CAGGGGCCCT CGATGCGGGG 1680
 TCAGTGTGTE TGGGGGCGAG GGCCTCCGAT GCGGGGTCAG TGGTGGGGGG GCGCAGGGCC 1740
 CCGATGTCGG GGTCACTGCG TGGGGGGGCG AGGGGCCCTT CGTGTCCAGG GCACCTTTGGT 1800
 ACACGTGCCC ACAAGGCACC TGTCTCAGAG GAGGGGCCCT GGCAGGCAGC GTGGCACTC 1860
 80 CCTCCGAGAG CCGAGCTCCA TGCTAACCTG CCGACAGCAA CCGCACAGAG CCACATTCCC 1920
 TGCTGCACCT GGTCTGCAGG GGTGTCCCAG GACAGGCCCA AGTCAGGCCA GCATGCAGCT 1980
 GCCCTCTTAC CTTGAAGATG GAGATGGGCT TTCCAGGGGA CATAAGGATG TCAGGCTTGG 2040
 ACCTCTTGGG CAGGAAAGGG TGCAAGTCTT GAGGGCCTGT GCGCCACAGC CCGCAGCACCC 2100
 AGGTGGACTG CAGCGCAGTG GGTGGGCCAG TGGCAGCCAG GAGAAAGCCC CCGCTCAGCA 2160
 GCGTGGGGTC TGCCCAACAG GGCTCCCCCA GGTCTGCCTT TGAGGGTGGC TGCCATGCCC 2220

5	TGGGGGATCC	TGGCATCTTT	ACTGGACTGG	AAGCAGGAGA	CAGAACAGTG	TCTGTCCCGG	2280
	GGTGACTTCA	TCAGGAGACC	GCCCACATAG	AGCTGGACCC	CGCAGCTGAA	GCGGAAATGT	2340
	GAGACAGGCT	GGCACCCTCG	GAAAACTGCG	CTTTGAGCCT	TGGTGTTCGG	TGCAGGTGTA	2400
	AAAGAAATAG	GTCTCCCGAG	TTTACAGCTT	GAATCAGGCG	TAGTGAATGG	CCCTGGAGAC	2460
	CACGAGGGGA	GAATTTAAAG	GCCCCGGCTG	GCAGGGTCTA	GGTGGCTGGC	AGAGGCACAT	2520
	GCAGACCTTG	CTGGAGGCTT	GCCCCGAGAC	GCTGGGCGGG	TGAGTCTCCG	TGCAGGATGT	2580
	GAGCAGCGTC	CTGGGCTCTT	ATCCGCGAGG	TGCCAGTAGC	GTGTGCAGGT	ACATACACGT	2640
	GCGTGCACAC	TGTATGACAC	CCCCGAAATG	TCTCAGGATG	TTGAAATGTG	TCCTTGGGGG	2700
10	CAGAAGTGTG	CCCAAGTTGAG	AATCTGCCCC	AGAGGAACAC	ACCCACACCA	GGCCTCAGGA	2760
	TTTGTGTGTT	ATCAAGTTCC	AAGGAAAAGG	AACATCTCAG	CGGGGCGTGG	TGGTTACGCG	2820
	CTGGAATCCC	AGCAGTTGAG	GCCAGGAGTT	CCAGAGCAGC	CTGGGCAACG	CAGTGAGAGA	2880
	CCCCATCTCT	ACAARAAAAA	AAAAAGAAAG	AAAGAAAATG	AGAGATCCAG	GTTTAAAAAT	2940
	TCATAAACAC	CACAAGGAAA	CAATACACTA	TGAGACCCAG	CAGAGCAAC	AGATTGACTC	3000
15	TAGACCCAGA	TACTAGAAIT	ATCAGAGAGA	ATATAAGTA	ACAGTGTTTT	ATATATCTAA	3060
	AGAAATAAAA	GAGATTCTTG	GAAACATGAA	AAAAAA			

A58 DNA sequence

	Gene name:	ESTs
	Unigene number:	Hs.157601
20	Probeset Accession #:	N07459
	Nucleic Acid Accession #:	AC005383
	Coding Sequence:	328-2751 (underlined sequences correspond to start and stop codons)

25	1	11	21	31	41	51	
	GACAGTGTTC	GCGGCTGCAC	CGCTCGGAGG	CTGGGTGACC	CGCGTAGAAG	TGAAGTACTT	60
	TTTATTGTC	AGACCTGGGC	CBATGCGGCT	TTAAAAAAGG	CGAGGGGCTC	TATGCACCTC	120
	CTTGGCGGTA	GTCTCTCCGA	CCTCAGCCCG	GTGGGGTCTG	GCCGCGCTCT	CCCAGGAGAG	180
30	ACAAACAGGT	GTCCCAAGTG	GCAGCGCGCG	CCCGGGCGCC	CCTCTGTGTA	TCCCGTAGCG	240
	CCCCCTGGCC	CGAGCCGCGC	CCGGGTCTGT	GAGTAGAGCC	GCCCGGGCAC	CGAGCGCTGG	300
	TGCGCGCTCT	CCCTCGGTTA	TATCAACATG	CCCCCTTTCC	TGTTGCTGGA	GGCGGTCTGT	360
	GTTTTCTGT	TTTCCAGAGT	GCCCCATCT	CTCCCTCTCC	AGGAAGTCCA	TGTAAGCAAA	420
	GAACCCATCG	GGAAGATTTC	AGCTGCCAGC	AAATGATGT	GGTGCTCGGC	TGCAGTGGAC	480
35	ATCATGTTTC	TGTTAGATGG	GTCTAACAGC	GTGGGAAAG	GGAGCTTTGA	AAAGTCCAAG	540
	CACTTTGCCA	TCACAGTCTG	TGACGGTCTG	GACATCAGCC	CCGAGAGGGT	CAGAGTGGGA	600
	GCATTCCAGT	TCAGTTCAC	TCCTCATCTG	GAATTCOCCT	TGGATTCAIT	TTCAACCCAA	660
	CAGGAAGTGA	AGGCAAGAA	CAGAGGATG	GTTTTCAAG	GAGGGCGCAC	GGAGACGGAA	720
	CTTGCTCTGA	AATACCTTCT	GCACAGAGGG	TTGCCTGGAG	GCAGAAATGC	TTCTGTGCCC	780
40	CAGATCTCTA	TCATGCTCAC	TGATGGGAAG	TCCACGGGGG	ATGTGGCAGT	GCCATCCAAG	840
	CAGCTGAAGG	AAAGGGGTGT	CACGTGTGTT	GCTGTGGGGG	TCAGGTTTCC	CAGGTGGGAG	900
	GAGCTGCATG	CACCTGGCAG	CGAGCCTAGA	GGGCAGCACG	TGCTGTGGCG	TGAGCAGGTG	960
	GAGGATGCCA	CCAACGGGCT	CTTCAGCACC	CTCAGCAGCT	CGGCGATCTG	CTCCAGCGCC	1020
	ACGCCAGACT	GCAGGGTCCA	GGCTCACCCC	TGTAGACACA	GGAGCTGGA	GATGGTCCGG	1080
45	GAGTTGCTG	GCAATGCCCC	ATGCTGGAGA	GGATCGCGGC	GGACCTTTGC	GGTGTGGCT	1140
	GCACACTGTC	CTCTCTACAG	CTGGAAGAGA	GTGTTCTTAA	CCCAACCTCG	CACCTGCTAC	1200
	AGGACCACTT	GCCCCAGCCC	CTGTGACTCG	CAGCCCTGCC	AGAATGGAGG	CACATGTGTT	1260
	CCAGAAAGAC	TGGACGGCTA	CCAGTGCTTC	TGCCCGCTGG	CCCTTTGGAG	GGAGGCTAAC	1320
	TGTGCCCTGA	AGCTGAGCCT	GGAATGCAGG	GTGACCTTCC	TCTTCTGCT	GGACAGCTCT	1380
50	GCGGGCACCA	CTCTGAGCGG	CTTCTGCGGG	GCCAAAGTCT	TGTTGAAGCG	GTTTGTGCGG	1440
	GCGGTGCTGA	GCGAGGACTC	TGCGGCCCGA	GTGGGTGTGG	CCACATACAG	CAGGAGCTTG	1500
	CTGGTGGCGG	TGCGGTGTGG	GGAATACAGG	GATGTGCTTG	ACCTGTGCTG	GAGCTCTGAT	1560
	GGCATTCCCT	TCCGTGGTGG	CCCAACCTTG	ACGGGCAGTG	CCTTGGCGCA	GGCGCCAGAG	1620
	CGTGGCTTGG	GGAGCGCCAC	CAGGACAGGC	CAGGACCGGC	CACGTAGAGT	GGTGGTTTTG	1680
55	CTCACTGAGT	CACACTCCGA	GGATGAGGTT	GGGGGCCAG	CGGCTCACGC	AGGGGGCGGA	1740
	GAGCTGCTCC	CTCTGGGTGT	AGGCAATGAG	GCGGTGCGGG	CAGAGCTGGA	GGAGATCACA	1800
	GGCAGGCCAA	AGCATGTGAT	GGTCTACTCG	GATCCTCAGG	ATCTGTTCAA	CCAAATCCTT	1860
	GAGCTGCAGG	GGAACTGTGT	CAGCGCGCAG	CGGCCAGGGT	GCCGGACACA	AGCCCTGGAC	1920
	CTGCTCTTCA	TGTTGGACAC	CTCTGCTTCA	GTAGGGCCCG	AGAAATTTGC	TCAGATGCAG	1980
60	AGCTTTGTGA	GAAGCTGTGC	CCTCAGGTTT	GAGGTGAACC	CTGAGGTGAC	ACAGGTCCGC	2040
	CTGGTGGTGT	ATGGCAGCCA	GGTGCAGACT	GCCCTCGGGC	TGACACCAAA	ACCCACCCGG	2100
	GCTGCGATGC	TGCGGGCCAT	TAGCCAGGCC	CCCTACCTAG	GTGGGGTGGG	CTCAGCCGGC	2160
	ACCGCCCTGC	TGCACATCTA	TGACAAAGTG	ATGACCGTCC	AGAGGGGTGG	CCGGCTGGTT	2220
	GTCCCCAAAG	CTGTGGTGGT	GCTCACAGGC	GGGAGAGCGG	CAGAGGATGC	AGCCGTTTCT	2280
65	GCCCCAAGAC	TGAGGAACAA	TGGCATCTCT	GTCTTGGTGG	TGGGGGTGGG	GCTGTCTTCA	2340
	AGTGAGGGTC	TGCGGAGGCT	TGCAGGTCCC	CGGATTTCCC	TGATCCAGGT	GGCAGCTTAC	2400
	GCGGACCTGC	GSTACCAACA	GGAGGTGCTC	ATTGAGTGGC	TGTGTGGAGA	AGCCAGGCAAT	2460
	CCAGTCAACC	CTCTCAAAAC	CAGCCCGTGC	ATGAATGAGG	GCAGCTGGGT	CCTGCAGGAT	2520
	GGGAGCTACC	GCTGCAAGTG	TGGGATGGGC	TGGGAGGGCC	CCCACTGCGA	GAACCGTGAG	2580
70	TGGAGCTCTT	GCTCTGTATG	TGTGAGCCAG	GGATGGATTG	TTGAGAGGCC	CCTGAGGCAC	2640
	ATGGCTCCCG	TGCAAGAGGG	CAGCAGCCGT	ACCCCTCCCA	GCAACTACAG	AGAAGGCGCTG	2700
	GGCAGTGAAG	TGTTGCCCTAC	CTCTGGAAT	GTCTGTGCCC	CAGGTCTCTA	GAATGTCTCG	2760
	TTCCCGCCGT	GGCCAGGACC	ACTATTCTCA	CTGAGGGAGG	AGGATGTCCC	AATCTCAGCC	2820
	ATGCTGCTTA	GAGACAGGAA	AGCAGCTGAT	GTCAACCCAC	AACGATGTGT	TTGAAAAGTT	2880
75	TTGATGTGTA	AGTAAATACC	CACCTTCTGT	ACCTGCTGTG	CCTTGTGTAG	GCTATGTCTAT	2940
	CTGCCACCTT	TCCCTTGAAG	ATAAACAGAG	GGTCTGTAAG	ACTTAAATTT	AGCGGCTGTA	3000
	CGTTCTCTTG	CACACAATCA	ATGCTCGCCA	GAATGTGTTT	GACACAGTAA	TGCCAGCAG	3060
	AGGCCTTTAC	TAGAGCACTC	TTTGGACGGC	GAAGGCCACG	GCCCTTCAAG	ATGGAAGCA	3120
	GCAGCTTTTC	CACCTTCCCA	GAGACATCTT	GGATGCAITT	GCATTGAGTC	TGAAGGGGGG	3180
80	CTTGAGGGAC	GTTTGTGACT	TCTTGGCCAC	TGCCCTTTGT	GTGTGGAAGA	GACTTGGAAA	3240
	GGTCTCAGAC	TGAATGTGAC	CAATTAACCA	GCTTGGTTGA	TGATGGGGGA	GGGGCTGAGT	3300
	TGTGATGGG	CCAGGTCTTG	GAGGGCCACG	TAAATCGGTT	CTGAGTCCGT	AGCAGTGTCC	3360
	ACCTGAAGG	TCTTC					

A59 Protein sequence

Gene name: ESTs
 Unigene number: Hs.157601
 Protein Accession #: none found
 Signal sequence: 1-17
 Transmembrane domains: none found
 VGM domains: 49-223; 341-518; 529-706
 EGF domains: 298-333; 715-748
 Cellular Localization: secreted

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1      11      21      31      41      51
|      |      |      |      |      |
15  MPPFLLLEAV CVFLFSRVPP SLPLQSEVHV KETICKISAA SKMMWCSAAV DIMFLLDGSN 60
    SVGKGSFERS KHFALTVCDD LDISPERVRV GAFQPSSTPH LEFPDLSFST QQEVKARIKR 120
    MVFKGGRRET ELAIKYLHR GLPGGRNASV PQILIIIVTDG KSGQDVALPS KQLKRGVTV 180
    FAVGVRFPRW BELHALASEP RGQHVLLAEQ VEDATNGLFS TLSSSAICSS ATFDCEVEAK 240
    PCRHRTLEVM REFAGNAPCW RGSRRTLAVL AAECPPFYSWK RVFLTHPATC YRTTCFPGCD 300
    90PCQNGGTC VPESLDGYQC LCPLAFGGGA NCALKLSLEC RVDLLFLDS SAGTTLDGFL 360
    RAKVVFKEFV RAVISEDSRA RVGVATYSRE LLVAVPVGEY QDVPPDLVWSL DGIPFRGGPT 420
    LTGSALRQAA ERGFGSAIRT GQDRPRRVVV LITESHSEDE VAGPARHARA RELLLLGVS 480
    EAVRAELEBI TGSPKHMVYV SDPQDLFNQI PELQKGLCSR QRPGRCTQAL DLVFMLDTS 540
    SVGPENFAQM QSFVRSALQ FEVNPDTQV GLVVYGSQVQ TAFGLDTKPT RAAMLRAISQ 600
    APYLCGVGSA GTALLHIYDK VMTVQRGAR GVPKAVVVLV GGRGAEDAAV PAQKLENGI 660
    SVLVVGVGPFV LSEGLRLLAG PRDLSIHVAA YADLRVHODV LIENLCSEAK QPVNLCKPSP 720
    CMNEGSCVLQ NGSYRCKCRD GWEGPHCENR EWSSCBVCVS QGMILETFLR HMAPVQEGSS 780
    RTPPSNYREG LGTEMVPTFW NVCAPGP
  
```

A60 DNA SEQUENCE

Gene name: Homo sapiens type II membrane serine protease mRNA
 Unigene number: Hs.63325
 Probeset Accession #: AA411502
 Nucleic Acid Accession #: NM 016425
 Coding sequence: 1-1314 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
|      |      |      |      |      |
40  ATGTTACAGG ATCTGACAG TGATCAACCT CTGAACAGCC TCGATGTCAA ACCCTGCGC 60
    AAACCCCGTA TCCCATGGA GACCTTCAGA AAGGTGGGGA TCCCATCAT CATAGCACTA 120
    CTGAGCCTGG CGAGTATCAT CATTGTGGT GTCCCTCATCA AGGTGATTCT GGATAAATAC 180
    TACTTCCTCT CGCGGACACC TCCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG 240
    CTGGACTGTG CCTTGGGGGA GAGCAGAGAG CACTGTGTCA AGAGCTTCCC CGAAGGGCCT 300
    GCAGTGGCAG TCCGCTCTCT CAAGGACCGA TCCACACTGC AGGTGCTGGA CTCGGCCACA 360
    GGGAACTGGT TCTCTGCTCT TTTCGACAA CTTACAGAA GCTCTGCTGA GACAGCCTGT 420
    AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG 480
    GATCTGGATG TTGTTGAAAT CACAGAAAAC AGCCAGGAGC TTCGCTGCG GAACTCAAGT 540
    GGGCCCTGTG TCTCAGGCTC CCTGGCTCTC CTGCACTGTC TTGCTGTGG GAAGAGCCTG 600
    AAGACCCCTC GTGGGTGGG TGCGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660
    AGCATCTCAG AGCAAAACA GCACGTCTGT GGAGGGAGCA TCCTGGACCC CCACTGGSTC 720
    CTCAGGCGAG CCCACTGCTT CAGGAACAT ACCGATGTGT TCAACTGGA GGTGCGGGCA 780
    GGCTCAGACA AACTGGGAG CTTCCTATCC CTGGCTGTGG CCAAGATCAT CATCATGAA 840
    TTCAACCCCA TGATCCCCAA AGACATGAC ATCGCCCTCA TGAAGCTGCA GTTCCCACTC 900
    ACTTCTCTAG GCACAGTCAG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCCTCCCA 960
    GCCACCCAC TCTGGATCAT TGGATGGGGC TTACGAAGC AGAATGGAGG GAAGATGTCT 1020
    GACATCTGTC TGCAGGCTTC AGTCCAGGTC ATTACAGCA CACGCTGCAA TGCAGACGAT 1080
    GCGTACCAGG GGGAGGTAC CAGAGAGATG ATGTGTGCG GCATCCCGGA AGGGGGTGTG 1140
    GACACCTGCC AGGGTGACAG TGGTGGGCC CTGATGTACC AATCTGACCA GTGCTCTGTG 1200
    GTGGGCATCG TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCAGG AGTATACACC 1260
    AAGGTCTCAG CCTATCTCAA CTGATCTTAC AATGTCTGGA AGGCTGAGCT GTAA
  
```

A61 Protein sequence:

Gene name: Homo sapiens type II membrane serine protease mRNA
 Unigene number: Hs.63325
 Probeset Accession #: AA411502
 Protein Accession #: NP_057509
 Signal sequence: none found
 Transmembrane domains: 31-53
 LDLa domain: 54-94
 Tryp_SPC domain: 204-429
 Cellular Localization: plasma membrane/ER

```

1      11      21      31      41      51
|      |      |      |      |      |
75  MLQDPDSQDP LNSLDVKPLR KPRIPMTIFR KVGIPYIIL LSLASIIIVV VLIKVILDKY 60
    YFLCGQPLHF IPRKQLCDGE LDCPLGDEE HCVKSPFFEGP AVAVRLSKDR STLQVLDSAT 120
    GNVFSACFDN FTEALAEAC EQMGYSSEKPT FRAVEIGPDQ DLDVVEITEN SQELRMENSS 180
    GPCLSGSLVS LHLACGKSL KIPRVVGGEE ASVDSHPWQV SIQYDKQEVV GSSILDPRWV 240
    LTAABCFRKH TDVFNWVRA GSDKLGSPFS LAVAKIIIE FFMVYKDNQ IALAKLQFPL 300
    TFGTVPKPC LFPEDEELTP ATPLNIIWNG FTKQNGGKMS DILLQASVQV IDSTRCNADD 360
    AYQGEVTRKM MCAGIEPEGGV DTCQGDSSGP LMYQSDQNHV VGIVSWGYGC GGPSTFGVYT 420
    KVSAYLNWYI NVWKAEI
  
```

A62 DNA SEQUENCE

Gene name: ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]
 Unigene number: Hs.105484
 Probeset Accession #: AA314779
 Nucleic Acid Accession #: none found
 Coding sequence: 103-579 (underlined sequences correspond to start and stop codons)

10

15

20

25

30

```

1      11      21      31      41      51
|      |      |      |      |      |
CCAAACAGAT  TTGCAGATCA  AGGAGAACCC  AGGAGTTTCA  AAGAAGCGCT  AGTAAGGTCT  60
CTGAGATCCT  TGCCTAGCT  ACATCCTCAG  GGTAGGAGGA  AGATGGCTTC  CAGAAGCATG  120
CGGCTGCTCC  TATTBCTBAG  CTGCTCGGCC  AAAACAGGAG  TCCTGGGTGA  TATCATCATG  180
AGACCCAGCT  GTGCTCCTGG  ATGGTTTAC  CACAAGTCCA  ATTGCTATGG  TTACTTCAGG  240
AAGCTGAGGA  ACTGCTCTGA  TGCCGAGCTC  GAGTGTCACT  CTACCGAAA  CGGAGCCCAC  300
CTGGCATCTA  TCCTGAGTTT  AAAGGAAGCC  AGCACCATAG  CAGAGTACAT  AAGTGGCTAT  360
CAGAGAAGCC  AGCCGATATG  GATTGGCCTG  CACGACCCAC  AGAAGAGGCA  GCAGTGGCAG  420
TGGATTGATG  GGGCCATGTA  TCTGTACAGA  TCCTGGTCTG  GCAAGTCCAT  GGGTGGGAAC  480
AAGCACTGTG  CTGAGATGAG  CTCCAATAAC  AACTTTTAA  CTGGAGCAG  CAACGAATGC  540
AACAGCGGCC  AACCTTCCT  GTGCAAGTAC  CGACCATAGA  BCAGAATCA  AGATTCTGCT  600
AACTCTGCA  CCAGCCCCGT  CCTCTTCCTT  TCTGCTAGCC  TGGCTAAATC  TGCTCATTAT  660
TTCAGAGGGG  AAACCTAGCA  AACTAAGAGT  GATAAGGGCC  CTACTACACT  GGCCTTTTAA  720
GGCTTAGAGA  CAGAACTTT  AGCATTGGGC  CCAGTAGTGG  CTCTAGCTC  TAAATGTTTG  780
CCCGCCATC  CCTTTCCACA  GTATCCTTCT  TCCCTCCTCC  CCTGTCTCG  GCTGTCTCGA  840
GCAGTCTAGA  AGAGTGCATC  TCCAGCCTAT  GAAACAGCTG  GGTCTTTGGC  CATAAGAAAT  900
AAAGATTGTA  AGACAGAAGG  AGAAGACTCA  GGAGTAAGCT  TCTAGACCCC  TTCAGCTTCT  960
ACACCCCTCT  GCCCTCTCTC  CATTCCTGCG  ACCCCACCCC  AGCCACTCAA  CTCCTGCTTG  1020
TTTTTCCTTT  GGCCTATAGG  AGGTTTACCA  GTAGAATCCT  TGCTAGGTTG  ATGTGGGCCA  1080
TACATTCCTT  TAATAAACCA  TTGTGTACAT  AAGAGAAAAA  AAAAAAATA  AAAAAAATA  1080

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A63 Protein sequence:

Gene name: ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]
 Unigene number: Hs.105484
 Probeset Accession #: AA314779
 Protein Accession #: none found
 Signal sequence: 1-22
 Transmembrane domains: none found
 C-type lectin domain: 47-156
 Cellular Localization: secreted

45

50

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1      11      21      31      41      51
|      |      |      |      |      |
MASRSMRLLL  LLSCLAKTGV  LGDIIMRPS  APGWFIKSN  CYGYFRKLRL  WSDALELCQS  60
YGNAGHLASI  LSLKEASTIA  EYISGYQRS  PIWIGLHDPQ  KRQQWQWIDG  AMYLRSWSG  120
KSMGGNKHCA  EMSSNNNFLT  WSSNECNKQ  HFLLCKYRP

```

A64 DNA SEQUENCE

Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 Probeset Accession #: X63629
 Nucleic Acid Accession #: X63629
 Coding sequence: 54-2543 (start and stop codons are underlined)

60

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80

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1      11      21      31      41      51
|      |      |      |      |      |
GCGGAACACC  GGCCCGCCGT  CGCGGCAGCT  GCTTCACCCC  TCTCTCTGCA  GCCATGGGEC  60
TCCCTCGTGG  ACCTCTCGCG  TCTCTCCCTC  TTCTCCAGGT  TTGCTGGCNG  CAGTGCCTGG  120
CCTCCGAGCC  GTGCCGGGCG  GTCTTCAGGG  AGGCTGAAGT  GACCTTGGAG  GCGGGAGGCG  180
CGGAGCAGGA  GCCCGGCCAG  GCGCTGGGGA  AAGTATTTCAT  GGGCTGCCCT  GGGCAAGAGC  240
CAGCTCTGTT  TAGCACTGAT  AATGATGALT  TCACCTGTGG  GAATGGCGAG  ACAGTCCAGG  300
AAAGAGGTTC  ACTGAAGGAA  AGGAATCCAT  TGAAGATCTT  CCTATCCAAA  CGTATCTTAC  360
GAAGACACAA  GAGAGATTGG  GTGGTTGCTC  CAATATCTGT  CCTGAAAAAT  GGCAGGGGTC  420
CCTTCCCCCA  GAGACTGAAT  CAGCTCAAGT  CTAATAAAGA  TAGAGACACT  AAGATTTTCT  480
ACAGCATCAC  GGGGCCGGGG  GCAGACAGCC  CCCCTGAGGG  TGTCTTCGCT  GTAGAGAAGG  540
AGACAGGCTG  GTTGTGTGTT  AATAAGCCAC  TGGACCGGGA  GAGGATTGCC  AAGTATGAGC  600
TCCTTGGCCA  CGCTGTGTCA  GAGAATGGTG  CCTCAGTGGG  GGACCCCATG  AACATCTCCA  660
TCATCGTGAC  CGACCAAGAT  GACCACAAGC  CCAAGTTTAC  CCAGGACACC  TTCCGAGGGA  720
GTGTCTTAGA  GGGAGTCTTA  CCAGGTACTT  CTGTGATGCA  GGTGACAGCC  ACAGATGAGG  780
ATGATGCCAT  CTACACCTAC  AATGGGGTGG  TTGCTTACTC  CATCCATAGC  CAGAAACCAA  840
AGGACCCACA  CGACCTCATG  TTCACAATTC  ACCGGAGCAC  AGGCACCATC  AGCGTCATCT  900
CCAGTGGGCT  GGAACGGGAA  AAAGTCCCTG  AGTACACACT  GACCATCCAG  GCCACAGACA  960
TGGATGGGGG  CGGCTCCACC  ACCACGCGAG  TGGCAGTAGT  GGAGATCCTT  GATGCCAATG  1020
ACAAATGCTC  CATGTTTGAC  CCCCAGAGT  ACGAGGCCCA  TGTGCTTGAG  AATGCAGTGG  1080
GCCATGAGGT  CGAGAGGCTG  ACGGTCACTG  ATCTGGAAGC  CCCCACCTCA  CCGGCTGGC  1140
GTGCCACCTA  CCTTATCATG  GCGGTGAGG  ACGGGGACCA  TTTTACCATC  ACCACCCACC  1200
CTGAGAGCAA  CCAGGGCATC  CTGACAACCA  GGAAGGGTTT  GGATTTTGAG  GCCAAAAACC  1260
AGCACACCTT  GTACGTTGAA  GTGACCAACG  AGGCCCCCTT  TGTGCTGAAG  CTCCTCAACT  1320
CCACAGCCAC  CATAGTGCTC  CAGGTGGAGG  ATGTGAATGA  GGCACCTGTC  TTTGTCCAC  1380
CCTCCAAAGT  CGTTGAGGTC  CAGGAGGGCA  TCCCACCTGG  GGAGCCTGTG  TGTGTCTACA  1440
CTGCAGAAGA  CCTGACAAG  GAGAATCAAA  AGATCAGCTA  CCGCATCTGT  AGAGACCCAG  1500

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5 CAGGGTGGCT AGCCATGGAC CCAGACAGTG GGCAGGTCAC AGCTGTGGGC ACCCTCGACC 1560
 GTGAGGATGA GCAGTTTGTG AGGAACAACA TCTATGAAGT CATGGTCTTG GGCATGGACA 1620
 ATGGAAGCCC TCCACCCTACT GGCACGGGAA CCCTTCTGCT AACACTGATT GATGTCAACG 1680
 ACCATGGGCC AGTCCCTGAG CCCCGTCAGA TCAACATCTG CAACCAAAGC CCTGTGGGCC 1740
 ACCTGTCTGA CATCACGGAC AAGGACCTGT CTCCCCACAC CTCCCTTTTC CAGGCCGAGC 1800
 TCACAGATGA CTCAGACATC TACTGGACGG CAGAGGTCAA CGAGGAAGGT GACACAGTGG 1860
 TCTTGTCCCT GAAGAAGTTC CTGAAGCAGG ATACATATGA CGTGCACTTT TCTCTGCTG 1920
 ACCATGGCAA CAAGAGCAG CTGACCGTGA TCAGGGCCAC TGTGTGCGAC TGCCATGGCC 1980
 ATGTGGAAC CTGCGCTGGA CCCTGGAAAG GAGGTTTCAT CCTCCCTGTG CTGGGGGCTG 2040
 TCCTGGCTCT GCTGTCTCTC CTGCTGGTGC TGCTTTTGTG GGTGAGAAAG AAGCGGAAGA 2100
 TCAGGAGGCC CCTCTACTC CCAGAAGATG ACACCGTGA CAACGCTTTC TACTATGGCG 2160
 AAGAGGGGGG TGGCGAAGAG GACCAGGACT ATGACATCAC CCAGCTCCAC CGAGGTCTGG 2220
 AGGCCAGGCC GAGGTGGTTC CTGCGCAATG ACGTGGCACC AACCATCATC CCGACACCCA 2280
 TGTACCGTCC TAGGCCAGCC AACCCAGATG AAATCGGCAA CTTTATAATT GAGAACCTGA 2340
 AGCGGGCTAA ACAGACACCC ACAGCCCGGC CCTACGACAC CCTCTGGTGG TTGCACTATG 2400
 AGGGCAGCGG CTCGGAACGG CGCTCCCTGA GCTCCCTCAC CTCTCCGCCC TCCGACCAAG 2460
 ACCAAGATTA GAATTATCTG AACGAGTGGG GCAGCGGCTT CAAGAAGCTG GCAGACATGT 2520
 ACGGTGGCGG GCAGGACGAC TAGGCGGCTT GCCTGCAGGG CTGGGGACCA AACGTCAAGC 2580
 CACAGAGCAT CTCCAGAGGG TCTCAGTTCC CCCTTCAGCT GAGGACTTCG GAGCTTGTC 2640
 GGAAGTGGCC CTGCAAGCTT GGCGGAGACA GGCTATGAGT CTGACGTTAG AGTGGTTGCT 2700
 TCCTTAGCCT TTAGGATGCG AGGAATGTGG GCAGTTTGAC TTCAGCATG AAAACCTCTC 2760
 CACCTGGGCC AGGGTTGCTT CAGAGGCCAA GTTCCAGAA GCCTCTTACC TGCCGTAATA 2820
 TGCTCAACCC TGTGTCTGGG GCTTGGGCTT GCTGTGACTG ACCTACAGTG GACTTTCTCT 2880
 CTGGAATGGA ACCTTCTTAG GCCTCCTGGT GCAACTTAAT TTTTCTTTT AATGCTATCT 2940
 TCAGAAAGCT AGAGAAAGTT CTTCAGAAAG GCAGCCAGA GCTGCTGGGC CCACTGGCCG 3000
 TCCTGCATTT CTGGTTTCCA GACCCCAATG CCTCCCATTC GGATGGATCT CTGCGTTTTC 3060
 ATACTGAGT TGCCTAGGTT GCCCTTATT TTTTATTTTC CCTGTGCGT TGCTATAGAT 3120
 GAAGGGTGAG GACAACTGTT TATATGTACT AGAATTTTT TATTAAGAA A

A65 Protein sequence:

Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 ProbeSet Accession #: X63629
 Protein Accession #: CAA45177
 Signal sequence: 1-24
 Transmembrane domain: 659-675 (second underlined sequence)
 Cellular localization: plasma membrane

40 1 11 21 31 41 51
 MGLERGLAS LLLLVQCNLQ CAASEPCRAV FREAEVTL EA GGAEQEPGQA LGKVFVGCPCG 60
 QEPALPSTDN DDFTVRNGET VQERRSLKER NPLKIPFSKR ILRRHKRDV VAPISVPEKG 120
 45 KGPFPQLNQG LKSNKDRDTK IYYSITGPGA DSPPEGVFAV EKETGALLN KPLDREBIK 180
 YLEFGEAVSE NGASVEDPMN ISILVTDQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT 240
 DEDDAIYTN GVVAYSIESQ EPEDFDLMP TIHRSTGTIS VISSGLDREK VPEYLTIIQA 300
 TMDGDGSTT TAVAVVEILD ANDNAEMFDF QKYEAHVPEH AVGHVQRLT VTDLDAPNSP 360
 50 AMRATYLLNG GDDGDHFTYT TPESNQGIL TTRKSLDFEA KNQHTLYVEV TNEAPFVLKL 420
 PSTATIVVE VSDVNEAPVF VEPKVVVEVQ SGIPTEGEPVC VYTAEDPDKE NQKISYRILR 480
 DEAGWLAMP DSGQVTAVGT LDREDEQFVR NNYEYVNLVA MDNGSPPTTG TGTLLLLTLD 540
 VNDHGVPVFP RQITICNQSP VRHLNITDK DLSHTSPFQ AQLTDSDIY WTAEVNEEGD 600
 TVVLSLKKFL KQDTYDVHLS LSEDEGNKQL TVIRATVDCD HGHVETCPGP WKGGFILVPL 660
 55 GAVLALLFL LVLALLVRKK RKIKFPLILP EDDTRDNVFP YGEGGGGEDD QDYDITQLHR 720
 GLEARPEVVL RNDVAPTIIP TPNYRPRPAN PDBIGNPIIE NLKAANTDPT APPYDITLVF 780
 DYECSGSDAA SLSSLTSSAS DQDQDYDILN EWGSRFKKLA DMYGGGEDD

A66 DNA SEQUENCE

Gene name: ATPase, Ca++ transporting, type 2C, member 1
 Unigene number: Hs.106778
 ProbeSet Accession #: N51919
 Nucleic Acid Accession #: AF189723
 Coding sequence: 1-2712 (underlined sequences correspond to start and stop codons)

70 1 11 21 31 41 51
 ATGATTCCTG TATTGACATC AAAAAAGCCA AGTGAATTAC CAGTCAGTGA AGTTGCAAGC 60
 ATTCTCCAG CTGATCTTCA GAATGGTCTA AACAAATGTG AAGTATAGTCA TAGGCGAGCC 120
 TTTCTAGGCT GGAATGAGTK TGATATTAGT GAAGATGAGC CACTGTGGAA GAAGTATATT 180
 TCTCAGTTTA AAAATCCCTT TATTATGCTG CTCTGGCTTC CTGCACTCAT CAGTGTTTTA 240
 ATGATCAGT TTGATGATGC CGTCAGTATC ACTGTGGCAA TACTTATCGT TGTACAGTT 300
 75 GCCTTTGTTT AGGAATATCG TTCAGAAAAA TCTCTTGAAG AATTGAGTAA ACTTGTGCCA 360
 CCAGATGCC ATTGTGTGCG TGAAGGAAAA TTGGAGCATA CACTTGGCCG AGACTTGGTT 420
 CAGGTGATA CAGTTTGCCT TTCTGTGGG GATAGAGTTC CTGCTGACTT ACCTTGTCTT 480
 GAGGCTGTGG ATCTTTCCAT TGATGAGTCC AGCTTGACAG GTGAGACAAC GCCTTGTCTT 540
 AAGGTGACAG CTCTTCAGCG AGCTGCAACT AATGGAGATC TTGCATOGAG AAGTAACATT 600
 80 GCCTTTATGG GAACACTGGT CAGATGTGGC AAAGCAAAGG GTGTTGTCTAT TGGAAACAGGA 660
 GAAATTTCTG AATTTGGGGA GGTTTTAAAT ATGATGCAAG CAGAAAGAGG ACCAAAAACC 720
 CCTCTGCAGA AGAGCATGGA CCTCTTAGGA AAACAACCTT CCTTTTACTC CTTTGTGATA 780
 ATAGGAATCA TCATGTTGGT TGGCTGGTTA CTGGGAAAAA ATATCCTGGA AATGTTTACT 840

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ATTAGTGTAA GTTTGGCTGT AGCAGCAATT CCTGAAGGTC TCCCATTTGT GGTACACAGT 900
ACGCTAGCTTC TTGGTGTATT GAGARTGGTG AAGAAAAGGG CCATTTGTGA AAAGCTGGCT 960
ATTGTTGAAA CTCTGGGCTG CTGTAAATBTG ATTTGTTTCTG ATAAAACTGG AACACTGAGC 1020
AAGAATGAAA TGACTGTTTAC TCACATATTT ACTTCAGATG GTCTGTCATG TGAGGTTTACT 1080
GGAGTTGGCT ATAAATCAATT TGGGGAAGTG ATTGTTGATG GTGATGTTGT TCATGGATTTC 1140
TATAACCCAG CTGTAGTACG AATTGTTGAG GCGGGCTGTG TGTGCAATGA TGCTGTAAAT 1200
AGAAACAATA CTCTAATGGG GAAGCCAACA GAAGGGGCTT TAATTGCTCT TGCAATGAAG 1260
ATGGGTCTTG ATGGACTTCA ACAAGACTAC ATCAGAAAAG CTGAATACCC TTTTAGCTCT 1320
GAGCAAAAGT GGATGGCTGT TAAGTGTGTA CACCGAACAC AGCAGGACAG ACCAGAGATT 1380
TGTTTTTATG AAGGTGCTTA CGAACAAAGTA ATTAAGTACT GTACTACATA CCAGAGCAAA 1440
GGGACAGACT TGACACTTAC TCAGCAGCAG AGAGATGTGT ACCAACAGA GAAGGCACGC 1500
ATGGGCTCAG CGGGACTCAG AGTCTTCTCT TTGCTTCTG GTCTGAACTG GGGACAGCTG 1560
ACATTCTCTG GCTTGGTGGG AATCATTGAT CCACCTAGAA CTGGTGTGAA AGAAGCTGTT 1620
ACAACACTCA TTGCTCTCAG AGTATCAATA AAAATGATTA CTGGAGATTC ACAGGAGACT 1680
GCAGTTGCAA AAGGTGCTTA TCTGGGATTG TATTCACAAA CTCCCGACTG AGTCTCAGGA 1740
GAAGAAATAG ATGCAATGGA TTTTCAGCAG CTTCACAAA TAGTACCAA GGTTCAGTA 1800
TTTTACAGAG TAGTCCCAAG GCACAAGATG AAAATTATTA AGTCGCTACA GAAGAACGGT 1860
TCAGTTGTAG CCAAGACAGG AGATGGAGTA AATGATGCAG TTGCTCTGAA GGCTGCAGAC 1920
ATTGGAGTTG CGATGGGCCA GACTGGTACA GATGTTTGA AAGAGGCAGC AGACATGATC 1980
CTAGTGTATG AAGGTGCTTA AACCATAATG TCTGCAATCG AAGAGGGTAA AGGGATTAT 2040
AATAACATTA AAAATTTGCT TAGATTCCAG CTGAGCACGA GTATAGCAGC ATTAACITTA 2100
ATCTCATGGG CTACATTAAT GAACCTTCTC AATCCTCTCA ATGCCATGCA GATTTTGTG 2160
ATCAATATTA TTATGGATGG ACCCCAGCTC CAGAGCCTTG GAGTAGAACC AGTGGATAAA 2220
GATGTCTATC GTAAACCTCC TCGCAACTGG AAGACAGCA TTTTGACTAA AACTTGATA 2280
CTTAAATATC TTGTTCTCAT AATAATCATT GTTGTGGGCA CTTTGTTTGT CTCTCGGCT 2340
GAGCTACGAG ACAATGTGAT TACACCTCGA GACACAACAA TGACCTTCAC ATGCTTTGTG 2400
TTTTTTGACA TGTTCATGCG ACTAAGTCC AGATCCGAGA CCAACTCTGT GTTTGAGATT 2460
GGACTCTGCA GTAATAGAAT GTTTTGCTAT GCAGTCTCTG GATCCATCAT GGGACATTA 2520
CTAGTTATTG ACTTTCTCTC GCTTCAGAAG GTTTTTCAGA CTGAGAGCCT AAGCATACTG 2580
GATCTGTTGT TTTCTTTGGG TCTCACCTCA TCAGTGTGCA TAGTGGCAGA AATTATAAAG 2640
AAGGTTGAAA GGAGCAGGGA AAAGATCCAG AAGCATGTTA GTTCGACATC ATCATCTTTT 2700
CTGAAGTAT GA
  
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A67 Protein sequence:

Gene name:

ATPase, Ca++ transporting, type 2C, member 1

Unigene number:

Hs.106778

Probeset Accession #:

N51919

Protein Accession #:

AAF27813

Signal sequence:

none found

Transmembrane domains:

60-82, 86-108, 252-274, 282-304, 757-779, 827-849, 856-878

Pfam domains:

Cation ATPase N [6-83], E1-E2 ATPase [89-324], Hydrolase [328-649], Cation ATPase C

[744-889]

Cellular Localization: not determined

45
 50
 55
 60

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1 11 21 31 41 51
MIPVLTSKGA SELPVSEVAS ILQADLQNGL NKCEVSHERRA FEGWNEFDIS EDEPLWKKYI 60
SQPKNPLIML LLASAVISVL MHQFDDAVSI TVAILIVVTV AFVQVYRSEK SLERLSKLVP 120
PECHCVREBK LEHTLARDLV PGDTVCLSVG DRVPADLRLE EAVDLSDIES SLTGRTTPCS 180
KVTAPQPAAT NGOLASRSNI APM3TLVRCG KAGGVVIGTG ENSEFGRVFK MMQAEAPKT 240
ELQKSMDDLK KQLSFYSEFI IGLIMLVGHL LKQDILEMFT ISVSLAVAAI PEGLEIVVTV 300
TLALGVMRMV KRAIVKLLP IVETLSCNV ICSDKTGTLT KNEMTVTHIF TSDGLEHART 360
GVQXNQFQEV IVDGDVVEGF YNPAVERIVE AGCVNDAVI RNNTLMGKPT EGALIALAMT 420
MGLDGLQDDY IRKAEYFFSS EQKXMAVXCV HRTQDDRFPI CFMKGAYEQV IKYCTTYQSK 480
GQTLTLTQQQ RDVYQGEKAR MGSAGLEVLA LASGPELQQL TELGLVGIID PFRTGVKEAV 540
TTLASAGVSI KMLTGDQSET AVAIALSELGL YSKTSQSVSG EELDAMDVQV LSQIVPKVAV 600
PYRASPRHMK KIRKSLQKNG SVVAMTGDGV NDAVALKAAD IGVMAGQTGT DVCKEADMI 660
LVDDDFQTIM SAIBEGRGYI NNINKFVRPQ LSTSLAALTL ISLATLMMWF NFINAMQILM 720
INIIMDGPFA QSLGVFVVDK DVIRKPPRNW KDSILTKNLI LKILVSBIII VGTILFVFWR 780
ELRDNVITPR DTTMTPTCFV PFDMPNALS RSQTKSVFEI GLCSNRMFCY AVLGSIMQQL 840
LVYFPPLQK VFQTESLSIL DLLFLGLTSS SVCIVARLIK KVERSRKIQ KVSSTSSSF 900
LEV
  
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A68 DNA SEQUENCE

Gene name:

bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)

Unigene number:

Hs.170195

Probeset Accession #:

BE616633

Nucleic Acid Accession #:

NM_001719

Coding sequence:

123-1418 (underlined sequences correspond to start and stop codons)

75
 80

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1 11 21 31 41 51
GGGCGCAGCG GGGCCCGTCT GCAGCAAGTG ACCGACGGCC GGGACGGCCG CTGCCCCCT 60
CTGCCACCTG GGGCGGTGCG GGGCCCGAGC CCGGAGCCCG GTTAGCGCGT AGAGCCGGCG 120
CGATGCACAT GCGCTACTCG CGAGCTGCGG CGCCGCACAG CTTGCTGGCG CTCTGGGCAC 180
CCCTGTTCCT CTGCGCTCC GCGCTGCGCG ACTTCAGCTT GGACAAAGAG GTGCACTCGA 240
GCTTCATCCA CGGCGGCTTC CGCAGCCAGG AGCGCGCGGA GATGCAGCGC GAGATCCTCT 300
CCATTTTGGG CTGCCCCAC CGCCCGCGCC CGCACCCTCA GGGCAAGCAC AACTCGGCAC 360
CCATGTTTAT GCTGGACCTG TACAACGCCA TGGCGGTGGA GAGGGGCGGC GGGCCCGCGC 420
GCCAGGGCTT CTTCTACCCC TACAAGGCCG TCTTCAGTAC CCAGGGCCCC CCTCTGCCCA 480
GCGTGCAGAA TAGCAATTC CTCACGACG CGACATGGT CATGACCTTC GTCAACCTCG 540
TGGAAATGAA CAAGGAATTC TTCCACCCAC GCTACCAACA TCGAGAGTTC CGGTTTGATC 600
TTTCCAGAT CCCAGAAGGG GAAGCTGTCA CGGCGCGCGA ATTCCGATC TACAAGGACT 660
  
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ACATCCGGGA ACGCTTCGAC AATGAGACGT TCCGGATCAG CGTTTATCAG GTGCTCCAGG 720
AGCACTTGGG CAGGGAATCG GATCTCTTCC TGCTCGACAG CCGTACCCCTC TGGGCTCCGG 780
AGGAGGGGCTG GCTGGTGTIT GACATCAGAG CCACCAGCAA CCACTGGGTG GTCAATCCGC 840
GGCACAACCT GGGCTTCGAG CTCTCGGTGG AGACGCTGGA TGGGCAGAGC ATCAACCCCA 900
AGTTGGCGGG CCGATTGGG CGGCACGGGC CCCAGAACRA GCAGCCCTTC ATGGTGGCTT 960
TCITCAAGGC CACGGAGGTC CACTTCGGCA GCATCCGGTC CACGGGAGC AAACAGGCA 1020
GCCAGAACCG CTCGAAGACG CCCAAGAAC AGGAAGCCCT GCGGATGGCC AACGTGGCAG 1080
AGAACAGCAG CAGCGACCAG AGGCAGGCCT GTAAGAAGCA CGAGCTGTAT GTCAGCTTCC 1140
GAGACCTGGG CTGGCAGGAC TGGATCATCG CGCTGAAGG CTACGCGGCC TACTACTGTG 1200
AGGGGGAGTG TGGCTTCCCT CTGAACCTCT ACATGAACGC CACCAACAC GCCATCGTGC 1260
AGACGCTGGT CCACTTCATC AACCGGAAA OGGTGCCAA GCCCTGCTGT GCGCCACGCG 1320
AGCTCAATGC CATCTCCGTC CTCTACTTCG ATGACAGCTC CAACGTCATC CTGAAGAAAT 1380
ACAGAAACAT GGTGGTCCGG GCTGTGGCT GCCACTAGCT CCTCCGAGAA TTCAGACCTT 1440
TTGGGGCCAA GTTTTCTCG ATCTCTCATT GCTCGCCTTG GCCAGGAACC AGCAGACCAA 1500
CTGCGCTTTG TGAACCTTTC CCCTCCCTAT CCCCACTTT AAAGGTGTGA GAGTATTAGG 1560
AAACATAGAG AGCATATGGC TTTTGATCAG TTTTTCAGTG GCAGCATCCA ATGAACAGA 1620
TCCTACAGC TGTGCAGGCA AAACCTAGCA GGAAGAAAA ACAACGCATA AAGAAAAATG 1680
GCCGGGCCAG GTCATTGGCT GGGAGTCTC AGCCATGCAC GGAATGTTT CCAGAGGTAA 1740
TTATGAGCGC CTACCAAGCA GGCACCCAG CCGTGGGAGG AAGGGGGCGT GGCAGGGGT 1800
GGGCACATTG GTGTCTGTGC GAAAGGAAAA TTGACCCGGA AGTTCCTGTA ATAAATGTCA 1860
CAATAAAACG AATGAATG

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A69 Protein sequence:
Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)

Unigene number: Hs.170195
Probeset Accession #: BE616633
Protein Accession #: NP_001710.1
Signal sequence: 1-30
Pfam domains: TGFb_propeptide [37-281]
Transmembrane domains: none found
Cellular Localization: secreted

35
40
45

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1 11 21 31 41 51
| | | | |
MEVRSRLRAAA PHSFVALWAP LFLRLSALAD FSLDNEVHSS FIHRRRLRSQE RREMQRRLS 60
ILGLEHPRPR HLQKHNESAP MFMLDLYNAM AVEEGGGPGG QGFSYFYKAV PSTQGPPLAS 120
LQDSHFLTDA DMVMSFVNLV EHDKEFFHPR YHRRFRFDL SKIPEGEAVT AAEFRITYDY 180
IREREDNETF RISVYQVLQE HLGREEDLEL LDRSTLWASE EGWLVDITA TSNHWVWVPR 240
HNLLQLQSVL TLGQSLINPK LAGLIGRHGP QNKQPFHVAF FKATEVHFRS IRSTGSKQRS 300
QMRSETPKNQ EALRMANVAE NSSSDQRQAC KKHLYVSFR DLGWQDWIIA PEGYAAYYCR 360
GECAFPPLNSY MNATNHAIVQ TLVVEFINPET VPKPCCAPTQ LNALSVLYED DSSNVILKKY 420
KRMVVRACGC H

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Cervical

50

A70 DNA sequence
Gene name: bone morphogenetic protein receptor IB (ALK-6)
Unigene number: Hs.87223
Probeset Accession #: AA250737
Nucleic Acid Accession #: NM_001203
Coding sequence: 274-1782 (underlined sequences correspond to start and stop codons)

55
60
65
70
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1 11 21 31 41 51
| | | | |
CGCGGGGCGC GGAGTCGGCG GGGCCTCGCG GCACGCGGCG AGTGCAGAGA CCGCGGCGCT 60
GAGGACGCGG GAGCCGGGAG CGCACGCGCG GGGTCGAGTT CAGCCTACTC TTTCTTAGAT 120
GTGAAGAGAA AGGAAGATCA TTTCAATGCC TGTGTATAAA GGTTCAGACT CTGCTGATT 180
CATAACCAAT TGGCTCTGAG CTATGACAAAG AGAGGAACA AAAAGTTAA CTACAGCC 240
TGCCATAAGT GAGAAGCAAA CTTCCTGAT AACATGCTTT TGCGAGTGC AGGAAAATTA 300
AATGTGGGCA CCAAGAAAGA GGATGGTGAG AGTACAGCCC CCACCCCGCC TCCAAAGTTC 360
TTGCGTTGTA AATGCCACCA CCATTGTCCA GAAGACTCAG TCAACAATAT TTGCAGCACA 420
GACGGATATT GTTTCAGAT GATAGAAGAG GATGACTCTG GGTGCGCTGT GGTCACTTCT 480
GGTTGCTAG GACTAGAAGG CTCAGATTTT CAGTGTGCGG ACCTCCCAT TOCTCATCAA 540
AGAAGATCAA TTGAATGCTG CACAGAAAGG AACGAATGTA ATAAGACCT ACACCTTACA 600
CTGCCCTCAT TGAAAAACAG AGATTTTGTT GATGGACCTA TACACACAG GGCTTTACTT 660
ATATCTGGA CTGCTCTGAG TTTGCTCTTG GTCCITATCA TATTATTTTG TTACTTCCGG 720
TATAAAGAC AAGAAACCA ACCTCGATAC AGCATTGGGT TAGAACAGGA TGAACCTTAC 780
ATTCTCTCTG GAGAAATCCCT GAGAGACTTA ATTAGCAGT CTCAGAGCTC AGGAAGTGGA 840
TCAGGCTCC CTCTGCTGGT CCAAAGGACT ATAGCTAAGC AGATTGAGT GGTGAACAG 900
ATTGGAAGAG TCGCTATAGG GGAAGTTTGG ATGGAAAGT GGCCTGGCGA AAGGTAGCT 960
GTGAAGATGT TCTTCAACAC AGAGGAAGCC AGCTGGTCA GAGAGACAGA AATATATCAG 1020
ACAGTGTGTA TGAGGCATGA AAACATTTTG GGTTCATTG CTGCAGATAT CAAAGGACA 1080
GGGTCTCTGA CCCAGTTGTA CCTAATCACA GACTATCATG AAAATGTTTC CCTTTATGAT 1140
TATCTGAAGT CCAACACCT AGACGCTAAA TCAATGCTGA AGTTAGCCTA CTCTCTGTC 1200
AGTGGCTTAT GTCATTTACA CACAGAAATC TTAGTACTC AAGGCAAAOC AGCAATTGCC 1260
CATCGAGTC TGAAGATTA AAACATTCTG GTGAAGAAA ATGGAACITG CTGTATTGCT 1320
GACCTGGGCC TGGCTGTAA ATTTATTAGT GATACAAATG AAGTTGAGAT ACCACCTAAC 1380
ACTCGAGTTG GCACCAACAG CTATATGCCT CCAGAGAGT TGGACGAGAG CTGAAACAGA 1440
AATCACTTCC AGTCTTACAT CATGGCTGAC ATGTATAGTT TTGGCCTCAT CTTTGGGAG 1500
GTTGCTAGGA GATGTGATC AGGAGGTATA GTGGAAGAA ACCAGCTTCC TTATCATGAC 1560
CTAGTGCCCA GTGACCCCTC TTATGAGGAC ATGAGGGAGA TTGTGTGCAT CAAGAAGTTA 1620

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CGCCCCCAT TCCCAAACCG GTGGAGCAGT GATGAGTGTC TAAGGCAGAT GGGAAACTC 1680
 ATGACAGAAAT GCTGGGCTCA CAATCCTGCA TCAAGGCTGA CAGCCCTGCG GGTAAAGAA 1740
 ACACITGCCA AAATGTGAGA GTCCAGGAC ATTAAGCTCT GATAGGAGAG GAAAAGTAAG 1800
 CATCTCTGCA GAAAGCCAAC AGGTACTCTT CTGTTTGTGG GCAGAGCAAA AGACATCAA 1860
 TAAGCATCCA CAGTACAGC CTGAACATC GTCTTGCTTC CCAGTGGGTT CAGACCTCAC 1920
 CTTTCAGGGA GCGACCTGGG CAAAGACAGA GAAGCTCCCA GAAGGAGAGA TTGATCCGTG 1980
 TCTGTTTGTG GCGGAGAAA CCGTTGGGTA ACTTGTTCAT GATATGATGC AT

A71 Protein sequence
 Gene name: bone morphogenetic protein receptor IB (ALK-6)
 Unigene number: Hs.72472 / Hs.87223
 Probeset Accession #: AA250737 / U89326
 Protein Accession #: NP_001194
 Signal sequence: 1-13
 Transmembrane domains: 128-144
 PFAM domains: activin_receptor [30-111], protein kinase [204-491]
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 MLRSAGKLN VTIKKEDGES TAPTPRPKVL RCKCHHCPE DSVNNICSTD GYCFMIEED 60
 DSGLPVVTSG CLGLEGGDFQ CRDTPIDHQR RSIECCTERN ECKNDLHPTL PFLNDRDFVD 120
 GPIHRRALLI SVTVCSLLLV LIILFCYFRY XQETPRYS IGLBQDETYI PPGESLRLDI 180
 EQSQSGSGSG GLPLLVQRTI AKQIQMVQKI GKGRYGEVWM GKNRGEKVAV KVPFTTEAS 240
 WPRETIYDT VLMRHENILG FIAADIKGTG SWTQLYLITD THENGSLYDY LKSTTLDAKS 300
 MLKLAYSSVS GLCHLHTEIF STQCKPAIAH RDLKSKNLLV KKNGTCCIAH LGLAVKFISD 360
 TNEVDIPENT RVGTGRYMPF EVLDESINRN HFQSYIMADM YSFGILILNEV ARRCVSGGIV 420
 EBYQLPYHDL VPSDPSYSDM REIVCIKKLR PSFPNRWSSD ECLRQMGKLM TECAHNHPAS 480
 RLTALEVRKKT LAKMSSESQDI KL

Bladder**A72 DNA SEQUENCE**

Gene name: Homo sapiens type II membrane serine protease mRNA
 Unigene number: Hs.63325
 Probeset Accession #: AA411502
 Nucleic Acid Accession #: NM_016425
 Coding sequence: 1-1314 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 ATGTTACAGG ATCTGACAG TGATCAACCT CTGAACAGCC TCGATGTCAA ACCCCTGCGC 60
 AAACCCCTTA TCCCATGGA GACCTTCAGA AAGGTGGGGA TCCCATCAT CATAGCACTA 120
 CTGAGCCTGG CAGATATCAT CATTTGTGTT GTCCCTCATCA AGGTGATTCT GGATAAATAC 180
 TACTTCTCTT GCGGGCAGCC TCTCCACTTC ATCCCGAGGA AGCAGCTGTG TGACGGAGAG 240
 CTGAGCTGTC CCTTGGGGGA GGACGAGGAG CACTGTGTCA AGAGCTTCCC CBAAGGGCCT 300
 GCAGTGGCAG TCCGCTCTC CAAGGACCGA TCCACACTGC AGGTGCTGGA CTGGGCCACA 360
 GGBAATCGST TCTCTGCTG TTTCGACAAC TTCACAGAG CTCTGCTGGA GACAGCCTGT 420
 AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG OCCAGACGAG 480
 GATCTGGATG TTGTTGAAT CACAGAAAC AGCCAGGAGC TTGCGATGCG GAACCTCAAT 540
 GGGCCCTGTC TCTCAGGCTC CTTGGTCTCC CTGCACGTGC TTGCTGTGCG GAAGAGCCTG 600
 AAGACCCCCC GTGTGGTGGG TGGGGAGGAG GCCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660
 AGCATCCAGT ACGACAACA GCACGTCTGT GGAGGGAGCA TCCTGGACCC CCACCTGGGTG 720
 CTACAGGCG GCTACAGCAG CAGGAACAT ACCGATGTGT TCAACTGGAA GGTGCGGGCA 780
 GGCTCAGACA AACTGGGCG CTTCCATCC CTGGCTGTGG CCAAGATCAT CATCATGAA 840
 TTCAACCCCA TGTACCCCAA AGACAATGAC ATCCCTCTCA TGAAGCTGCA GTTCCCACTC 900
 ACTTCTCTAG GCACAGTCAG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA 960
 GCCACCCAC TCTGATCAT TGGATGGGCG TTACGAGAG AGAATGGAGG GAAGATGTCT 1020
 GACATACTGC TGCAGCGGTC AGTCCAGGTC ATTGACAGCA CACGGTGCAG TGACAGAGAT 1080
 GCGTACCAGG GGGAAATCAC CGAGAAGATG ATGTGTGACG GCATCCCGGA AGGGGGTGTG 1140
 GACACCTGCG AGGGTGACAG TGGTGGGCC CTGATGTACC AATCTGAACA GTGGCATGTG 1200
 GTGGCATCG TTAGCTGGGG CTATGGCTGC GGGGGCCCGA GCACCCGAG AGTATACACT 1260
 AAGGTCTCAG CCTATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA

A73 Protein sequence:

Gene name: Homo sapiens type II membrane serine protease mRNA
 Unigene number: Hs.63325
 Probeset Accession #: AA411502
 Protein Accession #: NP_057509
 Signal sequence: none found
 Transmembrane domains: 31-53
 LDLa domain: 54-94
 Tryp_SPC domain: 204-429
 Cellular Localization: plasma membrane/ER

1 11 21 31 41 51
 MLQDFDSQPF LNSLDVKPLR KPRIPMETFR KVGIPPIIAL LSLASIIIVV VLKIVILDKY 60
 YFLOGQPLHF IPKQKLCQGE LDCPLGEDEE HCVKSFPEGR AVAVRLSKDR STLQVLDSAT 120

GNWFSACFDN FTEALARTAC RQMGYSEKPT FRAVEIGPDQ DLDVVEITEN SQELMRNNS 180
 GPCLSGSLVS LHCLACGKSL KTRPVVGGEZ ASVDSWVQV SIQYDKQHVC GGSILDPHV 240
 LTAHCFRKH TIVFMKVRG GSKLGSFSPS LAVAKIIE FNFMYPRDND IALMKLQFPL 300
 TFSGTVPIC LFFFDSELTAT ATPLWIIWG FTKQNGKMS DILLQASVQV IDSTRCHADD 360
 AVQGEVTEKM MCAGIPEGGV DTCQGDGGP LMYQSDQNHV VGIWSWGYGC GSPSTPGVYT 420
 KVSAYLNWY NVWKABL

A74 DNA SEQUENCE

Gene name: ESTs, Weakly similar to CGH7L collagen alpha 1(III) chain precursor [H.sapiens]
 Unigene number: Hs.19322
 Probeset Accession #: AA088458
 Nucleic Acid Accession #: AA088458
 Coding sequence: 862-1995 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 GCCCTTGGAC ACTGACATGG ACTGAAGGAG TAGAATGGAG CACGAGGACA CTGACATGGA 60
 CTAGAGAAAA AGGAGCTGGA GCAGGAGAAG GAGGTGCTGC TGCAGGGTTT GGAGATGATG 120
 GCCCGGGGCC CGGACTGGTA CCAGCAGCAG CTGCAACGAG TGCAGGAGCG CCAGCGCCGC 180
 CTGCGCCAGA GCAGAGCCAG GCGGACTTTT GGGGCTGCAG GAGAGCCCGG CCCACTGGGG 240
 CGGCTACTGC CCAAGGTACA AGAGGTGGCC CGGTGCTTGG GGGAGCTGCT GGCTGCAGCC 300
 TGTGCCAGCC GGGCCCTGCC CCCGTCTTCC TCCGGGCCCC CCTGCCCTGC CCGACGCTCC 360
 ACCTCACCCC CGGTCTGGCA GCAGCAGACC ATCTCATGCG TGAAGGAGCA GAACGACTTC 420
 CTCACCCAGG AGGTGACGCA GAGAGTGAG CGCATCACGC AGCTGGAGCA GGAAGAGTGG 480
 GCGCTCATTA AGCAGCTGTT TGAGGCCCGC GCGCTGAGCC AGCAGGACGG GGGACCTCTG 540
 GATTCCACCT TCATCTAGTC CTTGTGGGCC GCGTGGGCCC CCAGGGCCAG CCGGCACTC 600
 AGCCCTTCGA GGGTGGGCCG CCATCTCAGC CCACCTCTCT TGGCTGGAGA CCCCGGCGAG 660
 GCCCAGGCAC AGTCCCGGAG TGGGCGGCTT CCGCCGCCCC TTGCCAGATG GGCTCCCGAC 720
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A75 DNA SEQUENCE

Gene name: SCCA2 or 2b, serine (or cysteine) proteinase inhibitor
 Unigene number: Hs.227948
 Probeset Accession #: AB035089
 Nucleic Acid Accession #: AB035089
 Coding sequence: 9845-10219 (underlined sequences correspond to start and stop codons)

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	TGCCACCGCT	GTAGTAGTAG	TGGAATATAT	ATCTCCTTCA	ACTAATGAAG	AGTTCTGTTG	10140
	TAACTACCTT	TTCTTATCTT	TCTAAGGCA	AAATAAGACC	AACAGCAATC	TCTTCTATGG	10200
	CAGATCTCTA	TCCCAATAGA	TGCAATTAGT	CTGCTACTCC	ATTTAGAAAA	TGTTCACTTA	10260
	GAGGTGTTCT	GCTAACTTGA	TTGCTGGCAA	CAACAGATTC	TCTTGGCTCA	TATTTCTTTT	10320

5 CTATCTCATC TTGATGATGA TAGTCATCAT CAAGAATTGA ATGATTAAAA TAGCATGCC 10380
 TTCTCTCTTT CTCTTAATFAA GCCACATAT AAATGTACTT TTCCTCCAG AAAAATTTCC 10440
 CTGAGGAAA AATGTCCAAG ATAAGATGAA TCATTTAATA CCGTGTCTTC TAAATTGAA 10500
 ATATAATCT GTTCTGACC TGTTTAAAT GAACCAACC AAATCATACT TTCTCTTCAA 10560
 ATTTAGCAAC CTAGAAACAC ACATTTCCTT GAATTAGGT GATACCTAAA TCCTTCCTAT 10620
 GTTCTAAAT TTTGTGATTC TATAAAACAC ATCATCAATA AAATAATGAC ATAAATCAT 10680
 TTTTGTCTTA CCTGTTTCT CTCTGGAAG GGCAGGTGTC CAGTTACACA TAGGAAAGAT 10740
 AATTTAGAGA TATATTAATC ATATATAAAG GAAAATTAAA AACAGAGTAG TTCATGATGA 10800
 10 GCCTGGAGTA GAAGGCATAT CCCAGAACAG GAGGAGCCTT GTAAACCACA TAGGAACCTC 10860
 CTATTTTATG CTAAGGGGAT AAGAACTCA TTACAGGCTT TGATGGTGT TGTCAAAGA 10920
 GGGGCATAAA ATTATCATAT CCACATCTAG AAATACATC TCTGGCTACG CTGATATCAA 10980
 TGGATGCGAG GAAAGAACAG TGTGTTACC ATATATAAT TAGGAAATCA TTAGAGTATT 11040
 GGGAGTGGAA ATGGAGAGAA AGAAAGAGCC TGGGGGAATT ATTTAGGAAA TAATAGTTAC 11100
 AGAAGACAT CTAAGTTGCT GACCTATCTG ACTGGATGGA TGGAGAGATA TCTTGTCTT 11160
 15 GAGAGAAAAT GAACTTTTGG GTTTAAATTT GTACTTGATG AATTAGGTA CTTTAAATAT 11220
 TCAATGGAT TTGCTTGGCA GGCCTTGAA GATATAGTC TAAATCTCAG AAACAGATA 11280
 TGATCTGAG CTCTAAATTT GTGATATTCA ATATAAATC TTTAGAGTCA TTGGGATAAA 11340
 TATGCTAGTT GTAGCTAAAA GCAAAAATAA GATACTAGGG AGAAGGATA AAGTTAGAG 11400
 20 AAGAGAGAT CTAGAATTGA CCTTGAAGTA TATCAGCATG TGTAAAGATC AGGAATTGAT 11460
 CATTTTATT TTCCAGAAAG TAGCTTTTCT TAGGGTTCCA TATTACTCC CATAGATTCT 11520
 TCCC

A76 Protein sequence:

25 Gene name: SCCA2 or 2b, serine (or cysteine) proteinase inhibitor
 Unigene number: Hs.227948
 Probeset Accession #: AB035089
 Protein Accession #: BAB21525
 30 Signal sequence: none found
 Transmembrane domains: none found
 Serine Proteinase Inhibitor domain: 13-390
 Cellular Localization: secreted

35 1 11 21 31 41 51
 MNSLSEANTK FMDLQFQFR KSKENNIFYS PISITSALGM VILGAKDNTA QQISKVLHFD 60
 QVTENTTEKA ATYHVDKSGN VHQFQKLIT BFNKSTDAYE LKLANKLPGH KTYQLQEYL 120
 40 DAIRKPYQTS VESTDFANAE ESRKKINSW VESQTNKIK NLFFDGTIGN DITLVLVNAI 180
 YPKQWENKF KENTKEEFK WFNKNTYKSV QMMQYNSFN FALLEDVQAK VLEIPYKBD 240
 LSMIVLLENE IDGLQKLEEK LTAELKMSWT SLQNMRETCV DLHLPRFKME ESYDLKDTLR 300
 TMSWNIENG DADLSCHTWS HGLSVSKVLH KAPVEVTEEG VEAAATAVV VVLSOSPSTN 360
 ERFCCNPFLL FPIRQNKINS ILFYGRFSSP

A77 DNA SEQUENCE

45 Gene name: hypothetical protein FLJ13459
 Unigene number: none found
 Probeset Accession #: XM_047266
 50 Nucleic Acid Accession #: XM_047266
 Coding sequence: 485-1471 (underlined sequences correspond to start and stop codons)

55 1 11 21 31 41 51
 CTGACCTCAA GTGATCCACC CACCTCTGCC TCCCAAGTGG CTGGGATTAC AGGTGTGAGC 60
 CACCATGCCA GGCCTCTCTA ACCCTCTCAA GTCTGTTTC TCATCTGCAA AACAGAGGTA 120
 ATAGATCAG TATCTTCTTA ATGGAAGCAC CTGGACTACA TTTTCTTCAT TCATTGTTAT 180
 CATAATGAG GACTAACTTG TCTCCGTTG GGAGTTTGA ACCTAGACCT CATGTCTTCA 240
 TGACGTCAIC ACTGCCCCAG GCCAGCTGT GTCCCTACAC CAGCCCCAGC TGACGCATCT 300
 60 TCTTTTCTG CCGTAGAGA TGGTTACAT GCCTGGCGTG ATGCATCTG GCCTTGCAG 360
 ATCCTGGCGG GGCTGTGCCA AGCTGTGGC CTCCCTGCCC CTGAATACCG AGCCGCTGCT 420
 GTCAAGGTGG GCACCAAGT CTCTCTGACA CCACCGAGGA CCTTCCCTCC AGGGATCTCT 480
 TCACATGTGG ATTGACATCT TTCTCAAGA TGTGCTGCT CCACCCCCAG TTGACATCAA 540
 GCCTCGGAG CCAATCAGCT ATGAGCTCAG AGTTGTCTAT TGAACACCG AGGATGTGCT 600
 65 TCTGGATGAC GAGATCCAC TCACCGGAGA GATGTGAGT GACATCTATG TGAAGAGCTG 660
 GGTGAAGGGG TTGGAGCATG ACAAGCAGGA GACAGAGCTT CACTTCAACT CCTGACTCG 720
 GGAGGGGAAC TTCAATTGGC GCTTTGTGTT CCGCTTTGAC TACCTGCCCA CGGAGCGGGA 780
 GGTGAGCGTG TGGCGCAGGT CTGGACCTTT TGCTCTGGAG GAGGCGAGT TCCGCGAGCC 840
 TGCAGTGTCT GTCTGTGAGG TCTGGGACTA TGACCGCATC TCTGCCAATG ACTTCTCTTG 900
 70 ATCCCTGGAG TTGCAGCTAC CAGACATGGT GCGTGGGGCC CGGGGCCDGG AGCTCTGCTC 960
 TGTGAGCTB GCGCGCAATG GGGCCGGGOC GAGGTGCAAT CTGTTTGGCT GCGCCGCGCT 1020
 GAGGGGCTGG TGGCGGTAG TGAAGCTBAA GGAAGCAGAG GACGTGGAGC GGGAGGCGCA 1080
 GGAAGGCTCG CTGGCAGAA AGAAGCGAAA GCAGAGGAGG AGGAAGGGCC GGCAGAGA 1140
 CCTGGAGTTC ACAGACATGG GTGGCAATGT GTACATCTCT ACGGCAAGG TGGAGGCAGA 1200
 75 GTTGTAGCTG CTGACTGTGG AGGAGGCGCA GAAACGGCCA GTGGGGAAGG GCGGGAAGCA 1260
 GCTGAGGCTC CTGAGAAAC CCAGCGGCC CAAACTTCC TTCACTGGT TTGTGAACCC 1320
 GCTGAAGAAC TTGTCTTCT TCATCTGGCG CCGGTACTGG GGCACCTTGG TGCTGCTGCT 1380
 ACTGTGTCTG CTACCTCTCT TCCCTCTCT GATCTCTAC ACCATCCCTG GCCAGATCAG 1440
 CCAGGTCTTC TTGCTGCCC TCACAAAGTG ACTCTGCTG ACCTTGGACA CTACCCAGG 1500
 80 GTGCCAACCC TTCAATGCTT GCTCCTGAAA GTCTTTCTTA CCCATGTGAG CTACCCAGCA 1560
 GTCTAGTGCT TCCCTGAAAT AAACCTATCA CAGCCACTG

A78 Protein sequence:

Gene name: hypothetical protein FLJ13459

Unigene number: none found
 Probeset Accession #: XM_047266
 Protein Accession #: XP_047266
 Signal sequence: none found
 Transmembrane domains: 291-313
 C2 domain: 27-86
 Cellular Localization: plasma membrane / ER

1 11 21 31 41 51
 MWIDIFPDQDV PAPPFVDIKP RQPISYELRV VIWNTSDVVL DDENPLTGEM SSDIYVKSVM 60
 KGLEHDKQET DVHFNLSLTGE GNFWRFVFR FDYLPTEREV SVWRRSGPPA LEEAEFRQPA 120
 VLVLVQVMDYD RISANDFLGS LELQLPDMVR GARGPELCSV QLARNAGAPR CNLPRCRLR 180
 GWNVVLKE AEDVEREAQE AQAGKKRKQ RRRKGRPEDL EPTDMGGNVY ILTGKVBEP 240
 ELLTVEBAEK RPYGKGRKQF EPLEKPSRFK TSPNWFVNPL KTFVFFIWR YWRTLVLLLL 300
 VLLTVFLLLV FYTIPQIISQ VIFRPLHK

A79 DNA SEQUENCE

Gene name: Homo sapiens mRNA; cDNA DKFZp434K0322 (from clone DKFZp434K0322)
 Unigene number: Hs.161031
 Probeset Accession #: AL137708
 Nucleic Acid Accession #: AL137708
 Coding sequence: 1315-1791 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 GGCATTGATG CTGTGTGCGC GTGCGTGTGT GTGTGTGTGT GTGTGTGTGT GTGTGTGTGT 60
 GTGTGTGTGT GTCTGGAGTC ATGGCAGGGT CCCCTTCTGT CTGTCTCCTT GCTCTGCCCC 120
 AGACTGGGCG GCTGCGACAG TGAGGGTATC TGGCCTCAAC AGCTGCTTAT TCCCGATGGG 180
 ATGGCCTGGG CTGGGCCCTT GAGGCCAGGC TGACTTGGAC ATGGCAAGAG GGGTCCGAGG 240
 CTCCTGTGGG CAAAGCAGGG GAGGCCCAA TGTGGAGGAA CAGAGTCTCC TGGCTGGCTG 300
 CTGCTCTCTG GAGCGGGTGG AGTCAGGGAA GAGCTGAGCT GGGGAGTCAC CCTGGGCTGG 360
 GGGTCACCGT AGGCCCCATG TAGCACCTTG GTTCCCTGCG CTGTAGGTGA CAGGAGCCAG 420
 CCCAGCCAGG TGTCCTCCCT CCCAGGCCCT TAGGCAGGCG GGTACAGGGG CCAGCAGCTG 480
 CGCCCGCCCC ACCTTCCCTTC CCACCCACAT GCCGAAGGCT GGCACGGCAG GCAGGTGGAC 540
 GAGTCCAGAG AGCGGCTGAG TCAGTGTGTG TGGAAATGTC TGGCGCTCC CAGCTGCACC 600
 CTGCCCTTAC CTGCCCTTCA TCCTCAGGCG CTGCGGCCCT GAGGCCCTCG 660
 CAGGAATGCA CCTTAGCCCC AGGCCCTGCTC AGTGAGCTCC GCGCAGAGCC AGCCCTGCTC 720
 CTCCCGCCAT GACCTTCAGG ACCCTCTCTG GCTTCCAGT TCCCTGGGGT TGCAGTGAC 780
 ATGCTCCACC TGCAATCTCG GCAGAACATG GTGGGCCCCA GCTGTGGTGC GTGCTGGGGT 840
 AGAGGCAAGG AAGTGATGGG ACCGCAAGAG TGAGACCCCC AGGATGAGAG TGGGACCCCC 900
 AGGCAAGGCC GCGCTCCAGG GCGCCAGGAG AGAGAGAGCAG GAGGGAGAGG AGCTTCTCTG 960
 TGGAGGAGCG ATCTACAGT GGGGGCAAGG GTGCTCTGAG GTCCGGTGA GGCAGGGACT 1020
 AGGCTGCCCA GCGCTGCTCG GCTTGGCTGG GCGTGGGGCG TGCTGGGAGG TGGCTGGGAG 1080
 GCTGGGCTGG GGCAGCTTAA CTGGAGCTTT GGCAGGGTCC CAGAGCTTCC CTCCCTTCAG 1140
 CTCTCTGCTG CACAGAACCC TGCCCTCTGG CCACCCCTGT CTGCTCTCTT GCGCTGGCAG 1200
 ACCCAGCACT GGCCTCTGCT AGTCAGATGG GGTAGCGGGC AGGGGCCGGA GGGGCCACCC 1260
 TCCAGCTGCA CCCAGCTTCC TGGGCGCTCT CTTCACAAAC AGCAGGATAG AAGATGAGGG 1320
 CACCAACAGG TCTCTCCAG TGCCCGCGCC CCAGCTGGCA CCACAGCTAT ACCTGGGCTT 1380
 ATTCCAGACC TTGTGCGCGG GACCCCTGTG GAGTTGTGGG ATTCCAGAGA GGGGTGTGGG 1440
 GATAACCCAG CCAGATGGGG GCTGCACTG TCACAGATAG CACTCAGCCT GCGCTTACCC 1500
 CAGGGGCCCT GCTGGGCTCT CATTTGCCGG CCGCTTGGCG GCGGCGTCTT CTCTGCTTCC 1560
 TGCTCTCTCT GTGCTGCTGT CTGCTGCTGC CGCCGCCACA GGAAGAGGCC CAGGGACAAAG 1620
 GAGTCCGTGG GTCTGGGCGG TGCCCGCGCC ACCACCAACA CCCACTGGT GAGGAGCGGC 1680
 TCCTTGCTCA CTAGTCCAG AGAGGGCTTG AAATCCAGGC TCCAGAGCCC AGGCGAGCGA 1740
 GGGAGTTCA GCGCCAGGGA TGGTTTAACC CCACAGAGG CAGGGCGTTG AGGACCTTCC 1800
 TGGCAGGAAA AGTGGGTGAA CAGAGGTGAG AAGGAGGCCA TGCAACAGGG GCTGCCCTAT 1860
 GGGCCGAGGG GAGCCACAGC GGGTCTCTGA GGAAGGCAGG GGGTACCCCA GATGCCAGGT 1920
 TTTGGGTGGG TTTGGGCGGT CTCACAGAGC GAAGCCGAGC ATTGTGCTT GTTGGGTGGC 1980
 CTGGCTTGA GCGGGGGGGT CTGACCCAT GTCAITGCAAG GGTGCCCCGG GAGCCAGGGG 2040
 CTCTGATGAG GCATGATGTC AGCACCACTT GCGCTTGTTC CCAACTCACT CAGGTGCAA 2100
 CCTGATGAG ATGGCCTGGA GTCCAGCCCG GGGGATGCTC AGCAATGGGG GTGCTTCCAG 2160
 CTCTCCCTGG AGTTGCACTT TGGAGCCAG GAGGTGAAGG GCGCCGCTGC GCAGGACCAAG 2220
 CGGTTCTGGG AGTTTCCGGA AAGGGTGAAG GGGGAAGGCC AGACCCCATG CCTTGGGTGG 2280
 TGGGAGCTG ACAGGGCAGG GCGCTTGGG TGAGCCCAAC CCGCTGGCTC CCAGATCAGG 2340
 GTGGGCTTGA GGCAGGCGAG CGACCTGAGG CTTGGGGGCA CCGTGGACCC CTATGCCCGG 2400
 GTCAGGTTCT CCACCCAGGC CGACACAGAG CATGAGACAA AAGTGCACCG AGGCACGCTC 2460
 TGCCCGGTGT TTGACGAGAC CTGCTGCTTC CAGGTGAGTC AGGATGGTTC GCGCTGGGTG 2520
 GCGTGGACGG CTGGATGGGC CTGGGCTGGG TGGGCTGGG CAGCTGGGTG GCGCTGGGCA 2580
 GCTGGGTGGG CTTGAGCTAG GGCAGCAGGG CTTGGCTCAC GCGCTGCTCT CAGATCCCGC 2640
 AGGCGGAGCT GCGAGGGGCC ACCCTGCAAG TGCAGCTTTT CAACTTCAAG CGCTTCTCGG 2700
 GGCATGAGCC CTTGAGGCTG CTCCGTCTGC CACTGGGCAC CGTGGATCTG CAGCATGTTT 2760
 TGGAGCACTG GTACCTGCTG GGCOCGCCGG CTGCCACTCA GGTGAGGTGC TGGTCAACAG 2820
 GCCACAGCCC AAGGCAGAGC TGGCAGGGAC CCGCCCTAT GGGCCATCGG AAGACAGGC 2880
 CTGATGGGCA GCATTTTCGG GGGTCTGAGC CCCAATCTCG CCAGATCAC CCTCCCGGSC 2940
 TGAAGCCCTT CTGCTGCCCC ACAGCCCGAG CAGGTGGGGG AGCTGTGCTT CTCTCTCGG 3000
 TAGTGCCCA GCTCAGGCGG CTGAGCCGTG GTGGTCTGG AGGCTCGAGG CCGCTGTTCA 3060
 GGAATGCTAG AGCCCTACGT GAAGGTCTCA CTCTGCTGA ACCAGAGGAA TGGGAGAGAA 3120
 ABAAGACAG CCACCAAAA GGCACCGCG GCCCCTACT TCAATGAGGC CTTCACCTTC 3180
 CTGGTCCCTT TCAGCTAGGT CCAGATGTC GACCTGGTGC TGGCTGTCTG GAGCCGAGC 3240
 CTGCCCTCC GAAGTGAAGC GGTAGGCAAG GTGCACTGG GTGCCCGGCG CTGGGGCAG 3300

CCCTGTCAGC ACTGGGACAG CATGCTGGCC CACGCCCGGC GGGCCATTGC CCAGCGGCAC 3360
 CCCTGCGGC CAGCCAGGCA GGTGGACCGC ATGCTGGCCC TGCGGCCCG CCTTGCCCTG 3420
 CGCTGCGCT TGCCCACTC CTGAATGCAC CACATGCTC TGTCTCCCG CTGAGCCAG 3480
 GCCTTGCCC AGGCCGCCCT GCAGGACCAC TGCAATAAAC GCCTTCTCT GGC

A80 Protein sequence:

Gene name: Homo sapiens mRNA; cDNA DKFZp434K0322 (From clone DKFZp434K0322)
 Unigene number: Hs.161031
 Probeset Accession #: AL137708
 Protein Accession #: CAB70885
 Signal sequence: none found
 Transmembrane domains: 69-85
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 | | | | |
 MGHPVPSPSA PAPAGITTAIF GLIPDLVAGT FCELDKDSQEG CGDNPAKNGL QLSTDALSLA 60
 STPGPRWALI AGALAAGVLL VSCLLCAACC CCRHRKIKPR DKESVGLGSA RGTITTHLVR 120
 SGLLLTQSRG GLKSLRQSPG QRGEFSFRDG LTPTEAGR

A81 DNA SEQUENCE

Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 Probeset Accession #: X63629
 Nucleic Acid Accession #: X63629
 Coding sequence: 54-2543 (start and stop codons are underlined)

1 11 21 31 41 51
 | | | | |
 GCGGAACACC GGCCTGCGCT CGCGGCAGCT GCCTCAGCCC TCTCTCTGCA GCCATGGGGC 60
 TCCCTCGTGG ACCTCTCGCG TCTCTCTCC TTCTCCAGGT TTCTCTGGCG CAGTGGCGCG 120
 CCTCCGAGCC GTCCCGGGCG GTCTTCAGGG AGGCTGAAGT GACCTTGGAG GCGGGAGGCG 180
 CGGAGCAGGA GCCCGGCCAG GCCTGCGGGA AAGTATTTCAT GGGCTGCCCT GGGCAAGAGC 240
 CAGCTCTGTT TAGCACTGAT AATGATGACT TCACTGTGGG GAATGGCGAG ACAGTCCAGG 300
 AAGAAGGTC ACTGAAGGAA AGGAATCCAT TGAAGATCTT CCGATCCAAA CGTATCTTAC 360
 GAAGACACAA GAGAGATTGG GTGGTTGCTC CAATATCTGT CCTGAAAT GGCAGGGTC 420
 CCTTCCCCCA GAGACTGAAT CAGCTCAAGT CTAATAAAGA TAGAGACACC AAGATTTTCT 480
 ACAGCATCAC GGGCCCGGGG GCAGACAGCC CCCCTGAGGG TGTCTTCCCT GTAGAGAAAG 540
 ABACAGGCTG GTTGTGTTTG AATAAGCCAC TGGACCGGGA GAGGATTGCC AAGTATGAGC 600
 TCTTTGGCCA CGCTGTGTCA GAGAAATGGT CCTCAGTGGG GAGCCCATG AACATCTCCA 660
 TCATCGTAC CGACAGAAAT GACCAACAGC CCAAGTTTAC CCAGGACACC TTCCGAGGGA 720
 GTGTCTTAGA GAGAGTCTTA CCAGGTACTT CTGTGATGCA GGTGACAGCC ACAGATGAGG 780
 ATGATGCCAT CTACACCTAC AATGGGGTGG TTGCTTACTC CATCCATAGC CAAGAACCAA 840
 AGGACCCACA CTACCAATTC ACCCGAGCAC AGGCACCATC AGCGTCATCT 900
 CCAGTGGGCT GGCAGCGGAA AAGTCCCTG AGTACACACT GACCATCCAG GCCACAGACA 960
 TGGATGGGGA CGGCTCCACC ACCACGGCAG TGGCAGTAGT GAGATCTCTT GATGCCAATG 1020
 ACAATGCTCC CATGTTTGGC CCGAGAAAT AGGAGGCCCA TGTGCTTGAAG AATGCAGTGG 1080
 GCGATGAGGT GCGAGAGGCT AGCGTCACTG ATCTGGACGC CCGCAACTCA CCAGCGTGCC 1140
 GTGCCACTTA CCTTGTCTAG GCGGTGAGCG ACGGGGACCA TTTTACCATC ACCACCCACC 1200
 CTGAGAGCAA CCGGGGCATC CTGACAACCA GGAAGGGTGT GGAATTTTGA GGCRAAAACT 1260
 AGCACACCT GTACGTGAAA GTGACCAACG AGGCCCTTTT TGTGCTGAAG CTCCCAACT 1320
 CCACAGCCAC CATAGTGGTC CAGGTGGAGG ATGTGAATGA GGCACCTGTG TTTGTCCAC 1380
 CCTCCAAAGT CGTTGAGGTC CAGGAGGGCA TCCCACTGG GAGGCTGTGT TGTGTCTACA 1440
 CTGCAAGAGA CCGTGAACAG GAGAATCAAA AGATCAGCTA CGCATCCTG AGAGACCCAG 1500
 CAGGGTGGCT AGCCATGGAC CAGACAGTGG GGCAGGTTCAG AGCTGTGGGC ACCCTCGACC 1560
 GTGAGGATGA GCAGTTTGTG AGGAACAACA TCTATGAAGT CATGGTCTTG GCCATGACA 1620
 ATGGAAGCCG TCCCAACACT GGCACGGGAA CCTTCTGTCT AACACTGATT GATGTCAAG 1680
 ACCATGGCCC AGTCCCTGAG CCGCGTCAGA TCACCATCTG CAACCAAGC CCTGTGGCC 1740
 ACGTGTCTGA CATCAAGGAC AAGGACCTGT CTCCCAACAC CTCCCTTTTC CAGGCCAGC 1800
 TCACGATGA CTCAGACATC TACTGGACGG CAGAGGTCAA CGAGGAAGGT GACACAGTGG 1860
 TCTTGTCCCT GAAGAAGTTC CTGAGCAGG ATACATATGA CGTGCACCTT TCTCTGTCTG 1920
 ACCATGGCAA CAAGAGCAG CTGACGGTGA TCGGGGCCAC TGTGTGGCAG TGCCATGGCC 1980
 ATGTGGAAC CTGCGCTGGA CCGTGGAAAG GAGGTTTCAT CCTCCCTGTG CTGGGGGCTG 2040
 TCCGTGCTCT GCTGTCTCTC CTGCTGGTGC TGCTTTTGTG GTTGAGAAAG AAGCGGAAGA 2100
 TCAAGGAGCT CCTCTACTC CCAGAGATG ACACCCGTGA CAACGTCTTC TACTATGGCG 2160
 AAGAGGGGGG TGGCGAAGAG GACCAGGACT ATGACATCAC CCAGCTCCAC CGAGGTCTGG 2220
 AGGCCAGGCC GAGGTGGTT CTCCGCAATG ACGTGGCACC AACCATCATC CCGACACCCA 2280
 TGTACCGTCC TAGGCCAGCC AACCCAGATG AATCGGCAG CTTTATAATT GAGAACCTGA 2340
 AGCGGGCTAA CACAGACCCC ACAGCCCGCG CCTAAGACAC CCTCTTGGTG TTGACTATG 2400
 AGGGCAGCGG CTCGACCGCC GCGTCCCTGA GCTCCCTCAC CTCTCCGCC TCCGACCAAG 2460
 ACCAGATTA AGATTATCTG AACGAGTGGG CGAGCCGCTT CAAGAAGCTG GCAAGCATGT 2520
 ACGGTGGCGG GAGGAGCGAC TGGCGGCCCT GCGTCAGGG CTGGGGACCA AACGTGAGGC 2580
 CACAGAGCAT CTCGAGGGGG TCTCAGTTCC CCTTCAGCT GAGGACTTGG GAGCTTGTCA 2640
 GGAAGTGGCC GTAGCAACTT GGCGGAGACA GGCTATGAGT CTGACGTTAG AGTGGTTGCT 2700
 TCCTTAGCCT TTCAGGATGG AGGAATGTGG CGAGTTTGA TTAGCAGCTG AAAACCTCTC 2760
 CACCTGGGGC AGGGTTGCTT CAGAGGCCAA GTTCCAGAA GCCTCTTACC TGCCGTAAAA 2820
 TGCTCAAOCC TGTGTCTCTG GCTGGGCCCT GCTGTGACTG ACCTACAGTG GACTTTCTCT 2880
 CTGGAATGGA ACCTTCTTAG GCTTCTGGT GCAACTTAAT TTTTCTTTT AATGCTATCT 2940
 TCAAAACGTT AGAGAAAGTT CTTCAAAAGT CGAGCCGAGA GCTGCTGGGC CCAGTGGCGG 3000
 TCTCTGATTT CTGGTTTCCA GACCCCAATG OCTCCCATTC GAGTGGATCT CTGGTTTCT 3060
 ATACTGATG TGCCTAGGTT GCGCTTATT TTTTATTTC OCTGTGGGT TGCTATAGAT 3120
 GAAGGGTGA GACAATCGTG TATATGTACT AGAAGTTTTT TATTAAGAA A

A82 Protein sequence:

Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 Probeset Accession #: X63629
 Protein Accession #: CAA45177
 Signal sequence: 1-24
 Transmembrane domain: 659-675 (second underlined sequence)
 Cellular localization: plasma membrane

```

1      11      21      31      41      51
|      |      |      |      |      |
15  MGLPRGPLAS LLLLQVCNWLQ CAASEPCRAV FREAEVTLEA GGAEQEPGQA LGKVFMGCPG 60
    QEPALFSTDN DDFTVRNGET VQERRSLKER NPLKIFPSKR ILRRHKRDWV VAPISVPENG 120
    KGFFPQRINQ LKSNKORDYK IFYSITGPGA DFPFEGVFAV EKETGMWLLN KPLDREBIK 180
    YELFGHAVSE NGASVEDFMN ISIIVTQND HKPKFTQDTF RGSVLEGVLP GTSVMQVTAT 240
    DEDDAIYYTN GVVAISHSQ EPKDPHDLMF TIRRTGTIS VISSGLDREK VPETTLTIQA 300
    TDMDGGGSTT TAVAVVILLD ANDNAPMFDQ QKYBAHVPEV AVGHEVQRLT VTDLDAPNSP 360
    ANRATYLMG GDDGDHFTIT THPESNQIL TTRKGLDPEA RNQHTLYVEV TNEAPFVLK 420
    PTSTATIVVH VEDVNEAFVF VFPKVVVEVQ EGIPTGEFVC VYTAEDPDKE NQKLSYRILR 480
    DPAGWLAMP DSGQVTAVGT LDREDEQFVR NNIEVMVLA MDNGSPPTTG TGTLLTLLID 540
    VNDHGVPEEF RQITICNQSP VRHVLNITDK DLSPTSPFO AQLTDDSDIV WTAEVNEBGD 600
    TVVL6LKKFL KQDTYDVHLS LSDHGNKEQL TVIRATVCDC HGVETCPGP WKGGFILPVL 660
    GAVLALLFL LVLLLVRRK RKIKEPLLLP EDDTRDNVYF YGEGGGGEED QDYDITQLHR 720
    GLEARPEVVL RNDVAPTIIP TMYRPRPAN FDEIGNFILE NLKAANTDPT APPYDTLLVF 780
    DYEGSGSDAA SLSSLTSSAS DQDQDYDYLN EWGSRFKKLA DMVGGGEDD
  
```

A83 DNA SEQUENCE

Gene name: putative G-protein coupled receptor
 Unigene number: Hs.16085
 Probeset Accession #: F07953
 Nucleic Acid Accession #: NM_016334
 Coding sequence: 104-1471 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
40  AGCACCTGGG AAAAGGCAGA CCGTGTGAGG GGGCCTGTGG CCCCAGCGTG CTGTGGCCTC 60
    GGGGAGTGGG AAGTGGAGGC AGGAGCCTTC CTACACTTC GCCATGAGTT TCCTGATCGA 120
    CTCACGATC ATGATTACCT CCCAAATACT ATTTTGTGA TTGGGGTGGC TTTTCTTCAT 180
    GCGCCAAATG TTAAAGACT ATGAGATACG TCAGTATGTT GTACASGGA TCCTCTCCGT 240
    GAGTTTGCA TTTCTGTGA CCATGTTTGA GCTCATCATC TTTGAAATCT TAGGAGTATT 300
    GAATAGCAGC TCCCGTTATT TTCACTGGA AATGAACCTG TGGTAATTC TGCTGATCCT 360
    GGTTTTCATG GTGCCCTTTT ACATGGGCTA TTTTATGTG AGCAATATCC GACTACTGCA 420
    TAAACAACGA CCGCTTTTTC CCGTCTCTCT ATGGCTGACC TTTATGTATT TCTTCTGGAA 480
    ACTAGGAGAT CCGCTTTCCCA TTCTCAGCCC AAAACATGGG ATCTTATCCA TAGAACAGCT 540
    CATCAGCCGG GTTGTGTGTA TTGGAGTGAC TCTCAGGCT CTCTCTCTG GATTTGGTGC 600
    TGTCACCTGC CCATACACTT ACATGTCTTA CTTCCTCAGG AATGTGACTG ACACAGATAT 660
    TCTAGCCCTG GAACGGCGAC TGCTGCAAA CATGGATAT ATCATAAGCA AAAAGAAAG 720
    GATGGCAATG GCACGGAGAA CAATGTTCCA GAAGGGGGA GTGCATAACA AACCATCAGG 780
    TTTCTGGGGA AGATAAAAA GTGTACCAC TTCAGCATCA GGAAGTGAAG ATCTTACTCT 840
    TATTCAACAG GAAGTGGATG CTTTGGGAAG ATTAAGCAGG CAGCTTTTTC TGGAAACAGC 900
    TGATCTATAT GCTACCAAG AGAGAATAGA ATACTCCAAA ACCTTCAGG GGAATATTT 960
    TAAATTTCTT GGTACTTTT TCTCTATTTA CTGTGTTTGG AAAATTTTCA TGCTTACCAT 1020
    CAATATTGTT TTTGATCGAG TTGGGAAAC GATCTCTGTC ACAAGAGGCA TTGAGATCAC 1080
    TGTGAATTAT CTGGGAATCC AATTTGATGT GAAGTTTGG TCCCAACACA TTTCTTCTAT 1140
    TCTTGTGGA ATAATCATG TCACATCCAT CAGAGGATG CTGATCACTC TTACCAAGTT 1200
    CTTTTATGCC ATCTCAGCA GTAAGTCTCT CAATGTCTAT GTCTGTCTAT TAGCAGAT 1260
    AATGGGCATG TACTTTGTCT CTTCTGTGCT GCTGATCGA ATGAGTATG CTTTGAATA 1320
    CCGCACCATA ATCACTGAAG TCCCTGGAGA ACTGCAGTTC AACTTCTATC ACCGTTGTT 1380
    TGAATGTATC TTCTGTGTA GCGCTCTCTC TAGCATACTC TTCTCTATTT TGGCTCACAA 1440
    ACAGGCACCA GAGAAGCAAA TGGACCTTG AACTTAAGCC TACTACAGAC TGTAGAGGC 1500
    CAGTGGTTTC AAAATTAGA TATAAGAGGG GGGAAAAATG GAACCAAGGC CTGACATTTT 1560
    ATAAACAAC AAAATGCTAT GTAGCATTT TTCACCTTCA TAGCATACTC CTTCCCCCTC 1620
    AGGTGATACT ATGACCATGA GTAGCATCAG CCAGAACATG AGAGGGAGAA CTAATCAAG 1680
    ACAATACTCA GCAGAGAGCA TCCCGTGTGG ATATGAGGCT GGTGTAGAGG CGGAGAGGAG 1740
    CCAGAAACT AAAGGTGAAA AATCACTGG AACTCTGGGG CAAGACATGT CTATGGTAGC 1800
    TAGGCCAAAC ACGTAGGATT TCCGTTTAA GGTTCACATG GAAAGGTTA TAGCTTGGC 1860
    TTGAGATTGA CTCATTAAAA TCAGAGACTG T
  
```

A84 Protein sequence

Gene name: putative G-protein coupled receptor
 Unigene number: Hs.16085
 Protein Accession #: NP_057418.1
 Signal sequence: none found
 Transmembrane domains: 5-27, 42-64, 76-98, 110-132, 144-166, 289-311, 342-364, 380-402,
 424-446
 Cellular Localization: plasma membrane

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1      11      21      31      41      51

```

5 MSFLIDSSIM ITSQILFFGF GWLFFMRQLF KDYEIRQYVV QVIFSVPFAF SCIMFELIIF 60
 ELLGVLNSSS RYFHWKNNLC VILLILVFNV PFYIGYFIVS NIRLLHKQRL LFSCLMLWTF 120
 MYFFWKLQDP FPIILSPKHGI LSIEQLISRV GVIGVTLMAL LSGFGAVNCP YTYMSYFLRN 180
 VTDLDLLE RRLQYMDMI ISKKRMAMA RRTMFQKGEV HNKPSGFWGM IKSVTTSASG 240
 SENLTLIQQE VDLEELSRO LFLSTADLYA TKERIEYSKT PKGKYFNLFG YFFSIYCVWK 300
 LFMATINIVP DRVGKIDVET RGIETVNVY GIQFDVKFWS QHISFILVGI IIVTSIRGLL 360
 ITLTKEFYAI SSSKSSNVIV LLLAQIMGMV FVSVLLIRM SMPLEYRTII TEVLGELQFN 420
 FYHRNFDVIF LVSLALSSILF LYLAKKQAPK QKMAP

10 A95 DNA SEQUENCE:
 Gene name: TTK protein kinase
 Unigene number: Rs.169B40
 Probeset Accession #: M86699
 Nucleic Acid Accession #: NM_003318
 Coding sequence: 1026-3551 (underlined sequences correspond to start and stop codons)

20 1 11 21 31 41 51
 1 GGAATTCCTT TTTTITTTTT TTGAGATGG AGTTTCACTC TTGTTGGCCA GGCIGGAGTG 60
 2 CAATGGCACA ATCTCAGCTT ACTGCAACCT CGCCTCCCGG GGTTCAGCG ATTCTCCTGC 120
 3 CTCAGCCTCT CAGTAGCTG GGAATACAGG CATGTGCCAC CACCCCTGGC TAACTAATTT 180
 4 CTITTTCTAT TAGTAGAGAT GGGGTTTCAC CATGTGGTC AGGCTGGTCT TAAACTCCTG 240
 25 ACCTCAGGAG ATCCACTTGC CTGGCCCTCC CAAAGTGCTA GGATTACAGC CGTGAAACTG 300
 6 TGCTGGCTG ATCTTTTTT TGTGTGTGGA TTTTGAAAC AGGCTCTCCC TTGCTGCCCC 360
 7 AGGCTGGAGT GCAGTGGTGC GATCTGGCT CACTATAACC TCCACTCCT GGTTCRAGT 420
 8 GATCCTCCCA CTTTAGCCTC CTGAGTAGCT GTGATTACAG GGTGACCA CCACACCCCG 480
 9 CTAATTTTTT TATTTTATC AGAGACAGGG TTTCACCATG TTGCCCAGGC TGTCTCAAAA 540
 30 CTCTGGACT CAGGGATCC GCCTGCCTCC ACTTCCCAAA GTCCCGAGAT TACAGGTGTG 600
 10 AGTCACCATG CCGACCTTAA TAATTCITAA GTCAATTTT CTGGTCCATT TCATCCTTAG 660
 11 GGTCCACAGA ACAAATCTGC ATTAGCGGT ACAATAATCC TTAACITCAT GATTACAAAA 720
 12 AGGAAGATGA AGTGATTCTT GATTAGAAA GCGGAAGTAG TAAGCCACT GCACACTCCT 780
 13 GGAATGATAT CCTAAATCCA GATACAGTAA AATGGGGTA TGGGAAGGTA GAATACAAAA 840
 35 TTTGGTTTAA ATTAATATC TAAATATCTA AAAACATTTT TGGATACATT GTTGATGTGA 900
 14 AATGATAGCT GTACAGACTT CCTAGAAAAC AGTTTGGGTT CCATCTTTTC ATTTCCCCAG 960
 15 TGCAGTTTTC GGTAGAAATG GAATCCGAGG ATTTAAGTGG CAGAGAAATG ACAATTGATT 1020
 16 CCATAATGAA CAAAGTGAGA GACATTAANA ATAAGTTTAA AATGAAGAC CTACTGATG 1080
 40 AACTAAGCTT GAATAAAATT TCTGCTGATA CTACAGATAA CTCGGGAATC GTTAACCAAA 1140
 17 TTATGATGAT GGCACACAC CCAGAGGACT GGTGAGTTT GTTGTCTAAA CTAGAGAAAA 1200
 18 ACAGTGTTC GCTCACTGAT GCTCTTTTAA ATAAATGTAT TGGTCCGTAC AGTCAAGCAA 1260
 19 TTAGAGCGCT TCCCCAGAT AAATATGGCC AAAATGAGAG TTTTGCTAGA ATTCAGTGA 1320
 20 GATTGTCTGA ATTAAGGCT ATTCAAGAGC CAGATGATGC ACGTACTAC TTTCAAAATG 1380
 45 CCAGAGCAAA CTGCAAGAAA TTGCTTTTTC TTCAATATC TTTTGACAAA TTGAACTGT 1440
 21 CACAGGTATA GTCTAAAAA AGTAAACAC TTCTTCAAAA AGCTGTAGAA CCGGAGCAGT 1500
 22 TACCACATGA AATGCTGGAA ATTGCCCTGC GGAATTTAAA CCTCCAAAAA AAGCAGCTGC 1560
 23 TTTCAAGAGA AAGACAAATC AATTTATCAG CATCTACGGT ATTAAGTGC CAAGAATCAT 1620
 24 TTTCCGCTC ACTTGGGCTT TTACAGATA GGAACAACAG TTGTGATTCC AGAGGACAGA 1680
 50 CTACTAAAGC CAGGTTTTTA TATGGAGAGA ACATGCCACC ACAAGATGCA GAAATAGGTT 1740
 25 ACCGGAATTC ATGAGACAAA ACTAACAGTC ATGCCCATTT GGAAGAGTCC 1800
 26 CAGTTAACTT TCTAAATAGC CCAGATTGTG ATGTGAAGAC AGATGATTC GTTGTACCTT 1860
 27 GTTTTATGAA AGTCAAAATC TCTAGATCAG AATGCCGAGA TTTGGTTGAG CCGGATCTA 1920
 28 AACCAGTGG AATGATTCCT TGTGAATTAA GAAATTTAAA GTCTGTTCAA AATAGTCAAT 1980
 55 TCAAGGAACC TCTGGTGTCA GATGAAAGA GTTCGAACT TATTATTACT GATTCAATTA 2040
 29 CCTGATGAT TAAACGGAAC TCAAGTCTTC TAGCTAAAT AGAAGAAACT AAAGAGTATC 2100
 30 AAGAACAGGA GGTTCAGAG AGTAACAGGA AACAGTGCCA AGCTAAGAGA AAGTCAGAGT 2160
 31 GTATTAAGCA GATCTCTGCT GCATCTTCAA ATCACTGGCA GATTCGGGAG TTAGCCGAA 2220
 32 AAGTTAATAC AGAGCAGAAA CATACCACTT TTGAGCAACC TGTCTTTTCA GTTTCAAAA 2280
 60 AGTCACCAAC ATATCAACA TCTAAATGGT TTGACCCAAA ATCTATTTGT AAGACACCAA 2340
 33 GCAGCAATAC CTGGATGAT TACATGATCT GTTTTGAATC TCCAGTTGTA AAGATGACT 2400
 34 TTCCACCTGC TTGTCACTTG TCAACACCTT ATGGCCAAAC TGCTGTTCCT CAGCAGCAAC 2460
 35 AGCATCAAT ACTTGCCACT CCACCTCAAA ATTTACAGGT TTTAGCATCT TCTTCAGCAA 2520
 36 ATGAATGCAT TTGGTTTAAA GGAAGAATTT ATTCATATT AAAGCAGATA GGAAGTGGAG 2580
 65 GTTCAAGCAA GGTATTTTCA GTGTTAAATG AAAAGAAACA GATATATGCT ATAAATATG 2640
 37 TGAACCTAGA AAGAGCAGAT AACCACACTC TTGATAGTTA CCGGAACGAA ATAGCTTATT 2700
 38 TGAATAAATC ACACACACAG AGTGATAAGA TCATCCGACT TTATGATTAAT GAAATCAAGG 2760
 39 ACCAGTACAT CTACATGGTA ATGGAGTGTG GAAATATTGA TCTTAATAGT TGGCTTAAAA 2820
 40 AGAAAAATC CATTGATCCA TGGGAACGCA AGAGTACTG GAAATATATG TTAGAGGCAG 2880
 70 TTCACACAAT CCATCAACAT GGCATTGTTT ACAGTATCTT TAACCCAGCT AACTTTCTGA 2940
 41 TAGTTGATGG AATGCTAAG CTAAATGATT TTGGGATTGC AAACCAATG CAACAGATA 3000
 42 CAACAAGTGT TGTAAAGAT TCTCAGTTG GCACAGTTAA TTATATGCCA CCAGAGCAAA 3060
 43 TCAAGATAT CTCTCTCTCC AGAGAGAAAT GGAATCTTAA GTCAAGATA AGCCCAAAA 3120
 44 GTGATGTTG GTCCCTAGGA TGTATTTTGT ACTATATGAC TTACGGGAAA ACACCATTTT 3180
 75 AGCAGATAT TAATCAGATT TCTAAATTAC ATGCCATAT TGAATCTAAT CATGAAATG 3240
 45 AATTTCOCGA TATTCCAGAG AAGATCTTTC AAGATGTGTT AAGTGTGTT TTAAGAGGG 3300
 46 ACCCAACACA GAGGATATCC ATTCCTGAGC TCCTGGCTCA TCCATAATG CAAATTCAAA 3360
 47 CCAATCCAGT TAACCAATG GCCAAGGGA CCACTGAAGA AATGAATAT GTTCTGGGCC 3420
 48 AACTGTGTGG TCTGAATCT CCTAATCCA TTTTGAAGC TGCTAAACT TTATATGAAC 3480
 80 ACTATAGTGG TGGTGAAGT CATATTTCTT CATCTCCAA GACTTTTGAA AAAAAAGGG 3540
 49 GAAAAAATG ATTTCCAGTT ATTCGTAATG TCAGATAGGA GGTATAAAT ATATTGGACT 3600
 50 GTTATACCTT TGAATCCCTG TGGAAATCTA CATTTGAGA CAACATCACT CTGAAGTGT 3660
 51 ATCAGCAACA AAAATCCAGT GAGATTATCT TTAAGAGAAA ACTGTAAAA TAGCAACCAA 3720
 52 TATGCACT GTATATATG TAGACTTGT TTCTCTGTT TATGCTCTG TGAATCTAC 3780
 53 TTGACATCAT TTTACTCTG GAATAGTGGG TGGATAGCAA GTATATTCTA AAAAATTTG 3840

TAAATAAAGT TTTGTGGCTA AATGA

A86 Protein sequence:

5 Gene name: TTK protein kinase
 Unigene number: Hs.169840
 Probeset Accession #: M86699
 Protein Accession #: NP_003309
 Signal sequence: none found
 10 Transmembrane domains: none found
 Protein Kinase Domain: 510-775
 Cellular Localization: cytoplasmic and nuclear

1 11 21 31 41 51
 15 MNKVRDIKKN FKNEDLTDEL SLNKISADTT DNSGTVMQIM MANNPEDWL SLLKLKENS 60
 VPLSDALLNK LIGRYSQAIE ALPPDKYQGN ESPARIQVRF AELKAIQEPD DARDVFMAR 120
 ANCKQFAFVH ISFAQFELSQ GNVKSKQLL QRAVERGAVP LEMLEIALRN LNLQKQQLS 180
 EEEKKNLGS TVLTAQESFS GSLGHLQNRN NSCDNRQQT KARFLYGENM PQDAEIGYR 240
 NSLRQTNKTK QSCPPGRVPV NLNSPDCDV KTDDSVVPCF MKRQTSRSEC RDLVVPGRSKP 300
 20 SGNDSCELRN LKSVQNSHPK EPLVDEKSS ELIITDSITL KNTKESLLA KLEETKEYEC 360
 PEVPESNQKQ WQAKRKSECI NQNPAASSNH WQIPELARKV NTSQKHITFE QPVFVSXQS 420
 PPISTSKWFD PKSICKTPSS NTLDDVMSCF RFPVVKNDFF PACQLSTFYG QPACFQQQOH 480
 QILATPLQNL QVLASSANE CISEVKGRYS ILKQIGSGGS SKVFOVINEK KQIYAIKYN 540
 25 LEEADNQTLN SYRNEIAYLN KLQHSQDKII RLVDYEITDQ YIYMVMCCGN IDLNSWKKK 600
 KSIDPWERKS YWKNMLRAVH TIHQHGYVHS DLKPNFLIV DGLMKLIDFB IANQMPPDTT 660
 SVVKSQVGT VNYMPPPAIK DMSSEENK SKSKISPKSD VMSLGCILYV MTYGTTPFQ 720
 IINQISKLEH IIDENHIEF PDIPKDLQD VLKCKLRDP KQRIPIPELL AHPYVQIQTH 780
 FVNQMAKQTT EEMKYVLGQL VGLNSPNSIL KAAKTLREHY SGSEHNSSS SKTWEIKRKG 840
 K

A87 DNA SEQUENCE

Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)
 Unigene number: Hs.170195
 Probeset Accession #: BE616633
 35 Nucleic Acid Accession #: NM_001719
 Coding sequence: 123-1418 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 40 GGGCGCAGCG GGGCCCGTCT GCAGCAAGTG ACCGACGGCC GGGACGGCCG CCTGCCCOCT 60
 CTGCCACCTG GGGCGGTGCG GGCCCGGAGC CCGGAGCCCG GTTAGCGCGT AGAGCCGCG 120
 CGATGCACGT GGCCTCACTG CGAGCTGCGG CGCGGCACAG CTCTGTGGCG CTCTGGGCAC 180
 45 CCTGTTCCT GCTGCGCTCC GCCCTGGCGG ACTTCAGCCT GGACAAACGAG GTGCATCGA 240
 GCTTCATCCA CGCGCGCTTC CGCAGCCAGB AGCGGGCGGA GATGACGCGC GAGATCCTCT 300
 CCATTTTGGG CTGCGCCAC CGCCCGCGCC CGCACTTCCA GGGCAAGCAC AACTCGGCAC 360
 CCATGTCAT GCTGACCTG TACAACGCCA TGGCGGTGGA GGAGGGCGGC GGGCCCGCG 420
 GCCAGGGCTT CTCTACCCCT TACAAGGCCG TCTTCAGTAC CAGGGGCCCT CCTCTGGCCA 480
 50 GCCTCGAGA TAGCCATTTC CTCACCGAGC CCGACATGGT CATGAGCTTC GTCAACCTCG 540
 TGGAAACATGA CAAGGAATTTC TTCCACCCAC GCTACACCCA TCGAGAGTTC CGGTTTGATC 600
 TTTCACAGAT CCGCAAGGG GAAGCTGTCA CGGCAGCCGA ATTCCGGATC TACAAGGACT 660
 ACATCCGGGA CAGCTTCGAC AATGAGACGT TCCGGATCAG CGTTTATCAG GTGCTCCAGG 720
 AGCACTTGGG CAGGGAATCG GATCTCTTCC TGCTCGACAG CGGTACCCCT TGGGCTCCG 780
 55 AGGAGGGCTG GCTGGTGTTC GACATCACAG CCACCAAGCA CCACTGGGTG GTCAATCCGC 840
 GGCAACACT GGGCCCTGAG CTCTCGGTGG AGACGCTGGA TGGGAGAGC ATCAACCCCA 900
 AGTTGGCGGG CCGATTTGGG CGGCACGGGC CCCAGAACAA GCGGCCCTTC ATGGTGGCTT 960
 TCTTCAGGC CAGCGAGGTC CACTTCCGCA GCATCCGGTC CACGGGAGC AAACAGCGCA 1020
 GCCGAAACCG CTCCAGACG CCCAAGAAC AGGAAGCCCT GCGGATGGCC AACGTGGCAG 1080
 60 AGAACACGAG CAGCGACCAG AGGCAGGCTT GTAGAGACA CAGCTGTAT GTCAGCTTCC 1140
 GAGACCTGGG CTGCGAGGAC TGGATCATCG CGCTGAAGG CTACGCGGCC TACTACTGTG 1200
 ABGGGGAGTG TGCCTTCCCT CTGAACCTCT ACATGAACGC CACCAACCAAC GCCATCGTGC 1260
 AGACGCTGGT CCACCTCATC AACCCGAAA CGGTGCCAA GCCCTGCTGT GCGCCCAAGC 1320
 AGCTCAATGC CATCTCCGTC CTCTACTTGG ATGACAGCTC CAAGTTCATC CTGAAGAAAT 1380
 65 ACAGAAACAT GGTGGTCCGG GCCTGTGGCT GCCACTAGCT CCTCCGAGAA TTCAGACCTT 1440
 TTGGGGCCAA GTTTTCTCG ATCTTCCATT GCTCGCTTGG GCGAGGAACC AGCAGACCAA 1500
 CTGCTTTTGG TGAGACCTTC CCTTCCCTAT CCGCAACTTT AAGGTGTGA GAGTATTAGG 1560
 AAACATGAGC AGCATATGGC TTTTGATCAG TTTTTCAGTG CGAGCATCCA ATGAACAAGA 1620
 TCTTACAGC TGTGACGGCA AAACCTAGCA GSAACAAAAA ACACACGATA AAGAAAAATG 1680
 70 GCGGGCCAG GTCATTTGCT GGAAGTCTC AGCCATGCAC GGAAGTGTTC CCAGAGGTAA 1740
 TTATGAGGCG CTACAGCCA GGCACCCGAG CGTGGGAGG AAGGGGGCTG GGCAGGGGT 1800
 GGCACATG GTCTCTGTGC GAAAGGAAAA TTGACCCGGA AGTCTCTGTA ATAAATGTCA 1860
 CAATAAAAAG AATGAATG

A88 Protein sequence:

75 Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)
 Unigene number: Hs.170195
 Probeset Accession #: BE616633
 Protein Accession #: NP_001710.1
 80 Signal sequence: 1-30
 Pfam domains: TGF β propeptide [37-281]
 Transmembrane domains: none found
 Cellular Localization: secreted

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1      11      21      31      41      51
|      |      |      |      |      |
5  MHVRSLSRAAA PHSFVALWAP LFLRLSALAD FSLDNEVHSS FIHRRILRSQE RREMOREILS 60
   ILGLPHRPRP HLQKHN8AP MFMLDLYNAM AVEEGGPGG QGFSYPYKAV FSTQGPPLAS 120
   LQDSHFLIDA DMVMSFVNLV EEDKEFFHPR YHREFRFDL SKIPEGEAVT AAEFRIYKDY 180
   IRERFDNETF RISVYQLQE HLGRESDLFL LDRSLWASE EGMVFDITA TSNHWVNPR 240
   HNLGLQLSVE TLDGQSINPK LAGLIGRHP QNKQPFMVAF FKATEVHFRS IRSTGSKQRS 300
   QNRSKTPKNQ BALHMANVAE NSSSDQROAC KKHLYVSFR DLGWQDWILA PEGYAAYYCE 360
10  GECAFLNSY MNATNHAIVQ TLVHPINPET VFKPCCAPTQ LNAISVLYFD DSSNVILKKY 420
   RNMVVRACGC H

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A89 DNA SEQUENCE:

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15  Gene name:      Homo sapiens mRNA; cDNA DKFZp56401763 (from clone DKFZp56401763)
   Unigene number: Hs.27373
   Probeset Accession #: F13036
   Nucleic Acid Accession #: AC012478
   Coding sequence: 1-1896 (underlined sequences correspond to start and stop codons)

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20  1      11      21      31      41      51
   |      |      |      |      |      |
   ATGCGCGCGG TGCCGCTGCC CGCCCCGCTC CTGCGCGTGC TGCTGCTGCG GCTCCTGGCC 60
   GCTCCGCGCG CCGCGCGCAG CAGAGCCGAG TCGTCTCCCG CGCCGTGGCC CGAACCCGAG 120
25  CGDGAATCCG GGCCTACCGC CGGCCCGGGG CCGGGGAACA CCACCCGGTT TGGGTCTGGG 180
   GCGGCGGGCG GCAGCGGCAG CTCCAGCTCC AACAGCAGTG GCGACGCTT GGTGACCCGC 240
   ATTTCATCC TCTTCCGCGA CCTACCCACC CTCAGGCAG CGGTGATCGT GCGTTCGCC 300
   TTTACCAACC TCCTCATGCG CTGCTGCTG CTGCGCTCT TCAGTCCGG AAAGAGGTTA 360
   AAGAAGACAC GCAAGTATGA TATCATCACC ACTCCAGCAG AGCGAGTGA AATGGCGCCA 420
30  CTAAATGAAG AGGATGATGA AGATGAGGAC TCCACAGTAT TCGACATCAA ATACAGAGTG 480
   TCCTTGCCGG CTGCACTGAG ACGTCAGCTG CCAGGGTGCC AGACGCTACT GACAGTTCCT 540
   GTGCCCCGAC CCTCATCTCT CGACATGAC CTTCAGCAA GATGCAGTGG AAGGCCTGAT 600
   GGTGGAATCA GACCTGGTAA AACCTGTTT CCAGCCTGCT GGCATCTCT GGAAGTGTG 660
   TCAGTGCACA CCTGGGGTGT GAAGGACTGG ACCTGGGAAG CCTCTTGGGT CGGAGGTGTT 720
35  GAAACCAAAA CGAAGCTTAT GTATAAAACC CCAGCTCCAT CGTGCGTGT AGGCATCTGC 780
   TCAGACTGTC ACTGGCAAGC TCGTTTCCAC GTCAACCAA TGGAGTTGCT TCTGCCACCC 840
   TTTGGGCATC CCTTAAAGT GCCCCTACT TCTACTCCCG ATGGTTTTCG ACAAATGCAG 900
   CTGAATCTCA TGGAAAGCT GGATTCCTCT GCCTTACGCA GAACACCCG GGTCCATCT 960
   GCCAGGTGCT TGCCACTGGT CCGGCAGAAA ATGGCGGCTG CTGAAAGTGA CCTTCCAAAT 1020
40  CCTTGGTGGC ACTTCAGGCG CACAGGCTCT CCATAAAAA CCTTTACAC ACAAAACCATG 1080
   AGTACCTTGG CTTTGGATGT TTTCTGTGGT GCCGGCCAGC GGGGCACTTT TGTGAGAGAC 1140
   AGACAGATGA CTTGATCTCT CCAGGTTAGC TCTTCTCCA AACAGCTGCG CTGGAAGCCA 1200
   GCCCTAGAGA GTGGGTTTCC CCATCATCTC AGGCTTCTCA GAGAGTGTCC TCCGCTGAGC 1260
   ACCCATCTTG TCAGGTGGCG TCGTTTCAGAT GCCCGGGGAC AAGCCAGCCT GACGGGGAGG 1320
45  AGGGTGTTC GCGGTCCGCG GCAGTCTCTG CATGGCGGAG GGTGAGCGGG TACCGCACTC 1380
   TGCCTTTTGG TTTTGAAGAT TCTGTGTAGG CGCCATCCTC ACCTTGACCT CTTCTACAAA 1440
   ATCTGTCTCC CTTCTGTGTC CGTGGAAACAC CTACGGGAAG CCAAGAGAAG CTCAGTGACT 1500
   GTCCTTGGGT CATTTGAGCA GAGCCACAAA AAGGCAGCTG CTGCCACCGG GGAGCCTGTC 1560
   AAACGAGGCG CAGTGGGCA ATTGACCAGA CACACATGCC CTGGCTGGGG GATCACACAT 1620
50  GCGAACCTGC AGACAATTCC AGATACCCAA GGCCAGGAAG GCCACGTGA GATGTCTACT 1680
   CACCCGAGAG GAGACTTGGG TGGGGTGGCA AATTCTATT TGGAGGAAGA GGGTTTCCAG 1740
   GATGGCAGAT GGCAGAGAT GGTCTGATG TCTGAGGAAG GCCACCTAG TTTGACAGGA 1800
   TGTGAGAGGC TCACAGGTTT CCATCACTTC TCCAGCCATT CCAAGTCTTG GTCCTTCCTT 1860
   TCCCCCGGAC AGCCCTGTT TCTGTCCAGG CCTGA

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A90 Protein sequence:

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60  Gene name:      Homo sapiens mRNA; cDNA DKFZp56401763 (from clone DKFZp56401763)
   Unigene number: Hs.27373
   Probeset Accession #: F13036
   Protein Accession #: PGENESH predicted
   Signal sequence: 1-27
   Transmembrane domains: 94-115, 448-469
   Cellular Localization: not determined

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65  1      11      21      31      41      51
   |      |      |      |      |      |
   MRAVPLPAFL LFLLLALLLA APAARASRAE SVSAPNPEPE RESRPPPGPG PGNTTFPGSG 60
   AAGGGGSSSS NSSGDALVTR ISILLRLDFT LKAAVIVAPA FTILLIACLL LRVFRSGKRL 120
70  KTRKYDIIT TPAERVENAP LNEEDDED STVPDIKYRV SLPAALRRQL PGQYLLTVP 180
   VPPFFILDI LPARCSGRPD GGIRPQKTCF PAWHPFVESW SAATWGVKDW TNKPSVGVG 240
   ETKTNVMYT PAPSCVSGIC SDCEWQARFH VTMLLLLEP FGHFFKVPEPT STEHGFRQLQ 300
   LNLMEKLDSS ALRNRTRAPS ARCLPLVLA EMAAESDLFN FWHFSTAGS PIKTLYTQTM 360
75  STLGLDVFCG AGQRGTFCED RAVTKVLQGS SFSKQLRWKP ALESGFPHRL RLLRECPPLS 420
   THFVRLARD ARGQASLTCR RVFRPRQBL HGGSGAGTAT CLVLKILLR RHPHLDLFYK 480
   ICLPCCAVEH LREAKRSSVT VLASFQSPQ KAAAHGEFV KRGPSGLTR HTCPGWGITH 540
   ANLQTIPTDQ GQGGFRREVT HPGGDLGVA NFYLEEGEGF DGRQCKNVM SEEPPSLTG 600
   CERLTGSHH SESHKSWSYL SPKQPLFLSR P

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EMING**A91 DNA SEQUENCE**

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Gene name:      G protein-coupled receptor 64
Unigene number: Hs.184942

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Probeset Accession #: AA435577
 Nucleic Acid Accession #: NM_005756
 Coding sequence: 73-3117 (underlined sequences correspond to start and stop codons)

5
 10
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 65
 70
 75
 80

1 11 21 31 41 51
 AGCCAGCCCC AGGACGCGAG CGGCAGGTGT GCACAGAGGT TCTCCACTTT GTTTCTCGAA 60
 CTGCGCGTCA GGATGGTATT CTCTGTCAAG CAGTGTGGCC ATGTTGGCAG AACTGAAGAA 120
 GTTTTACTGA CGTTCAGAT ATTCCTTGTC ATCAITTTGTC TCCATGTCGT TCTGGTAACA 180
 TCCCTGGAAG AAGATACTGA TAATTCAGT TTGTCAACCAC CACCTGCTAA ATTATCTGTT 240
 GTCAATTTTG CCCCCTCTCT CAATGAGGTT GAAACACAAA GCCTCAATGA TGTTACTTTA 300
 AGCTTACTCC CTTCACAAAG AACAGAAAA ACTAAATCA CTATAGTAAA AACCTTCAAT 360
 GCTTCAGGCG TCAACCCCA GAGAAATATC TGCAATTTGT CATCTATTTG CAATGACTCA 420
 GCATTTTTTA GAGGTGAGAT CATGTTTCAA TATGATAAAG AAAGCACTGT TCCCAGAAAT 480
 CAACATATAA CGAATGGCAC CTAACTGGA GTCTCTGCTC TAAGTGAATT AAAACGCTCA 540
 GAGCTCAACA AAACCTTGCA AACCTAAGT GAGACTTACT TTATAATGTX TGCTACAGCA 600
 GAGGCCCAAA GCACATTAAT TTGTACATTC ACAATAAACC TGAATAATAC AATGAATGCA 660
 TGTCTCTCAA TAGCCCTTTT GGAAAGAGTA AAGATTGAC CAATGGAACA CTGCTGCTGT 720
 TCTGTACGGA TACCTTGCCC TTCTTCCCA GAAGAGTTGG GAAAGCTTCA GTGTGACCTG 780
 CAGGATCCCA TTGTCTGTCT TGCTGACCAT CCACBTGGCC CACCATTFTT TCCAGSCCAA 840
 TCCATCCGAG TGGTGCTCTG GGCCTCTGTG CTTTCCCAGG TCCCACAAAG TACCTCTTTT 900
 GCTGAGCTTC CAGATTATTC ACCTGTGACC CACAATGTTT CCTCTCCAAAT AGGGGAGATT 960
 CAACCCCTTT CACCCAGACC TTCAGCTCCC ATAGCTTCCA GCGCTGCCAT TGACATGCCC 1020
 CCACAGCTTC AAGCGATCTC TTCCCTATG CCCCACACCC ATGCTCCCGG CACCCCACTT 1080
 CCTGTGAAAG CCTCATTTTC CTCTCCACC GTGTCTGCCC CTGGAATGT CAACACTACC 1140
 AGCGCACCTC CTGTCCAGAC AGACATCTGC AACACCAGCA GTATTCTGTA TCTTGAGAAC 1200
 CAAGTGTGTC AGATGGAGAA GGCTCTGTCC TTGGGCGGCC TGGAGCTTAA CCTGCGAGGA 1260
 GAAATGATCA ACCAAGTCAG CAGACTCTCT CAITCCCCCG CTGACATGCT GCGCCCTCTG 1320
 GCTCAAGAT TGTGAAAGT AGTGGATGAC ATTGGCTTAC AGCTGAACCT TTCAACACG 1380
 ACTATAAGTC TAACCTCCCC TTCTTTGGCT CTGGCTGTGA TCAGAGTGAA TGCCAGTAGT 1440
 TTCACACAA CTACCTTTGT GGCACAAAG CCTGCAATTC TTCAGGTTTC TCTGAAACCC 1500
 CAAGCTCTCT AGAACAGTAT TGGCACATTT ACTCTTCTT CATCGCTGAT GAATAATTTA 1560
 CCAGCTCATG ACATGGAGCT AGCTTCCAGG GTTCAGTTCA ATTTTTTGA AACACCTGCT 1620
 TTGTTTCAGG ATCCTTCCCT GGAGAACCTC TCTCTGATCA GCTACGTCAT ATCATCGAGT 1680
 GTTGCACACC TGACCGTCAG GAACCTGACA AGAACGTGA CAGTCACATT AAAGCACATC 1740
 AACCCGAGCC AGGATGAGTT AACAGTGAGA TGTGTATTTT GGGACTTGGG CAGAAATGTT 1800
 GGCAGAGGAG GCTGTCTAGA CAATGGCTGC TCTGTCAAG ACAGGAGATT GAATGAAACC 1860
 ATCTGTACTT GTAGCCATCT AACAGCTTC GCGCTTCTGC TGGACCTATC TAGGACATCT 1920
 GTGCTGCTG CTCAATGAT GTCTCTGAGG TTCAATACAT ATATTGGTTG TGGGCTTTCA 1980
 TCAATTTTTC TGTCAGTAC TCTTGTAAOC TACATAGCTT TGGAAAAGAT CCGGAGGGAT 2040
 TACCTTCCA AAATCCTCAT CCAGCTGTGT GCTGCTCTGC TTCTGCTGAA CCGTGTCTTC 2100
 CTCTGAGACT CGTGGATGTC TCTGTATTAAG ATGCAAGGCC TCTGCTATC AGTGGCTGTA 2160
 TTCTCTCAT TTCTCTCTT GTCTCTATTC ACATGGATGG GCGTAGAAGC ATTCCATATG 2220
 TACCTGGCCG TTGCTAAAGT ATTTAACTAC TACATCCGAA AATACATCCT TAAATTCGCG 2280
 ATTGTGCGTT GGGGGGTACC AGCTGTGCTT GTGACCATCA TCTGACATAT ATCCCAGAT 2340
 AACTATGGGC TTGGATCTTA TGGGAATTC CCCAATGCTT CACCGGATGA CTCTGCTGG 2400
 ATCAACACA ATGCAGTATT CTACATTACG GTGGTGGGAT ATTCTGTGT GATATTTTTC 2460
 CTGAAGTCA GCATGTTTAT TGTGCTCTG GTTCAGCTCT GTCCGAATTA AAGAGAGAG 2520
 CAACGGGAG CCCCAGGAAA AACAGTATT CAAGACCTCA GAGATATGCG TGGCCTTACA 2580
 TTTTACTGCG GAATAACTTG GGGCTTTGCC TTCTTGGCT GGGGACCAAT TAACGTGACC 2640
 TTCTATGATC TGTTTGCCAT CTCTAATACC TTACAAGGAT TTTTCAATAT CATCTTTTAC 2700
 TGTGTGCTCA AAGAAATGTT CAGGAAGCAA TGGAGGCGGT ATCTTGTGT TGGAAAGTTA 2760
 GCGCTGGCTG AAATTTCTGA CTGAGTAAAC ACTGCTACTA ATGTTTAAA GAAGCAGACT 2820
 GTAAACCAAG GAGTGTCCAG CTCTTCAAT TCTTTACAGT CAAGCAGTAA CTCCACTAAC 2880
 TCCACACAC TGCTAGTGAA TAATGATTGC TCAGTACAG CAAGCGGAAA TGGAAATGCT 2940
 TCTACAGAGA GGAATGGGTT CTCTTTTAT GTTCAGATG GAGATGTGT GCTTCAGAT 3000
 TTCACTGAAA AACGACATAT GTTTAAGCAG AAGGAAGATT CCTGCAATGG GAAGGGCGT 3060
 ATGCTCTCA GAAGGACTTC AAAGCGGGA AGCTTACACT TTATTGAGCA AATGTGATTC 3120
 CTCTCTCTA AAATCAAAGC ATGATGCTTG ACAGTGTGAA ATGTCCAATT TTACCTTTTA 3180
 CACATGTGA GATGTATGAA AATCACTCA TTTTATTCTC GSCAACATCT GGAGAAGCAT 3240
 AAGCTAATTA AGGCGGATGA TTATTATTAC AAGAGAAAC CAGACATTA CACCATGGTT 3300
 TTTAGACATT TCTGATTTGG TTCTTATCT TTCAATTTAT AAGAGGTTG GTTTTAAACA 3360
 ATACACTAAG AATGACTCCT ATAAAGAAA CAAAAAAGG TAGTGAACIT TCAGCTACCT 3420
 TTTAAAGAGG CTAAGTTATC TTGATAACA TCATATAAAG CAACGTGTA CTTAGGCTG 3480
 TTGGTGAGTT TAGTTGTGCA TGCCCTTGTG GTATATAAGC TAAATCTTAG TGACCCATGT 3540
 GTCAAAAAATC TTACTTCTAC ATTTTATTGT ATTTATTTTC TACTGTGTA ATGTATTCCT 3600
 TTGTAGAAATC ATGGTTGTTT TGTCTCAGT GATAATTCA AAAATCCTTG CTCGTTCCGC 3660
 AAATCCTTAA GCTCCCTTTG GAGATGATAT AGGATGTGAA ATACAGAAAC CTCAGTGAAA 3720
 TCAGAAATA ATGATCCGAG CCAGACTGAG AAAATGTAAAG CAGACAGTGC CACAGTTAGC 3780
 TCATACAGTG CTTTGTAGCA AGTTAGGAAA AGATGCCCCC ACTGGGCAGA CACAGCCCTA 3840
 TGGGTCAATG TTTGACAAAC AGAGTGAGAG ACCATATTTT AGCCCCACTC ACCCTCTTGG 3900
 GTGACGAGCC TGTACAGCCA AACACAGCAT CCAATATGAA TACCCATCCC CTGACCGCAT 3960
 CCCCAGTAGT CAGATTATAG AATCTGCACC AAGATGTTTA GCTTTATACC TTGGCCACAG 4020
 AGAGGATGA ACTGTCTATC AGACCATGTG TCAGGAAAAAT TGTGAACGTA GATGAGGTAC 4080
 ATACACTGCC GCTTCTCAAA TCCCAGAGC CTTTAGGAAC AGGAGAGTAG ACTAGGATTC 4140
 CTCTCTTAA AAGGTATCAT ATATATGAAA AAAATCATA TTGCGTTCT TAAAAAGCA 4200
 ACTGCAATGG ACATTGTGTA TTGTATGAC TGGTACACTC TGGCCAGACC AGAGCTATAA 4260
 TTGTTTTTAA AATGTGTCTT GAAGAAATCA CAGTGACAG GGGAGTAGCT ATTGGGAACA 4320
 GGGAACTGTC CTACACTGCT ATTTGTGCTA CATGTATGGA GCCTTGATTG CTCAGTATTA 4380
 TATACAGGGT CTATCTTGCT TCTTACCCTAC ATCTGCTTGA GCAGTGCCCT AAGTACATCC 4440
 TTATTAGGAA CAATTTCAAC CCTTTTATG TAAGTCTTTC ACTAAGGTTT TCTTGATAT 4500
 ATTTCAAGTG AATGTTGGAT CTCAGACTAA CCATAGTAAT AATACACATT TCTGTAGTG 4560
 CTGACTGTGC TTTGCAATAT TTCTTTCTG ATTTATTTAA TTTTCTGTG TTTATATGTT 4620

AAAATCAAAA ATGTTAAAT CAATGAAATA AATTGTCAGT TAAGA

A92 Protein sequence

Gene name: G protein-coupled receptor 64
 Unigene number: Hs.184942
 Protein Accession #: NP_005747.1
 Signal sequence: 1-38
 GPS domain: 564-615
 Transmembrane domains: 624-646, 660-682, 688-710, 733-755, 783-805, 828-850, 858-880
 Cellular Localization: plasma membrane

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1      11      21      31      41      51
|      |      |      |      |      |
MVFSVRQCGH VGRTEEVLLT FKIFLVIICL HVVLVTSLEE DTDNSSLSPF PAKLSVVSFA 60
PSSNEVETTS LADVTLSLLP SNETEKTKIT IVKTFNAGSV KPQRNICNLS SICNDSAFFR 120
GEIMFYDKE STVPQNHIT NGTLTGVLSL SELKRSSELNK TLQTLSEYTF IMCATAEAQ9 180
TLNCTFTIKL NNTMNACAAI AALERVKIRP MEHCOCSEVRI PCPSSEELG KLCQDLQDPI 240
VCLADHPRGP PPSSSQSIPV VPRATVLSQV EKATSPAEPP DYSPTVHNVP SPIGHIQPLS 300
PQPSAPIASS PAIDMPPQSE TISSPMPQTH VSGTPPPVKA SFSSPTVSAP ANVNTTSAPP 360
VQTDIVNTSS ISDLENQVLQ MEKALSLSGL EPNLAGEMIN QVSRLLHSEF DMLAPLAQRL 420
LKVVDDIGLQ LNFSTNTLSL TSPSLALAVI RVNASSFNIT TFVAQDPANL QVSLETQAPE 480
NSIGTITLPS SLMMNLPAHD MELASRVQFN FFETPALFQD PSLENLSLIS YVSSSVANL 540
TVRNLTNVT VTLKHINPSQ DELTVRCVFW DLGRNGRGCG WSDNGCSEVD RRLNETICTC 600
SELTSPGVLL DLSRTSVLPA QMMALFITTY IGCGLSSIFL SVTLVYIAF EKIRRDYPSK 660
ILTLQCAALL LNLVLELLS WIALYKMQGL CISVAVFLHY PLLVSEFTWMG LBAFPMYAL 720
VKVENTYIRK YILKFCIVGW GVPVVVTII LTISPNDYGL GSYGKFPNGS PDDFCWINNN 780
AVFYITVVG YFCVIFLLNS MFIVVLVQLC RIKKKQLGA QRKTSIQLDR SIAGLTFLG 840
ITMGFAFFAN GFVNVTFMVL FAIENTLQGF FIFIFYCVAK ENVRKQWRRY LCCGRLRLAE 900
NSDWSKTATN GLKKQTVNQS VSSSNSLQS SSNSTNSTTL LVNDCSVHA SGNGMASTER 960
NGVSFSVQNG DVCLRDFTGK QHMFNEKEDS CNKGKRMALR RTEKRGSLHF IEQM
  
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Fibrosis

A93 DNA SEQUENCE

Gene name: RGF-like-domain; multiple 6
 Unigene number: Hs.12844
 Probeset Accession #: N67551
 Nucleic Acid Accession #: NM_015507
 Coding sequence: 241-1902 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
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CCGCAGAGGA GCGTCGGCCA GGCTAGCCAG GCGCGCCCCA GCGCCTCCCC AGGCCGCGAG 60
CGCCCTGCC GCGGTGCTTG GCCTCCCTTC CCAGACTGCA GGGACAGCAC CCGGTAACCTG 120
CGAGTGGAGC GGAGGACCCG AGCGGCTGAG GAGAGAGGAG GCGGCGGCTT AGCTGCTACG 180
GGGTCCGGCC GCGGCCCTCC CGAGGGGGGG TCAGGAGGAG GAAGGAGGAC CCGTGCAGAG 240
ATGCTCTGCG CCGGAGCGCT TGCGCTCCCG CTGCTGCTCT CCGGGTGGCC AGGTGGTTTC 300
GGGAACGGCG CAGTGCCTAT GCATCACGGG TTGTTAGCAT CGGCACBTCA GCCTGGGGTC 360
TGTCACTATG GACTAAACT GCGCTGCTGC TACGGCTGGA GAAGAAACAG CAAGGGAGTC 420
TGTGAAGCTA CATCGGAACC TGGATGTAAG TTGTTGAGT GCGTGGGACC AAACAAATGC 480
AGATGCCTTC CAGATACAC CGGAAAACCC TGCAGTCAAG ATGTGAATG GTGTGGAATG 540
AAACCCCGGC CATGCCAACA CAGATGTGTG AATACACACG GAAGCTACAA GTGCTTTTGC 600
CTCAGTGGCC ACATGCTCAT GCCAGATGCT ACCTGTGTGA ACTCTAGGAC ATGTGCCATC 660
ATAAACTGTC AGTACAGCTG TGAAGACACA GAAGAAGGGC CACAGTGCTT GTGTCATCC 720
TCAGGACTCC GCTTGGCCCC AAATGGAAGA GACTGTCTAG ATATTGATGA ATGTGCTCT 780
GGTAAAGTCA TCTGTCCCTA CAATCGAAGA TGTGTGAACA CATTGGAAG CTACTACTGC 840
AAATGTCACA TTGTTTCGA ACTGCAATAT ATCAGTGGAC GATATGACTG TATAGATATA 900
AATGAATGTA CTATGGATAG CCATACGTGC AGCCACCATG CCAATGCTT CAATACCCAA 960
GGGTCTTICA AGTGTAAATG CAAGCAGGGA TATAAAGGCA ATGGACTTCG GTGTTCTGCT 1020
ATCCCTGAAA ATTCTGTGAA GGAAGTCTTC AGAGCACCTG GTACCATCAA AGACAGAAATC 1080
AAGAAGTTTC TTGCTCACAA AAACAGCATG AAAAAAGAGG CAAAAATTAA AAATGTTACC 1140
CCAGAACCCA CCAGGACTCC TACCCCTAAG GTGAACCTGC AGCCCTTCAA CTATGAAGAG 1200
ATAGTTTCCA GAGGCGGGAA CTCTCATGGA GGTAAAAAAG GGAATGAAGA GAAATGAAA 1260
GAGGGGCTTG AGGATGAGAA AAGAGAGGAG AAAGCCCTGA AGAATGACAT AGAGGAGCGA 1320
AGCCTGCGAG GAGATGTGTT TTTCCCTAAG GTGAATGAAG CAGTGAATT CGGCCGTGAT 1380
CTGGTCCAAA GGAAAGCGCT AACCTCCAAA CTGGAACATA AAGATTAAAT TATCTCGGTT 1440
GACTGCAGCT TCAATCATGG GATCTGTGAC TGGAAACAGG ATAGAGAAGA TGATTTTGAC 1500
TGGAACTCTG CTGATCGAGA TAATGCTATT GGCTTCTATA TGGCAGTTCC GGCCCTGGCA 1560
GGTCACAAGA AAGACATGGC CCGATTGAAA CTCTCTCTAC CTGACCTGCA ACCCCAAAGC 1620
AATCTCTGTT TGCTCTTGA TTACCGGCTG GCCGGAGACA AAGTGGGAAA ACTTCGAGTG 1680
TTTGTGAAA ACAGTGAACA TGCCCTGGCA TGGGAGAAGA CCACAGTGA GGATGAAAAG 1740
TGAAGACAG GGAATAATCA GTTGTATCAA GGAACGTATG CTACCAAAAG CATCATTTT 1800
GAGCAGAAC TGGCAGGGG CAAAACCGGC GAAATCGCAG TGGATGGCGT CTGTCTTGTT 1860
TCAGGCTTAT GTCCAGATAG CCTTTTATCT GTGGATGACT GAATGTTACT ATCTTTATAT 1920
TTGACTTTGT ATGTCAGTTC CCGTGTGTTT TTGATATTGC ATCATAGGAC CTCTGGCAAT 1980
TTAGAATTAT TAGCTGAAA ATTGTAATGT ACCAACAGAA ATATTATTGT AAGATGCTTT 2040
TCTGTATATA GATATGCCAA TATTGCTTT AAATATCATA TCACTGTATC TTCTAGTCA 2100
TTCTGAATC TTTCACATT ATATTATAAA ATATGGAAT GTCAGTTTAT CTCCCTCTCT 2160
CAGTATATCT GATTTGTATA AGTAAGTTGA TGAGCTTCTC TCTACAACAT TTCTAGAAAA 2220
TAGAAAAAAA AGCAGAGAGA AATGTTTAAC TGTTTGACTC TTATGATACT TCTTGGAAAC 2280
TATGACATCA AAGATAGACT TTTGCCTAAG TGGCTTAGCT GGGTCTTCA TAGCCAAACT 2340
TGATATATTA AATCTTTGTT AATAATAATA TCCAAATCAT CAAAAAATA AAAAAA
  
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A94 Protein sequence:

Gene name: EGF-like-domain; multiple 6
 Unigene number: Hs.12844
 Probeset Accession #: N67551
 Protein Accession #: NP_056322.2
 Signal sequence: 1-21
 Transmembrane domains: none found
 MAM domain: 402-546
 EGF domain: 80-259
 Cellular Localization: secreted

1	11	21	31	41	51	
MPLPWSLALP	LLLSNVAGGF	GNAASARHNG	LLASARQPGV	CHYGTKLACC	YGWRNNSKGV	60
CEATCEPGCK	FGELVGNKC	RCFFGYTGCT	CSQDVNRCGM	KPRPCQHRCV	NTHGSYKFC	120
LSGHMLMPEA	TCVNSRTCAM	INCQYSCEDT	EEGFPQCLCPS	SGLRAPNGR	DCLDIDECAS	180
GKVICPYNR	CVNTFGSYTC	KCHIGFELQY	ISGRYDCIDI	NECTMDSHTC	SEHANCFTNQ	240
GSPKCKCKQG	YKGNGLRCSA	IPENSVKEVL	RAPGTIKDRI	KILLAHKNSM	KKKAKIKNVT	300
PEPTRTTTPK	VNLQPNYEE	IVSRGNSHNG	GKKGNEEKMK	EGLEDEKREE	KALKNDIEER	360
SLRGDVEFFK	VNEAGEFLGI	LVQRKALTSK	LEHKDLNISV	DCSPNHGICD	WKQDREDDFD	420
WNPADRNAT	GFYMAVFLA	GHKKDIKRLK	LLLPDLQPOS	NFCLLFYRL	AGDKVGLRV	480
FVKNNSNALA	WEKTTSEDEK	WETGKIQLYQ	GTDATKSIIF	EAERGKSKTG	ELAVDGVLLV	540
SGLCPSLLS	VDD					

GLIOBLASTOMA**A95 DNA SEQUENCE**

Gene name: ESTs
 Unigene number: Hs.293616
 Probeset Accession #: AW043782
 Nucleic Acid Accession #: none found
 Coding sequence: 38-1075 (underlined sequence corresponds to start and stop codon)

1	11	21	31	41	51	
AGCAACGACG	CCGGGCGAGG	GGAGCGGGG	CCGCGCCATG	TGGCTGCTGG	GGCGCTGTG	60
CCGTCTGCTG	AGCAGCGCGG	CGGAGAGCTA	GCTGCTCCCT	GGGAACAAC	TCACCAATGA	120
GTGCACATCA	CCAGGCAACT	TCATGTGCAG	CAATGGACGG	TGCATCCCGG	CGCGCTGGCA	180
GTGTGACGGG	CTGCGTACT	GCTTCGACAA	GAGTGATGAG	AAGGAGTGCC	CCAAGGCTAA	240
GTGAAATGT	GGCCCAACT	TCTTCCCTG	TGCCAGCGGC	ATCCATTGCA	TCATTGGTCG	300
CTTCCGCTGC	AATGGGTTTG	AGGACTGTCC	CGATGGCAGC	GATGAAGAGA	ACTGCACAGC	360
AAACCTCTCG	CTTTGCTCCA	CGCCCGCTA	CCACTGCAAG	AACCGCTCT	GTATTGACAA	420
GAGCTTCATC	TGCGATGGAC	AGAATAACTG	TCAAGACAAC	AGTGATGAGG	AAAGCTGTGA	480
AAGTCTCTCA	GAAACCGGCA	GTGGCGAGGT	GTGTGTGACT	TCAGAGAACC	AACITGTGTA	540
TTACCCGAGC	ATCACCTATG	CCATCATCGG	CAGCTCCGTC	ATTTTGTGTC	TGGTGTGGC	600
CGTCTGGCA	CTGGTCTTGC	ACCACCGAGC	GAAGCGGAAC	AACCTCATGA	CGCTGCCGCT	660
GCACCGGCTG	CAGCAGCTTC	TGCTGTCTGC	CGCGCTGGTG	GTCTGGGACC	ACCCGCCACA	720
CTGCAACGAT	ACCTACGAG	TCAATAATGG	CATCCAGTAT	GTGGCCAGCC	AGGCGGAGCA	780
GAATGCTCTG	GAGTATGGCT	CCCCACCTTC	CTACTCGGAG	GCTTGTCTGG	ACCAGAGGCC	840
TGCGTGGTAT	GACCTTCCCT	CACCGCCCTA	CTCTTCTGAC	AOSGAATCTC	TGAACCAAGC	900
CGACCTGCCC	CCCTACCGCT	CCCGGTCCGG	GAGTGCCAAC	AGTGCCAGCT	CCGAGGCAGC	960
CAGCAGCCTC	CTGAGCGTGG	AAGACACGAG	CCACAGCCCG	GGGCGACCTG	GCCCCAGGGA	1020
GGGCACTGCT	TGCGCCAGG	ACTCTGAGCC	CAGCCAGGGC	ACTGAAGAAG	TATAAGTCCC	1080
AGTATATCCA	AAGTCCATAT	GGGTAAATCT	GCTCTGACTT	GTGCGCATTC	TAACAATTTG	1140
TGCTCATGGG	AAGCTCTTTA	AGCACCTGTA	AGGATGTCTC	AAGTTACAGT	TTGGGATATT	1200
AACATATCTC	GCATTCCTCT	CCTCCCCCAG	ACTTCAGAGA	TGTTTTCTCG	GCGTCTCAGT	1260
TGACATGATC	TGTTGTGGGT	CTTTCTCTGC	AGGTCACTCT	TCCCTTGGGA	CCCGAGATCA	1320
CACCTCATTT	TTTCAATTTA	TTCTGTTTCT	GTGGAGAGAG	CAGCATATAA	AACAGTATTG	1380
AAATAGGCTG	GGAGAGAGCA	ATGTTTCTGT	GCTATATTTG	ATGCTCAGAA	GTGCAAGAGA	1440
CGCTGGACCC	AATTCTCTCT	GCTGGGTAGT	TACCTTATAG	CATTTGGGGA	TTTGGGTAG	1500
ATGATCTAAC	CAGGAGGCCA	TCATGTGATG	GTCAACCCCC	CAAAAAAATT	CCATTGAGC	1560
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AAGAAAACCT	TGGACGTGAG	TAACACCCCT	CAGCAGTCGC	AAGCTTATTT	TGGTTTGTG	1680
AAGGACTCTG	AAACCATCTA	CCCTGTATAA	ATCTGCGCTT	TAGAAATTGG	CCCAAGAAAG	1740
CTCATCTGTA	GAGCTTTCCT	CAGCAGCATA	TATCATCAGC	CTCATCTTAA	AATAGGCGAG	1800
GAGCCCTCTC	CATGAGTTTA	TCCAAGTTCT	CAGCTCTTAA	AATGCAGGCT	GCCAGAGCCC	1860
TACACCTGCC	CTGGCTCTAC	AGGCACTTAC	CTGTTTCTG	GACTGTCAAC	CTCCAGCTG	1920
ACCTGCCCCG	AGCCAAGGAA	TGAGGACCTA	ACTTGAATTG	GCCCAAGTTC	TGACCTGGCT	1980
GTATGTCCCT	GTGGCCCA	CCAGCCCTGT	CTTGTCTATT	CATGAGCCTG	CAACTGGC	2040
CTCCAAAGTT	CCCTTAACAC	TTGCAAGTTC	CTTTTACCT	GTGCTTTTGT	ACTTCAGGAC	2100
ACTGGTTTCT	ATCAGAGGTG	AGAGGCAATG	TCAATACCTC	CAGCAAGCTC	TCCGTGGCTC	2160
CTGCACTGTG	CAGCTCTCTC	TTCCCAAGGT	CCCAATACCA	GCACCTCTAG	TTAGAGTTAG	2220
GGTCAGGGTC	ACGCTCTCTC	CAACATCCCA	GTAGTTTCTC	CTCTGAGACA	CATGGGCAAG	2280
AGACAAATTG	GAGTCAAGAT	TTTCCATTTG	GATCTATTTT	AAATCTTTTA	GAAATGCATT	2340
TGAACACAGT	TGTTTGTGTT	TTCCCTTCTA	GTTAAGGGAC	TATTATATG	TGTATAGGAA	2400
AGCTGTCTCT	TTTTTGTGTT	TTCCCTTAA	AAGGTCCAAA	GAAAGATGCA	AAAGGAGATC	2460
ACACCTTTGC	CCCGCTGAGC	CCCGTGATAA	CAGTCACTC	CAGACTAACC	TGTGTGCCAG	2520
ACATTGTGTC	ATTGTTGCA	TTTGAAGTTA	TTATTATCA	AGTTCTTGAA	GGAGCAGAA	2580
AGAGGGACTC	CTCTCTCCCT	CCGTGTATAG	TCTCTATGTT	TGTGCTAGTT	TTCTTTTTTT	2640
TTCTCTGTGT	CCAGTCAGCC	ACAGGGCCCG	CCTCCCTGCA	GGAATAAGGG	GTAAAACTGT	2700
AGGTGTTGTT	TGGCAAGAAA	CCCACTGAC	TGNTAGGGG	TAAATGGAAA	CCAGTATGAG	2760
CCACTCCGGG	CAGCTGTAC	CCATTGAGAA	CTTCTTCCG	CAGCTGAGAA	AATGTTTCAGT	2820
AACCTGTTTG	ACGCTAATTA	AAACAGAGCT	TGCAGGAAGT	GGGCTAAGG	TGGCATTGAG	2880

5 TGATCCTGTT CTGTAGACTT TCTTTCTTT TTTAACCAG ATCCAAAGGA TGTACAGAA 2940
 AAGCTAGCCA CTGGTATTTT GTTTGTGTTA AAAAAAAGAA GAAAGAAAGA AAGAAAGAAA 3000
 AACGGAAAGG AACCTAGCTG CCTGTATCTT TCATTTTAA AATAGCACTT GAGTTATTTT 3060
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 TTTTAACTC ATTCCAACCA GGAAGCTTTT TTATACATGG CCTAAATCTA CGCCAAACCA 3540
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 15 TTTTAAAAA ATGCNACTAA GTGGTTAATA GTGTGTGACG CTCAAAGTTA ATGTAAACTG 3720
 GAAAGCTTGT GTGTGTTTGC TTTTGTGTGT TGTGTAGGCT TGGTTTGTGT TTTTAAATTT 3780
 TTATACITTC TAATAAATTT GCAGTTTCAT TCTTTCTGTT TGTGCAAAAG GWTMTAMARM 3840
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 TGGGGCGGGG GGGCCCACTG AGGTACGGGG ACCACGCGGG CCCAAACGGG ACCCCAGAG 3960
 20 GAAACCTGG CCAAGAAAAA GGTGCGGAGA ATTCTCCAC CCAAAAAA ACGCCCGGG 4020
 GGACTCAACC AGGAGGACCC AAGGGAACCC GATAGAGTAC G 4080

25 A96 Protein sequence:
 Gene name: ESTs
 Unigene number: Hs.293616
 Probeset Accession #: AW043782
 Protein Accession #: none found
 30 Signal sequence: 1-17
 Transmembrane domains: 169-191
 LDLa domains: 28-66, 70-108, 112-149
 Cellular Localization: plasma membrane

35 1 11 21 31 41 51
 MWLLGLPLCLL LSSAAESQLL PGNFTNECN IPGNFMCNNG RCIPGAWQCD GLEDCDFKSD 60
 EKECKKAKSK CGPTFFPCAS GIHCLIGFR CNCFEDCPDG SDEENCINNP LECSTARYHC 120
 40 RNLGLIDKSP ICDGQNNCND NDEKESCESS QBPSSQVFFV TSENQLVYYP SITTYAIGSS 180
 VIFVLVALL ALVLRBQRK NNLMTLFVHR LQHPVLLSRL VVLDHPHHCN VTYNVMNGIQ 240
 YVASQABQNA SEVGSPPSYS EALLDQRPAN YDLPPPPYS DTESLNQADL PFYRSRSGSA 300
 NSASSQRASS LLSVEATSES PQQPFQFQGT AEPRDSEPSQ GTRSV

45 LUNG

50 A97 DNA SEQUENCE
 Gene name: putative GPCR, Weakly similar to dJ365012.1
 Unigene number: Hs.256897
 Probeset Accession #: BE001836
 Nucleic Acid Accession #: BE001836
 Coding sequence: 1-2955 (underlined sequences correspond to start and stop codons)

55 1 11 21 31 41 51
 ATGGGCGTCA AATCTTTTTC CTTCACACT GGGAAATGATG GGCTAGACCC AGACCCAAATC 60
 ATGTTAGTGA TGTATAGGAT CAGTGCCCA GCTGGTGTGG AAGACAGTG GGTCACTAGT 120
 GGTTAGGACC CACATAGCAC TAAAGTCTT CAACATGCAA TTAGAAGCTC AATGTTGAC 180
 60 GGGAAATATG TTCACTCTAA AAAAGATGTT TCTATTAGAA TTTACTTACT CTTTCATGAA 240
 AACATAGATG CTTCCTCTTT CCGATTAGT GATGGCCATC AGTTAACCCA AGTGCACTCA 300
 GAGAAATCAA ATTCTGACAC AATCCAGCAA GTAACATATA AAACATGATG CCCAGTCGAA 360
 GAATATCAGC TGCTGCTTCA GGTGACCTAT AGAGATTCCA AGGAGAAAG AGATTGAGA 420
 AATTTCTGGA AGCTCTTGAA GCCTCCATTA TTATGGTCA C ATGGGCTAAT TAGAATTATC 480
 65 AGAGCAAAAG CTACCAAGCA CTGCAACAGC CTGAATGGAG TCCTGCACTG TACCCTGTGA 540
 GACAGCTACA CTTGGTTTCC TCCTCATGC CTTGATCCGC AGAACTGCTA CCTTCACAG 600
 GCTGGAGCAC TCCCAAGCTG TGAATGTCT CATCAACACC TCAGCTAGAG TGTCAATTC 660
 TGTGAGAGAA CAAGATTG GGGCACTTTC AAAATTAAATG AAAGGTTTAC AATGACCTT 720
 TTGAATTCAT CTTCTGCTAT ATACTCCAAA TATGCAATG GAATGAAAT TCAACTTAAA 780
 70 AAAGCATATG AAAGAATTCA AGGTTTGTAG TCGTTTCAGG TCACCCATTT TCGAAATGGA 840
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 ATTGAACATG TTGCGAGAA GGCTAAGACA GCCCTTCACA AGCTGTTTCC ATTAGAAGAC 960
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 AAGGATGATG AATATACCTT GCCTGACAG AGTGGCTACA GGGGAACAT CACAGCCAG 1080
 75 TGTGATGCT CTGGGTGGCA GGTGATCAGG GAGACTGTGT TGCTCTCTCT CTTGAAGAA 1140
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 80 GTACCAACT GGCAGTCTT ACTGCGGAA GAAAGTATG CCAGCTCAGG GTTACTAGAG 1440
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 AAATTCATT ACTGGAAGG GATTCCAGTG AACAAAAGCC AACTCAAAAG GGGTACAGC 1560
 TATCAGATTA AATGTGTCT CCAAAATACA TCTATTCCA TCAGAGGCCG TGTGTTAAT 1620
 GGGTCAGACC AATTCAGAG ATCCCTTCCA GAAACTATA TCAGCATGSC CTCGTGACT 1680
 CTGGGGAACA TTTACACCGT TTCCAAAAT GGAATGCTC AGGTCAATGG ACCTGTGATA 1740

5	TCCACGGTTA	TTCAAAACTA	TTCCATAAAT	GAAGTTTTC	TATTTTTC	CAAGATAGAG	1800
	TCAAACCTGA	GCCAGCCTCA	TTGTGTGTTT	TGGGATTTC	GTCATTTGCA	GTGGAAOGAT	1860
	GCAGGCTGCC	ACCTAGTGAA	TGAAACTCAA	GACATCGTGA	CGTGCCAAATG	TACTCACTTG	1920
	ACCTCCTTCT	CCATATTGAT	GTCACCTTTT	GTCCCTCTA	CAATCTTCCC	CGTTGTAAAA	1980
	TBGATCACCT	ATGTGGGACT	GGGTATCTCC	ATTGGAAGTC	TCAITTTATG	CCTGATCATC	2040
	GAGGCTTTGT	TTTGAAGCA	GATTAAAAAA	AGCCAAACCT	CTCACACACG	TCGTATTGTC	2100
	ATGGTGAACA	TAGCCCTGTC	CCTCTTGATT	GCTGATGCT	GCTTTATTGT	TGGTGCCACA	2160
	GTGGACACCA	CGGTGAACCC	TTCTGGAGTC	TGCACAGYTG	CTGTGTTCTT	TACACACTTC	2220
10	TTCTACCTCT	CITTTGTTCT	CTGGATGCTC	ATGCTTGGCA	TCCTGCTGGC	TTACCGGATC	2280
	ATCCTCGTGT	TCCATCACAT	GGCCACGAT	TTGATGATGG	CTGTGGGATT	TTGCTGGGT	2340
	TATGGGTGCC	CCTCATTTAT	ATCTGTCTAT	ACCATTGCTG	TCACGCAACC	TAGCAATACC	2400
	TACAAAGGA	AAGATGTGTG	TTGGCTTAAC	TGTCCCAATG	GAAGCAAACC	ACTCCTGGCT	2460
	TTTGTGTGCC	CTGCACTGGC	TATGTGGCT	GTGAACCTCG	TTGTGGTGGT	GCTAGTTCTC	2520
15	ACAAAGCTCT	GGAGGCCGAC	TGTTGGGAA	AGACTGAGTC	GGGATGACAA	GGCCACCATC	2580
	ATCCGGGTGG	GGAGAGGCT	CCTCATTTCTG	ACCCCTCTGC	TAGGGCTCAC	CTGGGGCTTT	2640
	GGATAGGAA	CAATAGTGGA	CAGCCAGAAAT	CTGGCTTGGC	ATGTTATTTT	TGCTTTACTC	2700
	AATGCATTCC	AGGCATTTT	TATCTTATGC	TTTGGAAATC	TCTTGGACAG	TAACTGGGA	2760
	CACTTCTGT	TCAACAGT	GTCTGCCTTA	AGTTCTTGA	AGCAAACAGA	AAAGCAAAC	2820
20	TATCAGATT	TATCTGCCAA	ACCCAAATTC	TCAAAGCCTT	TCAACCCACT	GCAAAACAAA	2880
	GGCCATTATG	CATTTTCTCA	TACTGGAGAT	TCCTCCGACA	ACATCATGCT	AACCTAGTTT	2940
	GCTCAAATG	AATAA					

A98 PROTEIN SEQUENCE

25	Gene name:	putative GPCR, Weakly similar to dJ365012.1
	Unigene number:	Hs.256897
	Protein Accession #:	none found
	Signal sequence:	1-17
	Pfam domain:	7tm_2 [561-820]
30	Transmembrane domains:	545-567, 571-593, 605-627, 641-663, 677-699, 721-743, 767-789
	Cellular Localization:	plasma membrane

35	1	11	21	31	41	51	
	MHALLLCPFSV	LNAGSGLSL	QSPVEBYQLL	LQVTYRDSKE	KRDLRNFLKL	LKPFLNWSHG	60
	LIRIIRAKAT	TDQNSLNGVL	QCTCEDSYTW	FPFSCIDPQN	CYLHTAGALP	SCCEHLNMLS	120
	QSVNFCERTK	IWGTFFKINER	PTNDLLNSSS	AIYSKYANGI	BIQLKKAYER	IQGFESVQVT	180
	QFRNGSIYAG	YEVVSSSSAS	ELLSAIERVA	EKAKTALHLK	FPLEDGSRFRV	FGKAQCNDIV	240
40	FGFGSKDDEY	TLPCSSGYRG	NITAKCESSG	NQVIRETCVL	SLLBELNKNF	SMIVGNATEA	300
	AVSSFVQNLIS	VIIKQNPSTT	VGNLASVVSI	LSNISLSLSL	SRFRVSNSTM	EDVISIADNI	360
	LNASVNTNWT	VLLREKYAS	SRLLETLENI	STLVPPPTALP	LNYSRKPIDW	KGIFVNSQL	420
	KRGYFYQXKM	CPQMTSIFIR	GRVLIGSDQF	QRSLPETIIS	MASLTGLNLL	PVSENGNAQV	480
	NGFVISTVIQ	MYSTNEVFLF	FSKLESNLSQ	PHCVFWDPSH	LQWMDAGCHL	VNETQDIVTC	540
45	QCIIHLSFPI	LMSFPVPSPI	FPVVKWITYV	GLGISIGSLI	LCLIIELFW	KQIKKSQTS	600
	TRRICMVNIA	LSLLIADVWF	IVGATVDVTV	NPSGVCTIAV	FFTHFFYLSE	PFWMMLGLIL	660
	LAYRIILVPH	RMQHLMMAV	GFCLGYGCP	IISVITIAVT	QPSNTYKRRD	VCNLNWSNGS	720
	KPLLAFFVPA	LAIVAVNFVV	VLLVLTKLWR	PTVGERLSED	DEATIIIRVGK	SLLILTPLLG	780
	LTWNGFIGITI	VDSQNLAMHV	IFALLNAPQV	RTVTITYCIV	K		

A99 DNA SEQUENCE

	Gene name:	putative G-protein coupled receptor
	Unigene number:	Hs.16065
55	Probeset Accession #:	F07953
	Nucleic Acid Accession #:	NM_016334
	Coding sequence:	104-1471 (underlined sequences correspond to start and stop codons)

60	1	11	21	31	41	51	
	AGCACCTGGG	AAAGGGCAGA	CGTGTGAGG	GGGCTGTGG	CCCCAGCGTG	CTGTGGCCTC	60
	GGGGAGTGGG	AAGTGGAGGC	AGGAGCCTTC	CTTACACTTC	GCCATGAGTT	TCCTGATCGA	120
	CTCCAGCATC	ATGATTACCT	CCCAAACTACT	ATTTTGTGGA	TTTGGGTGGC	TTTCTTTCAT	180
65	CGGCCAATTG	TTTAAAGACT	ATGAGATAGC	TCAGTATGTT	GTACAGGTGA	TCTTCTCGGT	240
	GACGTTTGCA	TTTCTCTGCA	CCATGTTTGA	GCTCATCATC	TTTGAAATCT	TAGGAGTATT	300
	GAATAGCAGC	TCCGTTTATT	TTCACTGGAA	AATGAACCTG	TGCGTAATTC	TGCTGATCCT	360
	GGTTTTCATG	GTGCTTTTAT	ACATTGGCTA	TTTTATTGTG	AGCAATATCC	GACTACTGCA	420
	TAAACAACGA	CTGCTTTTTT	CCGTCTCTCT	ATGGCTGACC	TTTATGTATT	TCTTCTGGAA	480
70	ACTAGGAGAT	CCCTTTCCCA	TTCTCAGCCC	AAAACATGGG	ATCTATATCCA	TAGAACAGCT	540
	CATCAGCCGG	GTGGGTGTGA	TTGGAGTGAC	TCTCATGGCT	CTTCTTCTCTG	GATTTGGTGC	600
	TGTCAACTGC	CCATACACTT	ACATGYCTTA	CTTCTCAGG	AATGTGACTG	ACACAGATAT	660
	TCTAGCCCTG	GAACGGGAGC	TGCTGCAAAC	CATGGATATG	ATCATAAGCA	AAAAGAAAG	720
	GATGSCAATG	GCACGGAGAA	CAATGTCTCA	GAAGGGGGAA	GTGCATAACA	AACCATCAGG	780
75	TTTCTGGGGA	ATGATAAAAA	GTGTTACCC	TTCAAGCATCA	GGAGTGAHAA	ATCTTACTCT	840
	TATTCAACAG	GAAGTGGATG	CTTGGGAAGA	ATTAAGCAGG	CAGCTTTTTC	TGGAAACAGC	900
	TGATCTATAT	GCTACCAAGG	AGAGAAATGA	ATACTCCAAA	ACCTTCAAGG	GGAAATATTT	960
	TAATTTTCTT	GCTTACTTTT	TCCTATTATTA	CTGTGTTTGG	AAAATTTTCA	TGGCTACCAT	1020
	CAATATTGTT	TTTGATTCAG	TTGGGAAAAC	GGATCCCTGC	ACAAGAGGCA	TTGAGATCAC	1080
80	TGTGAATTAT	CTGGGAATCC	AATTTGATGT	GAAGTTTGGG	TCCCAACACA	TTTCTCTCAT	1140
	TCTTGTGTGA	ATAATCATCG	TCACATCCAT	CRGAGGATTC	CTGATCACTC	TTACCAAGTT	1200
	CTTTTATGCC	ATCTCTAGCA	GTAACTCTTC	CAATGTCTAT	GTCCTGCTAT	TAGCACAGAT	1260
	AATGGGCATG	TACTTTGTCT	CCCTGTGCT	GCTGATCGCA	ATGAGTATGC	CTTTAGAAAT	1320
	CCGACCATTA	ATCACTGAAG	TCCTTGAGAA	ACTGCAGTTC	AACCTCTATC	ACCGTTGGIT	1380
	TGATGTGATC	TTCTGTGTCA	GCGCTCTCTC	TAGCATACTC	TTCTCTTATT	TGGCTCACAA	1440

	ACAGGACACCA	GAGAAGCAAA	TGGCACCTTG	AACCTAAGCC	TACTACAGAC	TGTTAGAGGC	1500
	CAGTGGTTTC	AAAATTGTAGA	TATAAGAGCG	GGGAAAATG	GAACCCAGGC	CTGACATTTT	1560
	ATAAACAAAC	AAATGCTAT	GGTAGCATTT	TTCACTTCA	TAGCATACTC	CTTCCOCTC	1620
5	AGGTGATACT	ATGACCATGA	GTAGCATFCG	CCAGAACATG	AGAGGGAGAA	CTAACTCAAG	1680
	ACAATACTCA	GCAGAGAGCA	TCCCGTGTGG	ATATGAGGCT	GGTGTAGAGG	CGAGAGGAG	1740
	CCAAGAAACT	AAAGGTGAAA	AATACACTGG	AACCTCGGGG	CAAGACATGT	CTATGGTAGC	1800
	TGAGCCAAAC	ACGTAGGATT	TCCGTTTAA	GGTTCACATG	GAAGAAGTTA	TAGCTTTGCC	1860
	TTGAGATTGA	CTCATTAAAA	TCAGAGACTG	T			
10	<u>A100 Protein sequence</u>						
	Gene name: putative G-protein coupled receptor						
	Unigene number: Hs.16085						
	Protein Accession #: NP_057418.1						
	Signal sequences: none found						
15	Transmembrane domains: S-27, 42-64, 76-98, 110-132, 144-166, 289-311, 342-364, 380-402, 424-446						
	Cellular Localization: plasma membrane						
	1	11	21	31	41	51	
20	MSFLIDSSIM	ITSOILFFGF	GNLFFMRQLF	KDYBIRQYVV	QVIFSUTFAF	SCTMFELIIF	60
	EILGVNLSSS	RYFRHKNMLC	VILLILVFMV	PFYIGYFIVS	NIRLLHKQRL	LFSCILLWLT	120
	MYFFWKLGGP	FPILSPFHGI	LSIEQLISRV	GVIGVTLMAL	LSGFGAVNCP	YTYMSYFLRN	180
	VTDTLILALE	RRLLQITMDMI	ISKKKRMAMA	RRTMFQKGEV	HNKPSGFMGM	IKSVTTESAG	240
25	SENLTLLIQE	VDALKEELSRQ	LFLETADLYA	TKERIEYSKT	FKGRYFNFLG	YFYSIYCVWK	300
	IFMATINIVP	DRVGKIDPVT	RGIEITVNYL	GIQFDVKFWS	QHISFILVGI	IIVTSIRGLL	360
	ITLTKFFXAI	SSSKSSNVTV	LLLAQIMGMX	FVSSVLLIRM	SMPLRYRTII	TEVLGELQPN	420
	FYHRWFVDIV	LVSLSSILF	LXLAHQAPE	KQMAP			
30	<u>A101 DNA SEQUENCE</u>						
	Gene name: ESTs, Weakly similar to CGHU7L collagen alpha 1(III) chain precursor [H.sapiens]						
	Unigene number: Hs.19322						
	Probeset Accession #: AA088458						
	Nucleic Acid Accession #: AA088458						
35	Coding sequence: 862-1995 (underlined sequences correspond to start and stop codons)						
	1	11	21	31	41	51	
40	GCCCTTGGAC	ACTGACATGG	ACTGAAGGAG	TAGAATGGAG	CACGAGGACA	CTGACATGGA	60
	CTGAAGAAAA	AGGAGCTGGA	GCAGGAGAAG	GAGGTGCTGC	TGCGGGTGT	GGAGATGATG	120
	GGCGGGGGCT	GGACTGGTA	CCAGCAGCAG	CTGCACAGAG	TGCAGGAGCG	CCAGCCCGCC	180
	CTGGGCCAGA	GCAGAGCCAG	CGCCGACTTT	GGGGCTTCAG	GGAGCCCCCG	CCCACTGGGG	240
	CGGCTACTGC	CCAGGCTACA	AGAGGTGGCC	CGGTGCTGGG	GGGAGCTGCT	GGCTGCACCC	300
	TGTGCCAGCC	GGGCCCTGCC	CCCGTCTCTC	TCCGGGCCCC	CCTGCCCTGC	CTTGACGTCC	360
45	ACCTCACCCC	CGGTCTGGCA	GCAGCAGACC	ATCCTCATGC	TGAAGGAGCA	GAACCGACTC	420
	CTCACCCAGG	AGGTGACCGA	GAGAGGTGAG	CGCATCACGC	AGCTGGAGCA	GGAGAGTCTG	480
	GCGCTCATTA	AGCAGCTGTT	TGAGGCCCGC	GCCTTGAGCC	AGCAGGACGG	GGGACCTCTG	540
	GATTCCACCT	TCATCTGATC	CTTGTGGGCC	GGGTGGGCC	CCAGGGCCAG	CTTGSCACTC	600
	AGCCCTTCGA	GGGTGGGGCG	CCCATCGCAC	CCACCTCTTC	TGGCTGBAGA	CCCCCGGCG	660
50	GCCAGGCCAC	AGTCCCGGAG	TGGGCCTCTT	CTTGGCCGCC	TTGCCAGATG	GGCTCCCGAG	720
	GCCTGCCGCC	GGCTGGTCCC	CGCACCGAGC	GCTTGACTCC	GTCTGGGCTC	CTGGTTGTGT	780
	ACATGGGCTG	GGGCTCTCTT	TGAGTCCGCA	TAGTCCGCG	CTACTACTGG	CCGCTGTCTG	840
	TGGACAGTGG	GGTACCCCTC	CATGAGTTAG	CGTCCCGCCG	TTTCCAGCGG	TGCGGCCCTG	900
	GGTCCCATCT	TCAGGGAAG	GCATCTCCCA	CGCCAGGCTG	CACCTCCAAC	AACGGGCAGC	960
55	AGAGGGCGCG	GGGGCGCTCC	GACGCGGGTC	CAAGGGCAGC	TTCCCGCTCA	ACCAGGGCAC	1020
	CAGGACGAGG	TGGCTGTAGC	TGGACCGGAC	GGAAGTAGAT	GGAGGGGGTG	GGGACGGCCT	1080
	GTAAGCGGGG	GGTGCTTGCC	TGGCTGGGGA	GCCCCAGGGA	TAGCGGTCCG	ACTTCAGGTT	1140
	CTGGCCAGAG	CTGAGGGACC	CTGGCTGCAG	CGGATCGGCA	CGCCGGGTGG	GGGAGAGCTT	1200
	GGCCTGCTAT	TGGCTCCGAC	AGACCTTGGG	GTGATGGCCT	TCCCGCTCTT	GGCGGGGAGG	1260
60	TGCGCCACG	TTGAGTCCCA	CACACATCC	TGTGAGCCTG	GCTCCGACGG	AGGGCCCTCA	1320
	GACAGCTCCC	AGGCACGTCA	TAGGCAAGGC	CTGTTTCCCG	CGACTCAGGA	TTTCCAGGCG	1380
	CTGGGGTCTC	GCTCACCCCC	CTTTGCTCTC	AGGCCGAGCC	TGTCCCGAGG	TTTCAGCTGG	1440
	GAGAGGCCAC	CTCCCTCAGC	CAAGGAAAGC	GAGAACCCCC	AGGGTACAGG	AGGAGGCTGG	1500
	GGCAGGTCCC	CTTGGGTGTC	ACTTCCCTCAG	CCCGTGCCCA	GGCCCACTCC	CGTGGTGTCT	1560
65	GGAGTACGCA	CTGGTGGGGG	GGCCCTGCTC	AGCCCACTCT	GGAGGGTCCC	AGTGTACCCA	1620
	GAAACAGGGG	CACGGCAACA	GCATCGATGG	GTTCTGCAGC	CCAGGGGCCC	CGATGGGGGG	1680
	TCAGTGTGTG	TGGGGCGCAG	GGCCTCGGAT	GGGGGGTCAG	TGCCTGGGGG	GGCGAGGGCC	1740
	CCCGATGCGG	GGTCAGTGCG	TGGGGGGCGC	AGGGCCCGCT	CGTGTCCAGG	GCACTTTGGT	1800
	ACACTGTCCC	ACAAGGCACC	TGTCTCAGAG	GAGGGGCCCT	GGCAGGCAGC	GTGGCAACTC	1860
70	CCCTCCGGAG	CCAGCTCCCA	TGCTAACCTG	CCCAAGCAG	CCCCACAGAG	CCACATTCCC	1920
	TGCTGCACCT	GGTCTGCAGG	GGTGTCCGAG	GACAGGCCCA	AGTCAGGCCA	GCATGCAGCT	1980
	GCCCTCTCTAC	CTTGAAGATG	GGAGTGGGCT	TTCCAGGGGA	CATAAGGATG	TCAGGCTCTG	2040
	ACCTCTCTGG	CAGGAAGAGG	TGCAGGTCTT	GAGGGCCTGT	CCCCACAGCG	CCAGCAGCTC	2100
	AGGTGAGCTG	CAGCGCAGTG	GGTGGGCCAG	TGGCAGCCAG	GGAGAAGGCC	CCGCTCAGCA	2160
75	GGCTGGGGTC	TGCCACCCAG	GGCCTCCCCA	CGTCTGCCCT	TGAGGGTGGC	TGCCATGGCC	2220
	TGGGGGATCC	TGGCATCTTT	ACTGGACTGG	AGGCAGGAGA	CAGACAGTGT	TCTGTCCCGG	2280
	GGTGACTTCA	TCAGGAGAGC	GCCCCACATG	AGCTGGAGCC	CGCAGCTGAA	GGGGAAGTGT	2340
	GAGACAGGCT	GGTACCTCCG	GAAAAACTGC	CTTTCAGCCT	TGGTGTCTCC	TGCAAGGTGA	2400
	AAAGAAATAG	GTCTCTCCAG	TTTACAGCTT	GAAATCAGGC	TAGTGAAGTG	CCCTGGAGAC	2460
80	CACGAGGGCA	GAAATTTAAAG	GCCCCGGCTG	GCAGGGTCTA	GGTGGCTGGC	AGAGGCACAT	2520
	GCAGACCCCT	CCTGGAGCCT	GCCCTAGGAC	GCTGGGGCGG	TCAGTCTCCG	TGCAGGATGT	2580
	GAGCAGCGTC	CCTGGGCTCT	ATCCCGAGGG	TGCCAGTAGC	GTGTGCAGGT	ACATACAGCT	2640
	GGGTGCACAC	TGTGATGACA	CCCGGAAATG	TCTCAGGATG	TTGAAATGTA	TCCTTGGGGG	2700
	CAGAAAGTGT	CCAGTGTGAG	AATCTGCCCC	AGAGGAACAC	ACCCACACCA	GGCCTCAGGA	2760
	TTTTGTGTGT	ATCAAGTTCC	AAGGAAAGG	AACATCTCAG	CCGGGCGTGG	TGTTTCAAGC	2820

5 CTGGAATCCC AGCACITGAG GCCAGGAGTT CCAGAGCAGC CTGGGCAACG CAGTGAGAGA 2880
 CCCCATCTCT ACBAARAAAAA AAAAAGAAAG AAAGAAAATG AGAGATCCAG GTTTAAAAAT 2940
 TCATAAACAC CACAAGGAAA CAATACACTA TGAGACCCAG CAGAAGCAAC AGATTGACTC 3000
 TAGACCCAGA TACTAGAAAT ATCAGAGAGA ATATAAGTA ACAGTGTTTT ATATATCTAA 3060
 AGAAATAAAA GAGATTCTG GAAACATGAA AAAAAA

A102 DNA SEQUENCE

10 Gene name: TMPSR53a
 Unigene number: Hs.298241
 Probeset Accession #: AI538613
 Nucleic Acid Accession #: AB038157
 Coding sequence: 202-1566 (underlined sequences correspond to start and stop codons)

15 1 11 21 31 41 51
 | | | | |
 ACCGGGCACC GGACGGCTCG GGTACTTTTCG TTCTTAATTA GGTATGCCCC GTGTGAGCCA 60
 20 GGAAGGGCT GTGTTTATGG GAAGCCAGTA AACTGTGGCC CTACTATCTC TTCGTGGTGG 120
 CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGG TGGAGGCCGA GCCGGATGTC 180
 AGAGGTCCTG AAATAGTCCAC CATGGGGGAA AATGATCOGC CTGCTGTGTA AGCCCCCTTC 240
 TCATTCCGAT CGCTTTTTCG CCTTGATGAT TTGAAATAAA GTCCGTGTGC ACCAGATGCA 300
 GATGCTGTG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTTTTTTCC AATCATCGTC 360
 25 ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGGTC TGGGCATCCA CTTOGACTGC 420
 TCAGGGAGAT ACAGATGTGG CTATCCCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480
 GAGTCTCTCG ATTGCAAGAA CGGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540
 AATGCCGTGC TCCAGTGTGT CACAGCTGCT TCGTGAAGA CCAATGTGTC CGATGACTGG 600
 AAGGGTCACT AGCAAAATGT TGCTGTGCCC CAACTGGGTT TCCCAAGCTA TGTGAGTTCA 660
 GATAACCTCA GAGTGAAGTC GCTGGAGGGG CAGTTCGGGG AGGAGTTTGT GTCCATCGAT 720
 30 CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACCACT CAGTATATGT GAGGGAGGGA 780
 TGTGCTCTCG GCCACGTGGT TACCTTCGAG TGCACAGCCT GTGCTCATAG AAGGGGCTAC 840
 AGCTCAGCA TCGTGGGTGG AAACATGTCC TTGCTCTCGC AGTGGGCCCG GCAGGCCAGC 900
 CTTGAGTTCC AGGGCTACCA CCTGTGCGGG GGCTCTGTCA TCACBCCCTC GTGATCATC 960
 35 ACTGCTGCAC ACATGTTTTA TGACTGTGAC CTCCCAAGT CATGGACCAT CCAAGTGGGT 1020
 CTAGTTTCCC TGTGGACAA TCACBCCCA TCCCACTGG TGSAGAGAT TGTCTACCAC 1080
 AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATCGCCC TTATGAAGCT GCGCGGGCTC 1140
 CTACCGTTCA ATGAAATGAT CCAGCCTGTG TGCTGCCCC ACTCTGAAGA GAACCTTCCC 1200
 GATGGAAAG TGTGCTGGAC GTCCAGATGG GGGGCCACAG AGGATGGAGC AGGTGAAGCC 1260
 40 TCCCTGTCC TGAACCAAGC GGCCTCCCT TTGATTCCA ACAAGATCTG CAACCAAGG 1320
 GACGTGTACG GTGGCATCAT CTCCGCCCTC ATGCTCTGCG CGGGCTACCT GACGGGTGGC 1380
 GTGGACAGCT GCGAGGGGGA CAGCGGGGGG CCCCTGGTGT GTCAAGAGAG GAGGCTGTGG 1440
 AAGTTAGTGG TACAGACCTG CTTTGGCATC GGTGCGCAG AGGTGAACAA GCTGGGGTGG 1500
 45 TACACCGCTG TCACCTTCTT CCTGGACTGG ATCCACAGAC AGATGGAGAG AGACTAAAA 1560
 ACCTGAAGAG GAAGGGGACA AGTAGCCACC TGAGTTCTCT AGGTGATGAA GACAGCCCGA 1620
 TCCCTCCCTG GACTCCCGTG TAGGAACCTG CACACGAGCA GACACCTTG GAGCTCTGAG 1680
 TTCCGGCAAC AGTAGCAGGC CCGAAAGAGG CACCTTCCA TCTGATTCCA GCACAACTT 1740
 CAAGCTGCTT TTTGTTTTTT GTTTTTTTGA GGTGGAGTCT CGCTCTGTGG CCCAGGCTGG 1800
 50 AGTGCAGTGG CGAAATCCCT GCTCACTGCA GCTCCGCTT CCCTGTGTC AGCGATTCTC 1860
 TTGCTCAGC TTCCCGATTA CTTGGGACCA CAGGTGCCCG CCACCAACCC CACTAATTT 1920
 TTGTATTTT AGTAGAGCA GGGTTTACC ATGTTGGCCA GGTCTCTCTC AAACCCCTGA 1980
 CCTCAATGA TGTGCTGCTT TCAGCTTCCC AAGTGTCTGG GATTAAGAGC ATGGGCCACC 2040
 ACAGCTAGCC TCACGCTCCT TTCTGATCTT CACTAAGAAC AAAAGAAGCA GCAACTTGCA 2100
 55 AGGGCGGCTT TTCCCACTGG TCCATCTGCT TTTCTTCCA GGGGTCTGAC AAATTTCTCT 2160
 ACAGATAGC ACCTCACTG CACTCACTG CAAAGCCACC AACAGCCACT CAGAAAGAC 2220
 GCACCAGCC AGAAGTGCAG AACTGCAGTC ACTGCAGTT TTCATCTCTA GGGACCAAG 2280
 CCAAAACCCAC CCTTCTTACT TCCAAGACTT ATTTTCACAT GTGGGAGAGT TAATCTAGGA 2340
 ATGACTCGTT TAAGGCTAT TTTCTAGAT TCCTTGTAGC ATTTGGTGTCT TGACGTATTA 2400
 60 TTGCTCTTG ATTCCAAATA ATATGTTTCC TTCCCTCAA AAAAAA AAAAAA 2460
 AAAAAA

A103 Protein sequence:

65 Gene name: TMPSR53a
 Unigene number: Hs.298241
 Probeset Accession #: AI538613
 Protein Accession #: BAB20077
 Signal sequence: none found
 Transmembrane domains: 43-65, 239-261
 70 Tryp_SPC domain: 216-444
 Cellular Localization: plasma membrane

75 1 11 21 31 41 51
 | | | | |
 MGENDFPAVE APFSFRELFG LDDLKISFVA PDADAVAAQI LSLPLKFFP ITVIGIIALI 60
 IALAIGLGIH FDCSGKYRCR SBFKIELIA RCDGVSDCKD GEDEYRCRVV GQNAVLLQVP 120
 PAASWKTMCs DDWKGHYANV ACAQLGPPSY VSDNLRVSS LEGQFREBPV SIDHLLPDDK 180
 VTALHESVYV REGCASHGVV TLQCTACGHR RGYSSRIVGG NMSLLQWPNW QASLQFQGYE 240
 80 LCGGSVITPL WITTAARCVY DLYLPSWTI QVGLVSLDN PAPSHLVEKI VHSKYKPKR 300
 LGNDIALAKL AGPLTFNEMI QPVCLPNSRZ NFPDGVKWT SGGWATEDGA GDASPVLNHA 360
 AVPLISNKIC NHRDVYGGII SPSEMLCAGYL TGGVDSQCGD SGGPLVCQR RLWKLVGATS 420
 FGIGCAEVNK PGVITRTSTF LDNIHQMER DLKT

A104 DNA SEQUENCE

Gene name: Homo sapiens G protein-coupled receptor (H077175)

Unigene number: Hs.208229

Probeset Accession #: AI819198

Nucleic Acid Accession #: NM_032551.1

Coding sequence: 1-1197 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
|      |      |      |      |      |
10  ATGCACACCG TGGCTACGTC CGGACCCAAAC GCGTCTCTGGG GGGCACCAGGC CAACGCCCTCC 60
    GCGTGGCCGG GCTGTGGCGC CAACGCCCTCG GACGGCCGAG TCCCTTCGCC GCGGGCCGTG 120
    GACGCCCTGG TCGTACCGCT CTCTTTCGGG GCGCTGATGC TCGTGGGCTT GGTGGGGAAC 180
    TCGCTGGTCA TCTACGTCAT CTGCCGCCAC AAGCCGATGC GGACCCGTAC CAACTTCTAC 240
15  ATCGCCAAAC TGGCGGCCAC GGACGTGACC TTCTCTCTGT GCTGCGTCCC CTTCACGGCC 300
    CTGCTGTACC CGCTGCCCGG TTGGGTGCTG GCGGACTTCA TGTGCAAGTT CGTCAACTAC 360
    ATCCAGCAGG TCTCGGTGCA GGCCACGTGT GCCACTCTGA CCGCCATGAG TGTGGACCTC 420
    TGGTACGTGA CGGTGTTCCC GTTGGCGGCC CTGCACCCGC GCACGCCCGC CTGGCGCTG 480
    CTGTACAGCC TCAGCACTCG GTTAGGCTCT GCGCGCGTGT CTGCGCGGCT GCTCGCCCTG 540
20  CACCGCTCTG CACCCGGGCC GCGCGCTTAC TGCAGTGAAG CCTTCCCCAG CCGCGCCCTG 600
    GAGCGCGCCT TCGCACGTGA CAACCTGCTG GCGCTGTACC TGTGCGGCT GCTCGCCACC 660
    TCGCGCTGCT ATGCGGCCAT GCTGCGCCAC CTGGGCGCGG TCGCGGTGG CCGCGCCGCC 720
    GCGGATAGCG CCGTGCAGGG SCAGGTGCTG GCAGAGCGCG CAGGCGCGCT GCGGGCTAAG 780
    GTCCTCGCGC TGGTGGCGGC CGTGGTCTCT CTCTTTCGCC CCTGCTGGGG CCGCATCCAG 840
25  GCTCTCTCTG TGTTCGAGGC CTGGGCGGCC GCGGGCTCCT GGCACCCAG CAGTACGCC 900
    GCGTACGCGC TTAAGACCTG GCGTCACTGC ATGTCTTACA GCAACTCTGC GCTGAACCCG 960
    CTGCTCTACG CCTTCTCTGG CTGCACTTTC CGACAGGCTT TCGCGCGGCT CTGCCCCCTG 1020
    GCGCGCGCGC GCGCGCGCGC CCGCGCGCGC CCGCGACCTT CCGACCCGCT CAGCCACAC 1080
    GCGGAGCTTC ACCGCTCTGG GTCCACCCG GCGCGCGGCA GCGCGGAGC GCCAGGGAG 1140
30  AGTGGGCTGG CCGCGCGCGC GCTGTGCGTC CTGGGCGGAG ACAACGCCCC TCTCTGA

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A105 Protein sequence

Gene name:

Homo sapiens G protein-coupled receptor (H077175), mRNA

Unigene number:

Hs.208229

Protein Accession #:

AI819198

Signal sequence:

none found

Pfam domains:

7tm_1 [59-323]

Transmembrane domains:

43-65, 86-108, 122-144, 159-181, 203-225, 260-282

Cellular Localization:

plasma membrane

```

1      11      21      31      41      51
|      |      |      |      |      |
45  MHTVATSGPM ASWGAANAS GCPGOGANAS DGPVPSPEAV DANLVPLFFA ALMLLGLVGN 60
    SLVIVVICRH KPMRTVINFY IANLAATDVT FLCCVPPFTA LLVPLGWL GDMCKFVNY 120
    IQGVSVQATC ATLTAMSVDR WYTVFPLRA LRRTPRLAL AVSLSTNVGS AAVSAFVLAL 180
    RRLSPGPFRY CSEAFPSRAL ERAFALYNLL ALYLLPLLAT CACYAAMLR LGRVAVRPAP 240
    ADSALQQQVL AERAGAVRAK VSRLLVAAVL LPAACWGPFI LFLVLQALGP AGSWHFRSYA 300
50  AYALHTMAHC MSYNSALNP LLYAFILGSHF RQAFERKVCPC APRFRPRPRR PPSDFPAEHL 360
    ARLHRLGSHF APARAQKPGS SGLAARGLCV LGEDNAPL

```

A106 DNA SEQUENCE

Gene name:

Integrin, beta 8

Unigene number:

Hs.52620

Probeset Accession #:

AA479726

Nucleic Acid Accession #:

NM_002214

Coding sequence:

680-2990 (underlined sequences correspond to start and stop codons)

```

1      11      21      31      41      51
|      |      |      |      |      |
60  CCCAGAGCGG CCTCCCCCTG TTGCTGGCAT CCCAGCTTC CTCCCTTGCC AGCCAGGACG 60
    CTGCGGACTT GCTTTTCCCG GCTGCTCGCG AGACGGGGCT GCAAGGTGCG AACTAATGGT 120
    GTTGGCTTCC CTGCCACCTT GTGGAAGCAA CTGCGCTGAT TGATGCGCCA CAGACTTTT 180
65  TCCCTTCGAC CTGCGCGCGG TACCTTCCCA CAGATCCAGC ATCACCAGT GAATGTACAT 240
    TAGGTTGTTT TCCCCCCAG CTTCGGGCTT TGTFTGGGTT TGATTGTGTT TGGCTCTTCG 300
    CTAAGCTGAT TTATGCAGCA GAAGCCCCAC CGCTGAGAGA GAAACAAAAG CTCTTTTCTT 360
    TGTCCCGGAG CAGGCTGCGG AGCCCTTGCA GAGCCCTCTC TCCAGTCGCT GCGGGGCTCT 420
    TGGCCGTGGA AGGAGTGTCT TCTCGCGGAG ACCGCGGGAC CCGCGCTGCC GAGCGGGGAG 480
70  GCGCGTAGGG GCGCTGAGAT GCGAGCGGCT GCGCGGGGCC GCTTAAGTGC ACGGCTTGCT 540
    CCGAGCGCGG GGGTCCGCTT GCTAGGCTTG CGGAAACGCT CCTAGGACA CTGCGCGCGG 600
    GCGCGGAGG TCGCCCGGGA GCGCGAGCCC GCGTCCGGAA GGCAGCAGG CCGCGGGCGC 660
    GGGCGGGGCT GTTTTGCAAT ATGTGCGGCT CGGCCCTGCG TTTTITTACC GCTGCTTTG 720
    TCTGCTGCA AAGCAACCGG CGAGGTCCCG CCTGTTCTCT CTGGGCGAGC TGGGTGTTT 780
75  CACITGTGCT TGGACTGGGC CAAGGTGAAG ACAATAGATG TGCATCTTCA AATGACGAT 840
    CCTGTGCGAG GTCCCTTGCG CTGGGTCCAG AATGTGGATG GTGTGTCAA GAGGATTTCA 900
    TTTCAAGTGG ATCAAGAAGT GAACGTGTG ATATGTGTTT CAATTTAATA AGCAAGGCT 960
    GCTCAGTTGA TTCAATAGAA TACCATCTG TGCATGTTAT AATACCCACT GAAATGAAA 1020
    TTAATACCA GGTGACACCA GGAGAAGTGT CTATCCAGCT GCGTCCAGGA GCCAAGCTA 1080
80  ATTTTATGCT GAAAGTTCAT CCTCTGAAGA AATATCTGTT GGATCTTTAT TATCTTTTG 1140
    ATGTCTCAGC ATCAATGTC AATAATATAG AAAAAATTA TCCGTTGGA AACGATTTAT 1200
    CTAGAAAAT GGCATTTTTC TCCGTTGACT TTGCTCTTGG ATTTGGCTCA TACGTTGATA 1260
    AAGCAGTTTC ACCATACATT AGCATCCACC CCGAAGGAT TCATAATCAA TGCACTGACT 1320
    ACAATTTAGA CTGATGCTCT CCCCATGGAT ACATCCATGT GCTGTCTTTG ACAGAGACA 1380
    TCACTGAGTT TGAGAAAGCA GTTCATAGAC AGAAGATCTC TGGAAACATA GATACACAG 1440

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5 AAGGAGGTTT TGACGCCATG CTTCAGGCAG CTGTCTGTGA AAGTCATATC GGATGGCGAA 1500
 AAGAGGCTAA AAGATTGCTG CTGGTGATGA CAGATCAGAC GTCTCATCTC GCTCTTGATA 1560
 GCAAAATTGGC AGGCATAGTG GTGCCCAATG ACGGAAACTG TCATCTGAAA AACACCGTCT 1620
 AGGTCAAAATC GACAAACCATG GAACACCCCT CACTAGGCCA ACTTTCAGAG AAATTAATAG 1680
 ACAACACAT TAATGTCATC TTTCAGTTT AAGGAAACAC ATTTTCATTG TATAAGGATC 1740
 TTCTACCCCT CTTCGCCAGG ACCATTGCTG GTGAAATAGA ATCAAAGGCT GCAAACCTCA 1800
 ATAATTTGGT AGTGGGAAGC TATCAGAAGC TCATTTCAGA AGTGAAAGTT CAGGTGGAAA 1860
 ACCAGGTACA AGGCATCTAT TTTAACATTA CCGCCATCTG TCCAGATGGG TCCAGAAAGC 1920
 CAGGCATGGA AGGATGCGA AACGTGACGA GCAATGATGA AGTTCTTTTC AATGTAACAG 1980
 10 TTAACAATGAA AAGATTGATG GTACACAGGAG GAAAAAATA TGCATAATC AAACCTATTG 2040
 GTTTTAATGA AACCGCTAAA ATTCATATAC ACAGAAACTG CAGCTGTCTG TGTGAGGACA 2100
 ACAGAGGACC TAAAGGAAAG TGTGTAGATG AAACCTTTCT AGATTCCAAG TGTTCCTAGT 2160
 GTGATGAGAA TAAATGTCAT TTGATGAAG ATCAGTTTTC TTCTGAGAGT TGCAAGTCAC 2220
 15 ACAAGGATCA GCCTGTTTGC AGTGTGCGAG GAGTTTGTGT TTGTGGGAAA TGTTCATGTC 2280
 ACAAAATTAA GCITGGAAAA GTGTATGGAA AATACTGTGA AAAGGATGAC TTTTCTTGTC 2340
 CATATCACCA TGGAAATCTG TGTGCTGGGC ATGGAGAGTG TGAAGCAGGC AGATGCCAAT 2400
 GCTTCAGTGG CTGGGAAGGT GATCGATGCC AGTGCCCTTC AGCAGCAGCC CAGCACTGTG 2460
 TCAATTCAAA GGGCCAAAGT TGCAGTGGAA GAGGCACGTG TGTGTGTGGA AGGTGTGAGT 2520
 20 GCACCGATCC CAGGAGCATC GGCCGCTTCT GTGAACACTG CCGCACTGTG TATACAGCCT 2580
 GCAGGAAATA CTGCAATGAT ATGCAATGCC TTCAACCTCA CAATTGTGCT CAGGCTATAC 2640
 TTGATCAGTG CAAACCTCA TGTCTCTCA TGGAAACACA GCATTATGTC GACCAAACTT 2700
 CAGAATGTTT CCGTAGCCTT AGCTACTTGA GAATATTTT CATCATTTTC ATAGTTACAT 2760
 TCTTGATTGG GTTGCTTAAA GTCTGTATCA TTAGACAGGT GATACTACAA TGGATAGTA 2820
 25 ATAAATTTAA GTCTCTATCA GATTACAGAG TGTGAGCCTC AAAAAAGGAT AAGTTGATTC 2880
 TGCAGAGTGT TTGCAAGAGA GCAGTCACCT ACCGACGTGA GAAGCCTGAA GAATTAATAA 2940
 TGGATATCAG CAAATTAAT GCTCATGAAA CTTTCAGGTG CAACTTCTAA AAAAGATTTT 3000
 TTAACACTT AATGGGAAAC TGGAAATGTT AATAATTGCT CCTAAAGATT ATAATTTTAA 3060
 AAGTCACAGG AGGAGACAAA TTGCTCACGG TCATGCCAGT TGCTGTGTGT ACACTCGAAC 3120
 30 GAAGACTGAC AAGTATCCTC ATCATGATGT GACTCACATA GCTGCTGACT TTTTCAGAGA 3180
 AARATGTGTC TTACTACTGT TTGAGACTAG TGTGTTGTA GCACCTTACT GTAATATATA 3240
 ACTTATTATG ATCAGCATAG AATGTAGATC CTCTGAAGAG CACTGATTAC ACTTTACAGG 3300
 TACCTGTTT CCGTAGCCTT CCGCAGAGAG ACAATGCTGT GAGAGAGTTT AGCATTTGTT 3360
 CACTACAGG GTACAGTAAT CCGTGCACGT GACATGTGAG GAAAAAATA ATCTGCCAAG 3420
 35 TATATTCTAA GGTGCGCAAA CACTTCAACA GTTGGTGGT GAATAGACAA GAACAGCTAG 3480
 ATGAATAAAT GATTCGTGTT TCACCTTTTC AAGAGGTGAA CAGATACAAC CTTAATCTTA 3540
 AAAGATTATT GCTTTTAAA GTGTGTAGTT TTATGCAATG GTGTTTATGG TTGCTTAT 3600
 TTGCAAGAT GATACATAT TCCAGCAATC TCTCCTCTTT GCCTTTATGT TTTGTTTCT 3660
 TTTTACAGG ATAAGTTTAT GTATGTCACA GATGACTGGA TTAATTAAGT GCTAAGTTAC 3720
 40 TACTGCCATA AAAAATAAAT AATACAATGT CACTTTATCA GAATACTAGT TTTAAAGCT 3780
 GAATGTTAA

A107 Protein sequence:

45 Gene name: Integrin, beta 8
 Unigene number: Hs.52620
 Probeset Accession #: AA479726
 Protein Accession #: NP_002205.1
 Signal sequence: 1-39
 Transmembrane domains: 682-704
 50 EGF domain: 552-584
 TNF domain: 54-469
 Cellular Localization: plasma membrane

55 1 11 21 31 41 51
 | | | | |
 MCGBALAFT AAFVCLQNDR RGPASFLWAA WVPFLVLGLG QGENDRCASS NAASCARCLA 60
 LGPECGWCVQ EDFISGSRSE ERCDIVSNLI SKCCSVDSIE YPSVHVIIPT ENBINTQVTP 120
 60 GEVSIQLRPG AEANFMLKVH PLKKYFVDLY YLVDVSAAMH NNIEKLNSVG NDLSRKMAFF 180
 SRDFRLGFGS YVDKTVSPYI SIHPERIHNQ CSDVNLDCMP PHGYIEVLSI TENITEFEKA 240
 VHRQKISGNI DTPEGGFDM LQAAVCESHI GWRKEAKRLI LVMTDQTSIL ALDSKLGLIV 300
 VPNDGNCHLK NNYYVKESTM EHPSLGQLSE KLIDNNINVI FAVCGKQFHW YKDLLELLFG 360
 65 TIAGBIESKA ANLNNLVVEA YQKLISEVKV QVENQVQGIY FNITAI CPDG SRKPGMGSCR 420
 NVTSENDEVL NVTVTMKKCD VTGKNYAI KPIGFNEIAX IHIHNCSCQ CEDNRGPKGK 480
 CVDETFLDSK CFQCDENKCH FDEPQFSSES CKSHHDQFVC SGRGVCVCGK CSCHKIKLKG 540
 VYGYKEKDD FSCPYHHGNL CAGHGCEEAG RCQCPSQWEG DRQCPSAAA QHCVNSEKQV 600
 CSGRGTCVCG RCECTDERSI GRFCEHCPTC YTACKENWNC MQCLHPENLS QAILDQCKTS 660
 70 CALMEQHYV DQTECFSSP SYLRIFPIIF IVTFILGLLK VLIIRQVILQ WNSNKIKSSS 720
 DYRVSASKKD KLILQSVCTR AVTYREKPE EIKMDISXIN AHETFRCNF

A108 DNA sequence

75 Gene name: ESTs
 Unigene number: Hs.128899
 Probeset Accession #: AA983251
 Nucleic Acid Accession #: AA983251
 Coding sequence: 1-1749 (underlined sequences correspond to start and stop codons)

80 1 11 21 31 41 51
 | | | | |
 ATGCTGTCTG GCTTCTTGAT GAGTCCCACT ACCCAGCACA GAGCACAGTA CACTCCCGGA 60
 GGAAGAAAC TTCCGTGGGA GGCTTCCATC GGTGCGCACA CCTCCCGAGG GCGAGGCAGC 120
 GACCGGAGGA GCGAGAGCCG GCCGGAGGCT GCGCGGCTCC TGTGGGACCG CGCTGCAGCC 180
 GGGGAGGCGG AGAAGGGGAA CCGGGCGGAG CCGCCCGCCT GGATCCGCGC CCAGCAGCAG 240

5	CGCGGGCCGC	CGCCAGCTGG	GCAGGCTCCC	GGGACTGOGG	CTGGGGGCGC	GCAGGACCCCT	300
	CGCCTGCGTC	CTGGACGTTT	CCGGGGGAGG	GTCCGATTGC	CAGTGAAACC	TCAGAGAGCT	360
	TCGCGACGAC	AGCCCCGGGG	GCCTTCTGAC	TGCATCCCGA	GATTTCCATC	AGCGAGTGCA	420
	ACTCATAAGG	CAGTCCCTAA	GGGACCCGGG	CCACCGGCTG	AGGACGGGGA	TGGCTTAGGA	480
	GCTCTGTGAC	CTAGGGCCCG	GCCTCGTCCG	CTCCTGGGCG	TCGCGCCAGA	GGGAGTGCC	540
	CCCGCGGGA	AGCGCCGGGG	GACAGTCACT	GACBAGGCC	GGGGTCCGCC	GGGGCCACGA	600
	CTTCTGGGAG	ACCGTCTTGC	GCTCTCTGGA	GACGCGCTGT	CCGCGCCAG	GGTGGTGCCA	660
	TGTGGGGGCG	TCGCGGCTCG	TCCGTCTCCT	CATCCTGGAA	CGCGGCTTCG	CTCCTGCAGC	720
10	TGCTGCTGGC	TGCGCTGCTG	GCGCGGGGGG	CGAGGGCCCA	GCGCGAGTA	CTGCCACGGC	780
	TGGCTGGACG	CGCAGGGCGT	CTGGCGCATC	GGCTTCCAGT	GTCCCGAGCG	CTTCGACGGC	840
	GGCGACGCCA	CCATCTGCTG	CGCGAGCTGC	GCGTTGCGCT	ACTGCTGCTC	CAGCGCCGAG	900
	GGCGCGCTGG	ACCAGGGCGG	CTCGACAAAT	GACCGCCAGC	AGCGCGCTGG	CGAGCCTGGC	960
	CGCGCGGACA	AAGACGGGCC	CCGACGGCTC	GGCAGGCTTT	CATGTCTTAG	GGGTACCCAA	1020
15	GGAGACGGGG	AGGCTGGGCC	CCACCCGCTG	AGGGCTTGGC	AGCGGTGCTC	CCCTGAAGGC	1080
	TCGCCGAAAG	GAGGCGGGCT	CTCAGGGCTT	TTCCCGGGGC	TGCTGCCCGC	TGCCAGACGC	1140
	CGCGGATTCC	CATCTTCTCC	ACCGGGGGCG	CCCTCTCCCG	TGCAGCGGCC	CGCCTTGCC	1200
	ATCTACGTGC	GTGTGGCTCC	TGTTGGCTCC	GTTTGTGTCG	CCCTTATCAT	CTTGGGTCC	1260
	CTGGTGGCAG	CGTGTGCTG	CAGATGTCTC	CGGCTTAAGC	AGGATCCCCA	GCAGAGCCGA	1320
20	GCOCAGGGGG	GTAACCGCTT	GATGGAGACC	ATCCCATGTA	TCCCTAGTBC	CAGCACTCC	1380
	CGGGGTTCGT	CTCACGCCCA	GCTGCAGACA	GCTGCAGATT	CCAGCTCCAG	CGCCAACTCC	1440
	GGGGCCGGGG	CGCCCCAAC	AAGTTCACAG	ACCAACTGTT	GCTTGCCTGA	AGGGAACCATG	1500
	AACACGCTGT	ATGTCAACAT	GCCACGAAT	TTCTCTGTGC	TGAACCTGTA	GCAGGCCACC	1560
	CAGATTGTGC	CACATCAAGG	GCAGTATCTG	CATCCCCCAT	ACGTGGGGTA	CACGTTGCAG	1620
25	CACGACTCTG	TGCCCATGAC	AGCTGTGCCA	CCCTTTCATG	ACGCGCTGCA	GCTTGGCTAC	1680
	AGCAGATTTC	AGTCCCGCTT	CCCTCACACC	AACAGTGAAC	AGAAGATGTA	CCAGCGGGTG	1740
	ACTGTATAAC	CGAGAGTCA	TGGTGGGTTT	CTTACAGTAA	GGGAGACGAA	GGCAGGGGTG	1800
	GATCTCGAG	GTGGAGTCC	GCACATGTGG	GTGGTATTTA	TGGCAGGATT	CCCTTGGATG	1860
	GCTTCATTTC	CCCCCAGACT	GTATGAAATC	ATCTCCGAAT	TAGCATTTCT	GGATATGTTT	1920
30	CATCCAGGTT	ATCATTGATT	TATGATGAA	AACCGGCTTC	AGCTGGAGAT	GACTGTGATG	1980
	TGCTGATGG	GCTGTATACA	AATGCTTGAG	TCCGAAAGTG	CCTTGAGATA	TGGTTGACGA	2040
	AAGAAATTTA	TAAACTGATA	AATTAAGGAT	TTTATTATAT	TGTTATTATT	TATTTCTTTT	2100
	TGTTGTTTGA	CTGCACAGGA	TCAAATGCC	TGTTATCTCC	CTTTTACTGG	GACTTTTFTT	2160
	TTTTTTTTTT	TTTTTTTTTA	TCAGACAGGG	TCCTGCTCTG	TTGCCAGGC	TGGAGTGCCG	2220
35	TGGTGCGATC	TGGGCTCACT	GCAACTTCAG	CTTCTGGGAT	TCAGGCAACA	CTCCTGCCCT	2280
	AGCCTCCAC	GTGGCTGGGA	TTACAGGTGC	CTGCCGCCAT	GGCTAAATTT	TTGTATTTTT	2340
	TGTAGAGATG	GGGTTTCAAC	ATGTTGGCTG	GGCTGGTCTC	ACTCTCTGTA	CTCAAGCAA	2400
	TCGCGCTGTC	TCAGCCTCC	AAAGTGGCTG	GATTACAGGC	GTGAGCCACC	GCCCCAGCC	2460
	TGAGCCTTTT	TTTTTTCTA	ATGCATCCAA	GGTTAAGGGG	AAGAGCGAAA	TAACAGGACT	2520
40	ATTCATAAAG	GAAACCTGTT	TGAATCTGTT	GAGATCAGTC	ATCAGTCTCA	GTATTCACCA	2580
	GGCACACCTT	AATTTCAATG	TAAAAAGATA	TATATATTTT	GTCTATTTTT	GTGCTTTTGG	2640
	GGGCTTATTT	TGTGCTTTT	TACCTTATGT	AGAGATCTTA	TTACAAGATG	ATTTTCTACA	2700
	TTAAAAAGAG	TCGAAATAA	ATTGTATAGT	TACTTAACCTA	ATGAAGACAT	TTCAAGATC	2760
	TGGGATGATT	TGAATCTTGA	AGTAGTAGGT	GGTATAGTCA	TAAACCAATT	CATCCCCCTC	2820
45	TTGATTGTAT	CTTAATTTTC	TGGCTTTAAG	GTGACATCTG	AGAGGTAAATG	CATTTCTTTT	2880
	TATATTGAAA	TCATAAACA	TCACCCGCTG	CTTCTCTGAG	TTACTTTTAA	TTTTGCGCTG	2940
	TGGTATGGT	TTGGGCTTTC	CTTCTGTTTG	GTTTTCAGAG	CCCATGCTCT	ATATAGTCTT	3000
	GAGTCAAGT	AATTTCTATA	CTTGTAAATG	AAGATCAGTA	TTCTGCTCTA	GATCTGATAA	3060
	AAAAATTTTC	TGTCCTTAGT	TATAAAATTT	CAAGAAATG	TGTTACAAAG	ATACTTAGTA	3120
50	TAGCTCCTCA	GCCATAACCT	GAGACTTGGG	ATGAAATTTA	AACAGATAC	GATTACTTTT	3180
	GCAGATCATA	AGGCTTTTTA	TACTCTTGT	ATCAAAATGG	CTTATTTTTC	AGGCACTAAG	3240
	GATTGTATAG	AGAAAGCTTT	TTCAACGAAG	GATTGCTCTT	CTTCTCCAC	ACGTGCTCTG	3300
	AITTCCTCTC	TCTTTCAGGC	CTCAACAGGC	ACTGTATTCA	TGCGCAATGT	TCCAAATAT	3360
	CAATTCAGT	TGAATTTAT	TGTGTGTTCT	TTACTTATAT	AAAAAAGAT	AACTTAAGG	3420
55	ATGTGCAAGT	ACATTTCCAA	CTGCTAGCAC	AACCAATAT	TTGTAATTA	ACAATCGCT	3480
	GTATGATATG	GTCTTCTACA	CATTATATGC	TATAGATATC	TATCGATCAT	CTTCTATTC	3540
	TGTTTCATGA	CTGAATAATG	TAAACCAAGT	GTGCGCAAT	GGTATCATCA	ATGATACTCA	3600
	TTTTTAAATA	ACCAAGGCA	GGGAAATATC	ATTTTACTTA	TAAATAATA	TTTATGATG	3660
60	TGAAAAAATA	AAAAAATA	AAAAAATA				

A109 Protein sequence

Gene name: ESTs
 Unigene number: Hs.128899
 Protein Accession #: none found
 Signal sequence: 1-11
 Transmembrane domains: 402-424
 Cellular Localization: not determined

70	1	11	21	31	41	51	
	MLSGFLMSPS	TQHRAYTTPG	GKKLPWEASI	GAHTSRGRGS	DRSRSRPFA	AGLLMDRAAA	60
	GEAEKGNRGE	PPAWIRAQQQ	PRPPFAGQAP	GTAAAGQADP	RLRPGRSRGR	VRLPVKPFPEA	120
	SGRQPRGSPD	CIPRFPSSA	THKAVPKGTG	PPAEDGDGLG	APGPRARRRR	LLGVAAEGSG	180
75	PRGKRGTVS	DEARGSPGPR	LLGDRPALSG	DALSAPRVVP	CGALAARPS	HPGTPLRSCS	240
	CCWLRCWRNG	RGPSGEYCHG	WLDAGQVWRI	GFQCPFRFDG	GDATICCGSC	ALRYCCSSAE	300
	ARLDQGGCDN	DRQQAGGEPG	RADKDGPRRL	GRASCLRGTQ	GDGEGAPPV	RAWQRCSPFG	360
	SPKGRQLLRA	FPGLLEPRRE	RGFSSSPRGG	PSPLQRPALF	LYVFLIVGSG	VVFVAFILGS	420
80	LVAACCCRCI	RPKQDPQQSR	APFGNRLMET	IFMIPSASTS	RGSRRQSSST	AASSSSSSAQ	480
	GARAPPTRSQ	TNCCLEPGTM	NNVYVMPMTN	FSVINCQOAT	QIVPHQGGYL	HPFYVGYTVQ	540
	HDSVPMTAVP	PFMDGLQPGY	RQIQSPFPHT	NSEQKMPAV	TV		

A110 DNA SEQUENCE:

Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]

Unigene number: Hs.100686
 Probeset Accession #: AA487468
 Nucleic Acid Accession #: AA487468
 Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

5

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1      11      21      31      41      51
|      |      |      |      |      |
10 CGGCACCAAG AGCACTGGCC AAGTCAGCTT CTCTGAGAG AGTCTCTAGA AGACATGATG 60
   CTACACTCAG CTTTGGGTCT CTGCTCTCTA CTCGTACAG TTCTCTCCAA CCTTGCCATT 120
   GCAATAAAAA AGGAAAAGAG GCCTCTCAG ACACTCTCAA GAGGATGGGG AGATGACATC 180
   ACTTGGGTAC AAACCTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAAGCCATTA 240
   ATGGTTATTC ATCACCCTGA GGAATGTCAA TACTCTCAAG CACTAAAGAA AGTATTTGCC 300
   CAAATGAAG AAATACAAGA AATGGCTCAG AATAAGTTCA TCATGCTAAA CCTTATGCAT 360
15 GAAACCACTG ATAAGANTTT ATCACCCTGAT GGGCAATATG TGCCTAGAAT CATGTTTGTA 420
   GACCCCTCTT TAACAGTTAG AGCTGACATA GCTGGAGAT ACTCTAACAG ATTGTACACA 480
   TATGAGCCTC GGGATTACCC CCTATTGATA GAAAACATGA AGAAAGCATT AAGACTTATT 540
   CAGTCAGAGC TATAAGAGAT GATAGAAAAA AGCCTTCACT TCAAGAAGT CAAATTTCAT 600
   GAAGAAACC TCTGGCACAT TGACAATAC TAAATGTGCA AGTATATAGA TTTTGTAA 660
20 TTACTATTTA GTTTTAA ATAGTCTTAT TAAATAAAT GTTTTAA 720
   TCTGAAAAA AAAAAAAA AAAAAAAA

```

25 A11 Protein sequence:
 Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
 Unigene number: Hs.100686
 Probeset Accession #: AA487468
 Protein Accession #: none found
 Signal sequence: 1-23
 Transmembrane domains: none found
 Cellular Localization: secreted

30

```

35 1      11      21      31      41      51
   |      |      |      |      |      |
   MMLHSALGLC LLLVTVSENL ALAIKCEKRP PQTLSRQWGD DITWVQTYEE GLFYAQSKSK 60
   PLMWIHLED CQYSQALKKV FAQNEIQEM AQNKFIHLNL MHSTTDKLS PDGQYVPRIM 120
   FVDPSTLVRA DIAGRYSNRL YTYEPEDLEL LIENMKALR LIQSEL

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40

A112 DNA SEQUENCE
 Gene name: Homo sapiens type II membrane serine protease mRNA
 Unigene number: Hs.63325
 Probeset Accession #: AA411502
 Nucleic Acid Accession #: NM_016425
 Coding sequence: 1-1314 (underlined sequences correspond to start and stop codons)

45

```

50 1      11      21      31      41      51
   |      |      |      |      |      |
   ATGTTACAGG ATCCTGACAG TGATCAACCT CTGAACAGCC TCGATGTCAA ACCCCTGCBC 60
   AAAACCCGTA TCCCATGGA GACCTTCAGA AAGGTGGGGA TCCCATCAT CATAGCACTA 120
   CTGAGCCTCG CGAGTATCAT CATGTGGT GTCTCATCA AGGTGATTCT GGATAAATAC 180
   TACTTCTCT GCGGGCAGCC TCTCCACTTC ATCCGAGGA AGCAGCTGTG TGACGGAGAG 240
   CTGAGACTGC CTTTGGGGGA GGAAGAGGAG CACTGTGTCA AGAGCTTCCC CGAAGGGCTT 300
55 GCAGTGGCAG TCCGCCCTCTC CAGGACCGA TCCACACTGC AGGTGCTGGA CTCGGCCACA 360
   GGGAACTGAT TCTCTGCTG TTTGACACAC TTACAGAAAG CTCTGCTGA GACAGCCTGT 420
   AGGCAGATGG GCTACAGCAG CAAACCCACT TTCAGAGCTG TGGAGATTGG CCCAGACCAG 480
   GATCTGGATG TTGTTGAAT CACAGAAAC AGCCAGGAGC TTGCTATGCG GAACCTAAGT 540
   GGGCCCTGTC TCTCAGGCTC CTTGGTCTCC CTGCACGTGC TTGCTGTGG GAAGAGCCTG 600
60 AAGACCCGCC GTGTGGTGG TGGGAGGAG GCTCTGTGG ATTCTTGGCC TTGGCAGGTC 660
   AGCATCCAGT ACACAAACA GCAAGTCTGT GAGGGAGCA TCCCTGGACC CCACTGGGTC 720
   CTCACGGCAG CCCACTGCTT CAGGAACAT ACCGATGTGT TCAACTGGAA GGTGGGGCA 780
   GGCTCAGACA AACTGGGCAG CTTCCTCATCC CTGGCTGTGG CCAAGATCAT CATCAITGAA 840
   TTCACCCCA TGTACCCCAA AGACAAATGAC ATCGCCCTCA TGAAGCTGCA GTTCCCACTC 900
65 ACTTTCAG GCACAGTCAG GCCCATCTGT CTGCCCTTCT TTGATGAGGA GCTCACTCCA 960
   GCCACCCAC TCTGGATCAT TGGATGGGGC TTTACGAAGC AGAATGGAGG GAAGATGTCT 1020
   GACATACTGC TGCAGGCTC AGTCCAGGTC ATTGACAGCA CACGGTGCAA TGCAGACGAT 1080
   GCCTACCAAG GGAAGTTCAC CAGAAAGATG ATGTGTGAG GCATCCCGGA AGGGGGTGTG 1140
   GACACCTGCC AGGGTGACAG TGGTGGGCC CTGATGTACC AATCTGACCA GTGGCATGTG 1200
70 GTGGGATGCS TTAGCTGGG CTATGGCTGC GGGGGCCGA GCACCCGAGG AGTATACACC 1260
   AAGGTCTCAG CCTATCTCAA CTGGATCTAC AATGTCTGGA AGGCTGAGCT GTAA

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75 A113 Protein sequence:
 Gene name: Homo sapiens type II membrane serine protease mRNA
 Unigene number: Hs.63325
 Probeset Accession #: AA411502
 Protein Accession #: NP_057509
 Signal sequence: none found
 Transmembrane domains: 31-53
 LDLA domain: 54-94
 Tryp_SPC domain: 204-429
 Cellular Localization: plasma membrane/ER

80

1	31	21	31	41	51	
MLQDFSDQDP	INSLEDVKPLR	KPRIPMETFR	KVGIPILIAL	LSLASIIIVV	VLIKVILDKY	60
YFLCGQPLHF	IPRQLCDGE	LDCPLGEDZE	HCVKSPPEGP	AVAVRLSKDR	STLQVLDSAT	120
GNWFSACFDN	FTEALAEIAC	RQMGYSKPT	FRAVEIGPDQ	DLDVVEITEN	SQELMRNNS	180
GPCLSGSLVS	LBCLACGKSL	KTPRVVGGEE	ASVDSNFWQV	SIQYDKQHV	GGSLDPHNV	240
LTAACFCRKH	TDVFNWVKRA	GSDKLGSFPS	LAVAKIIIE	FNMYPKDN	IALMGLQFPL	300
TFSGTVRPIC	LPFFDEELTP	ATPLNIIIGW	FTKQNGGKMS	DILLQASVQV	IDSTRCNADD	360
AYQGEVTEKM	MCAGIPBBGV	DTCCGDSGGP	LMYQSDQWHRV	VGIVSWGYGC	GGPSTPGVYT	420
KVSAYLNWY	NVWKAEL					

A114 DNA SEQUENCE:

Gene name: TTK protein kinase
 Unigene number: Hs.169840
 Probeset Accession #: M86699
 Nucleic Acid Accession #: NM_003318
 Coding sequence: 1026-3551 (underlined sequences correspond to start and stop codons)

1	11	21	31	41	51	
GGAATTCCTT	TTTTTTTTTT	TTTGAGATGG	AGTTTCACTC	TTGTTGGCCA	GGCTGGAGTG	60
CAATGGCACA	ATCTCAGCCT	ACTGCACCT	CCGCTCCCG	GGTTCACGCG	ATTCTCCTGC	120
CTCAGCCTCT	CAAGTAGCTG	GGATTACAGG	CATGTGCCAC	CACCCCTGGC	TAACATAATT	180
CTTTTCTATT	TAGTAGAGAT	GGGGTTTCAC	CATGTGTGTC	AGGCTGGTCT	TGAACCTCTG	240
ACCTCAGGTG	ATCCACITGC	CTTGGCTCC	CAAAAGTGCTA	GGATTACAGC	CGTGAACCTG	300
TGCCCTGGCTG	ATTTCTTTTT	TGTTGTGGGA	TTTTTGAAC	AGGGTCTCCC	TTGGTCCGCC	360
AGGCTGGAGT	GCAGTGGTGC	GATCTTGGCT	CACATATAACC	TCCACCTCCT	GGTTTCAAGT	420
GATCCTCCCA	CTTTAGCCTC	CTGAGTAGCT	GTGATTACAG	GCCTGCCACCA	CCACACCCGG	480
CTAATTTTTG	TATTTTATT	AGAGACAGGG	TTTCACCATG	TTGGCCAGGC	TGTTCTCAAA	540
CTCTGGACT	CAAGGGATCC	GCCIGCTCC	ACTTCCCAA	GTCCCGAGAT	TACAGGTGTG	600
AGTCACCATG	CCTGACCTTA	TAAATCTTAA	GTCTTTTTC	CTGGTCCATT	TCTTCTCTAG	660
GGTCTCTACA	ACAAATCTGC	ATTAGGCGGT	ACAAATATCC	TAACTTCTAT	GATTCACAAA	720
AGGAAGATGA	AGTGATTCT	GATTTAGAAA	GGGGAAGTAG	TAAAGCCACT	GCACACTCCT	780
GGATGATGAT	CCTAAATCCA	GATACAGTAA	AAATGGGGTA	TGGGAAGGTA	GAATACAAAA	840
TTTGTGTTAA	ATTAAATTATC	TAAATATCTA	AAAACATTTT	TGGATACATT	GTGATGTGA	900
ATGTAAGACT	GTACAGACTT	CCTAGAAAAC	AGTTTGGGTT	CCATCTTTTC	ATTTCCCTAG	960
TGCAGTTTTC	TGTAGAAATG	GAATCCGAGG	ATTAAAGTGG	CAGAGAATTG	ACAATTGATT	1020
CCATAATGAA	CAAAAGTGAGA	GACATTAATA	ATAAGTTTAA	AAATGAAGAC	CTTACTGATG	1080
AACATAAGCT	GAATAAAATT	TCTGCTGATA	CTACAGATAA	CTCGGGAAGT	GTAAACCAAA	1140
TTATGATGAT	GGCAAAACAC	CCAGAGGACT	GGTTGAGTTT	GTTCCTCAAA	CTAGAGAAAA	1200
ACAGTGTTC	GCTAAGTGT	GCTCTTTTAA	ATAAATGTAT	TGGTGGTAC	AGTCAAGCAA	1260
TTGAAGCGCT	TCCCCAGAT	AAATAGGCC	AAATGAGAG	TTTGTCTAGA	ATTCAAGTGA	1320
GATTGTGCTGA	ATTAAGAGCT	ATTCAAGAGC	CAGATGATGC	ACGTGACTAC	TTTCAAAATG	1380
CCAGAGCAAA	CTGCAAGAAA	TTTGCTTTTG	TTTATATATC	TTTTGCACAA	TTTGAAGTGT	1440
CACAGGTTAA	TGTCAAAAAA	AGTAAACAA	TTCTTCAAAA	AGCTGTAGAA	CGTGGAGCAG	1500
TACCCTCTAGA	AAATGCTGAA	ATTGCCCTGC	GGAAATTTAA	CCTCCAAAAA	AGACAGCTGC	1560
TTTCAGAGGA	GAAAGAGAG	AAATTTATCAG	CATCTACGCT	ATTAAGTCCC	CAAGAAATCAT	1620
TTTCCGCTTC	ACTTGGGCT	TTACAGATA	GGAAACAACAG	TTGTGATTTCC	AGAGGACAGA	1680
CTACTAAGTC	CAGGTTTTTA	TATGGAGAGA	ACATGCCACC	ACAGAGTGCA	GAATAGGTT	1740
ACCGGAATTC	ATTGAGACAA	ACTAACAAAA	CTAAACAGTC	ATGCCCATTT	GGAAAGATCC	1800
CAGTTAACTT	TCTAAATAGC	CCAGATTGTG	ATGTGAAGAC	AGATGATTTA	GTGTGACCTT	1860
GTTTTATGAA	AGACAAAC	TCTAGATCAG	AATGCCGAGA	TTTGGTTGTG	CCTGGATCTA	1920
AACCAAGTGG	AAATGATTCC	TGTGAATTAA	GAATTTTAA	GTCTGTTCAA	AAATAGTCATT	1980
TCAAGGAACC	TCTGGTGTCA	GATGAAAGAA	GTCTGAACT	TATTTATTA	GATTCATATA	2040
CCCTGAAGAA	TAAACCGGAA	TCAAGTCTTC	TAGCTAAATT	AGAAAGAACT	AAGAGATATC	2100
AGAGACCCGA	GGTTCCAGAG	AGTAAACAGA	AACAGTGCCA	AGCTAAGAGA	AGTCAAGAGT	2160
GATTAACCA	GAATCCCTGC	GCATCTTCAA	ATCACTGGCA	GATTCGGAG	TTAGCCCGAA	2220
AAGTTAATAC	AGAGCAGAAA	CATACCACTT	TTGAGCAACC	TGCTTTTTCA	GTTCACAAAC	2280
AGTCACCACC	AATATCAACA	TCTAAATGGT	TTGACCCAAA	ATCTATTGTT	AAGACACCAA	2340
GCAGCAATAC	CTTGCTAAG	TACATGAGCT	GTTTGAAGC	TCCAGTTGTA	AAGAAATGACT	2400
TTCCACCTGC	TTGTCAAGTG	TCAACACCTT	ATGCCCAACC	TGCCGTGTTT	CAGCAGCAAC	2460
AGCATCAAA	ACTTGCCTAC	CCACTTCAA	ATTACAGGT	TTTAGCATCT	TCCTCAGCAA	2520
ATGAATGCTAT	TTCCGTTAAA	GGAAGAAATT	ATTCCATATT	AAAGCAGATA	GGAGTGGAG	2580
GTTCAAGCAA	GGTATTTTCA	GTGTTAAATG	AAAAGAAACA	GATATATGCT	ATAAATATG	2640
TGAATTAAG	AGAGCAGAT	AACCAAACTC	TTGATAGTTA	COGGAACGAA	ATAGCTTATT	2700
TGAATAAAT	ACAACAACAC	AGTGATTAAGA	TCAATCCGACT	TTATGATTAT	GAATCACCG	2760
ACCAATACAT	CTACATGGTA	ATGGAGTGTG	GAAATATTGA	TCTTAATAGT	TGGCTTAAA	2820
AGAAAAATC	CATTGATCCA	TGGGAACGCA	AGAGTTACTG	GAATAATATG	TTAGAGGCAG	2880
TTACACAAT	CCATCAACAT	GGCATTGTTT	ACAGTATCT	TAAACAGCT	AACTTTCTGA	2940
TAGTTGATGG	TATTCAGAG	CTAATTGATT	TTGGGATTGC	AAACCAATG	CAACCAAGTA	3000
CACCAAGTGT	TGTTAAAGAT	TCTCAGGTTG	GCACAGTTAA	TTATATGCCA	CCAGAGCAAA	3060
TCAAGATAT	GCTTCTCTCC	AGAGAGAAATG	GGAAATCTAA	GTCAAAGATA	AGCCCCAAAA	3120
GTGATGTTTG	GTCCCTTAGGA	TGTATTTTGT	ACTATATGAC	TTACGGGAAA	ACACCAATTC	3180
AGCAGATAAT	TATTCAGATT	TCTAAATTAC	ATGCCATTAAT	TGATCCCTAAT	CATGAAATTTG	3240
AATTTCCCGA	TATTCAGAG	AAAGATCTTC	AAAGTGTGTT	AAAGTGTGTT	TTAAAAAGGG	3300
ACCCAAACCA	GAGGATATCC	ATTCCTTGAGC	TCTTGGCTCA	TCCATATGTT	CAAAATCAAA	3360
CTCATCCAGT	TAAACCAATG	GCCAAAGGGA	CCACTGAAGA	AATGAATATT	GTTCCTGGGC	3420
AACCTGTTGG	TCTGAATTTT	CCTAATCTCA	TTTGAAGAGC	TGCTAAAAC	TTATATGAAC	3480
ACTATAGTGG	TGGTGAAGT	CATAATCTCT	CATCTCCCAA	GACTTTTGAA	AAAAAAGGG	3540
GAATAAATG	ATTGCGAGTT	ATTCGTAATG	TCAGATAGGA	GGTATAAAAT	ATATTGGACT	3600
GTTATACTCT	TGAATCCCTG	TGGAAATCTA	CATTGGAAGA	CAACATCACT	CTGAAGTGT	3660
ATCAGCAAAA	AAAATTCAGT	GAGATTATCT	TTAAAAAGAA	ACTGTAAAAA	TAGCAACCA	3720

TTATGGCACT GTATATATTG TAGACTTGTT TTCTCTGTTT TATGCTCTTG TGTAACTTAC 3780
 TTGACATCAT TTTACTCTTG GAATAGTGGG TGGATAGCAA GTATATTTCTA AAAAATTCTG 3840
 TAAATAAAGT TTTTGGGCTA AATGA

A115 Protein sequence:

Gene name: TTK protein kinase
 Unigene number: Hs.169840
 Probeset Accession #: MB6699
 Protein Accession #: NP_003309
 Signal sequence: none found
 Transmembrane domains: none found
 Protein Kinase Domain: 510-775
 Cellular Localization: cytoplasmic and nuclear

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1      11      21      31      41      51
|      |      |      |      |      |
MNXVRDIKMK FKNEDLIDEL ELNKKISADTT DNSGTVNQIM MMANNPEDWL SLLLKLEKNS 60
VPLSDALLNK LIGRYSQAIE ALPPDKYQON ESFARIQVRF AELKAIQEPD DARDYFQMAR 120
ANCKKPAFVH ISPAQFELSQ GNVKSKQLL QKAVERGAVP LEMLEIALRN LNLQKKQLLS 180
EEKKNLBSAS TVLTAQSFSS GSLGHLQNRN NSGDSRGQTT KARFLYGENM PPQDAEIGYR 240
NSLRQTNTKX QSCFFGRVPV NLLNSPDCDV KTDDSVVPCF MKRQTSRSEC RDLVVPGSKP 300
SGNDSCELRN LKSVQNSHFV EPLVSDKSS ELIITDSITL KNTLESSLLA KLEETKEYQE 360
PEVESNQKQK WQAKKKSECI NQNPAASSNH WQIPELARKV NTEQKHTTFE QPVFSVSKQS 420
PPISTSKWFD EKSICKTPSS NTLDDYMSCF RTPVVXNDFF PACQLSTFYG QPACFQQQOH 480
QILATPLQNL QVLASSANE CTSVKRIYS ILKIQSGSGS SKVPQVLNEK KQIYAIKYVN 540
LEBADNQILD SYRNEIAYLN KLQGHSDKII RLYDYRITDQ YIYMVMCEGN IDLNSWLKKK 600
KSIDPWRRKS YWNMLRAVH TIHQHGLVES DLKPFANFLIV DGLMLKIDFG IANQMOPDTI 660
SVVKDSQVGT VNYNPPPAIK DMSSSRENGK SKSKISPKSD VWSLGCILYI MTYGMTFPQQ 720
IINQISKLHA IIDFNHEIEF PDIEKDLQD VLKCCLEKRP KQRISIPELL AHFYVQIQTH 780
FVNQAKGTTT BEMKYVLGQL VGLNSPNSIL KAAKTLRYRY SGGSEHNSSS SKTFEKKRGK 840
X

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OVARIAN

A116 DNA SEQUENCE

Gene name: G protein-coupled receptor 39
 Unigene number: Hs.85339
 Probeset Accession #: AA349893
 Nucleic Acid Accession #: NM_001508
 Coding sequence: 1-1362 (underlined sequences correspond to start and stop codons)

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1      11      21      31      41      51
|      |      |      |      |      |
ATGGCTTCAC CCAGCCTCCC GGGCAGTGAC TGCTCCCAA TCATTGATCA CAGTCATGTC 60
CCCGAGTTTG AGGTGGCCAC CTGGATCAAA ATCACCCTTA TTCTGGTSTA CCTGATCATC 120
TTCTGTATGG GCCTTCTGGG GAACAGCGCC ACCATTCCGG TCACCCAGGT GCTGCAGAA 180
AAGGATATCT TGCAAGAGGA GGTGACAGAC CACATGTTGA GTTTGGCTTG CTGGACATCT 240
TTGGTGTTC TCATCGGCAT GCCATGGAG TTCTACAGCA TCATCTGGAA TCCCTGACC 300
ACGTCCAGCT ACACCTGTGC CTGCAAGCTG CACACTTTC TCTTGGAGGC CTGCAGCTAC 360
GCTACGCTGC TGACGTGCT GACACTCAGC TTTGAGCGCT ACATCGCCAT CTGTCAOCC 420
TTCAAGTACA AGCTGTGTC GGGACCTTGC CAGGTGAAGC TGCTGATTGG CTTCGTCTGG 480
GTCACTCTCG CCCTGGTGGC ACTGCCCTTG CTGTTTGCCA TGGGTACTGA GTACCCCTTG 540
GTGAACGTGC CCAGCCACCG GGTCTCTACT TGCAACCGCT CCAGCACCGG CCACCACGAG 600
CAGCCCGAGA CTTCCATAT GTCCATCTGT ACCACCTCT CCAGCCGCTG GACCGTGTTC 660
CAGTCCAGCA TCTTGGCGCG CTTCGTGGTC TACCTGTGG TCCTGCTCTC CBTAGCCTTC 720
ATGTGCTGGA ACATGATGCA GGTGCTCATG AAAAGCCAGA AGGCTCGCT GGCCTGGGGC 780
ACGCGGCTTC CACAGCTGAG GAAGTCCGAG AGCGAAGAGA GCAGGACCGC CAGGAGGCAG 840
ACCATCATCT TCTTGGGCTT GATTGTTGTT ACATTGGCGG TATGCTGGAT GCCCAACGAG 900
ATTGAGAGGA TCAATGGCTC GGCCAAACCC AAGCAGGACT GAGCAGGGTC CTACTTCGG 960
GCGTACATGA CTCTCTCTCC CTCTCGGAG ACCTTTTCTT ACCTCAGCTC GGTCTCAAC 1020
CGCTCTCTGT ACACGGTGTG CTGCGCAGCAG TTTGCGCGGG TGTTCGTGCA GGTGCTGTGC 1080
TGCGCGCTGT CGCTGCGACA CGCCAAACCC GAGAAGCGCC TGCGGTACA TGCGCACTCC 1140
ACCAACGACA GCGCCGCTT TGTGCGCGC CGTTGCTCT TCGCGTCCCG GCGCCAGTCC 1200
TCTGCAAGGA GAACGTGAGG GATTCTCTTA AGCACTTTTC AGAGCGAGGC CGAGCCCCAG 1260
TCTAAGTCCG AGTATATGAG TCTCGAGTCA CTAGAGCCCA ACTCAGCGCC GAAACGAGC 1320
AATTCTGCTG CAGAGAATGG TTTTCAGGAG CATGAAGTTT GA

```

A117 Protein sequence:

Gene name: G protein-coupled receptor 39
 Unigene number: Hs.85339
 Probeset Accession #: AA349893
 Protein Accession #: NM_001508, NP_001409
 Signal sequence: none found
 Pfam domains: 7tm_1 [72-172, 224-344]
 Transmembrane domains: 32-54, 68-90, 111-133, 151-173, 221-243, 280-301, 320-342
 Cellular Localization: plasma membrane

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1      11      21      31      41      51
|      |      |      |      |      |
MASPSLPGSD CSQIIDHSHV FEFEVATWIK ITLILVYLII FVMGILGNSA TIRVTQVLQK 60

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KGYLQKEVTD BMVSLACSDI LVFLIGMPME FYSIIWNPLT TSSYTLSCKL HTFLFEACSY 120
 ATLLHVLTLF FERYIAICHP FRYKAVSGPC QVKLLIGFVW VTSALVALPL LFAMGTEYPL 180
 VNVPSHRLGT CNRSSTRHHE QPETSNMISIC TMLSRRTVVF QSSIFGAEVU YLVVLLSVAF 240
 MCRNMOMVLM KSQKGSLAGG TRPPQLRKSE SEESRTARRQ TIIFLRLIVV TLAVCHMPNQ 300
 IRRIMAAAKP KHDWTRSYFR AYMILLFPSE TFFYLSSVIN PLLYTVSSQQ FRFVFQVLC 360
 CRLSLQHANH EKRLRVHAHS TTDSARFVQR PLLFASRRQS SARRTEKIFL STFQSEAEFQ 420
 SKSQSLSLSE LEPNSGAKPA NSAAENGFOE HEV

A118 DNA sequence

Gene name: bone morphogenetic protein receptor IB (ALK-6)
 Unigene number: Hs.87223
 Probeset Accession #: AA250737
 Nucleic Acid Accession #: NM_001203
 Coding sequence: 274-1782 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 CGCGGGGCGC GGAGTCGGCG GGGCTTCGCG GGACGCGGGC AGTGGCGAGA CCQCGGCGCT 60
 GAGGACGCGG GAGCGGGGAG CGCACGCGCG GGGTGGAGTT CAGCCTACTC TTCTCTAGAT 120
 GTGAAAGGAA AGGAAGATCA TTTCATGCTT TGTGATAAAA GGTTCAGACT TCTGCTGATT 180
 CATAACCATT TGGCTCTGAG CTATGACAAG AGAGGAAACA AAAAGTTAAA CTTCACAGCC 240
 TGCCATAAGT GAGAAGCAAA CTTCCTTGAT AACATGCTTT TCGGAAGTGC AGGAAATTA 300
 AATGTGGGCA CCAAGAAAGA GGATGGTGAG AGTACAGCCC CCACCCCGCG TCCAAAGGTC 360
 TTGCGTTGTA AATGCCACCA CCATTGTCCA GAAGACTCAG TCACCAATAT TTGCAGCACA 420
 GACGATATT GTTTCACBAT GATAGAAGAG GATGACTCTG GGTTCGCTGT GGTCACTTCT 480
 GGTTCGCTAG GACTAGAGG CTGAGATTTT CAGTGTCCGG AACTCCCAT TCCTCATCAA 540
 AGAAGATCAA TTGAATGCTG CACAGAAAGG AACGAATGTA ATAAAGACCT ACACCTACA 600
 CTGCTCCAT TGAAGAACAG AGATTTTGTG GATGGACCTA TACACCACAG GGCCTTACTT 660
 ATATCTGTGA CTGCTCTGAG TTGCTCTTGG GTCCCTATCA TATTATTGTT TTACTTCCGG 720
 TATAAAGGAA AAGAAAGTCA ACCTCGATAC AGCATTTGGT TAGAACAGGA TGAAGCTTAC 780
 ATTCTCTCTG GAGAAATCCT GAGAGACTTA ATTGAGCAGT CTCAGAGCTC AGGAAGTGGA 840
 TCAGGCTTCC CTCTGCTGCT CCAAGGACT ATAGCTAAGC AGATTCAGAT GGTGAACACG 900
 ATTGGAAGAG GTGCTATGCG GGAAGTTTGG ATGGGAAGT GGCCTGGCBA AAGGTAGCT 960
 GTGAAAGTGT TCTTCACCAC AGAGGAAGCC AGCTGGTTCA GAGAGACAGA AATATATCAG 1020
 ACAGTGTGTA AGGAAAGTCA AACATTTTGG GGTTCATGCT CTGACAGATAT CAAAGGGACA 1080
 GGTCTCTGGA CCCAGTTGTA CCTAATCACA GACTATCATG AAAATGGTTC CCTTTATGAT 1140
 TATCTGAAGT CCACCACTCT AGACGCTAAA TCAATGCTGA AGTTAGCTTA CTCTTCTGTC 1200
 AGTGGCTTAT GTCAATTTACA CACGAAATC TTTAGTACTC AAGGCAAAAC AGCAATTGCC 1260
 CATCGAGATC TGAAGAGTAA AACATTTCTG GTGAAGAAAA ATGGAACCTG CTGTATGCT 1320
 GACCTGGGCC TGGCTGTGTA ATTTATTAGT GATACAAATG AAGTTGACAT ACCACCTAAC 1380
 ACTCAGTTGG GCACCAAAAG CTATATGCTT CCAGAAAGTGT TGGACGAGAG CTGGAACAGA 1440
 AATCACTTCC AGTCTGTGAT CATGGCTGAC ATGTATAGTT TTGGCTTCAT CCTTTGGGAG 1500
 GTTGTAGGAA GATGTGTATC AGGAGGTATA GTGGAAGAAAT ACCAGCTTCC TTATCATGAC 1560
 CTAGTGCCCA GTGACCCCTC TTAIGAGGAC ATGAGGGAGA TTGTGTGCAT CAGGAAGTTA 1620
 CGCCCTCTAT TCCCAAAACG GTGGAGCAGT GATGAGTGTG TAAGGCAGAT GGGAAACTC 1680
 ATGACAGAAAT GCTGGGCTCA CAATCCTGCA TCAAGGCTCA CAGCCCTGCG GGTTAAGAAA 1740
 ACACCTGCCA AAATGTGAGA GTCCCAAGGAC ATTAACTCT GATAGGAGAG GAAAAGTAA 1800
 CATCTCTGCA GAAAGCCAAAC AGGTACTCTT CTGTTTGTGG GCAGAGCAAA AGACATCAA 1860
 TAAGCATCCA CAGTACAGC CTTGAACATC GTCCCTGCTT CCAGTGGGTT CAGACCTCAC 1920
 CTTTCAGGAA GCGACCTGGG CAAAGACAGA GAAGCTCCCA GAAGGAGAGA TTGATCCGTG 1980
 TCTGTTGTA GCGGAGAAA CCGTTGGGTA ACTTGTTCAA GATATGATGC AT

A119 Protein sequence

Gene name: bone morphogenetic protein receptor IB (ALK-6)
 Unigene number: Hs.72472 / Hs.87223
 Probeset Accession #: AA250737 / UB9326
 Protein Accession #: NP_001194
 Signal sequence: 1-13
 Transmembrane domains: 128-144
 PFAM domains: activin_receptor [30-111], protein kinase [204-491]
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 MLRSAGKLN VETKKGOGES TAPTPRPKVL RCKCHEHCPS DSVNNICSTD GYCFTMIERD 60
 DSGLPVVTSG CLGLESGDFQ CRDTPIPHQR RSIECCTERN ECKDLHPTL PFLKRRDFVD 120
 GPIHRRALLI SVTVCALLLV LILFCYFRY KQETREPRYS IGLEQDETYI PGESLRDLI 180
 EQSQSSGSGS GLPLLVQRTI AKQIQMVQKI GKGRYGEVVM GKWGSEKVAV KVFFTTESAS 240
 WPRETEYQYI VLMRHNILG FLAADIKGTG SWTQLYLTID YHNGSLYDY LKSTTLDAKS 300
 MLKLYSSVS GLCHLHTEIF STQGKPAIAH RDLKSKNILE KNGTCCIAAD LGLAVKFIED 360
 TNEVDIPFWT RVGTIKRYMP EVLDESLENH HFQSYIMADM YSFLILWEV ARRCVSGGIV 420
 EBYQLPYHDL VPSDPSYEDM REIVCIKKLR PSFPNRWSSD ECLRQMGKLM TECWAHPAS 480
 RLTLALRVKTY LARMSQSQDI XL

A120 DNA SEQUENCE

Gene name: LIV-1 protein, estrogen regulated
 Unigene number: Hs.79136
 Probeset Accession #: U41060
 Nucleic Acid Accession #: NM_012319.2
 Coding sequence: 138-2405 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51

5	CTCGTGGCGA	ATTGGGACG	AGACCGCGTG	TTGGGCGCTG	GTAGAGATT	CTCGAAGACA	60
	CCAGTGGGCG	CTGTGGGAAC	CAAACCTGGG	CGCGTGGCGG	GGCCGTGGGA	CAACGAGGCC	120
	GCGGAGACGA	AGGCCCAATG	GCGAGGAAGT	TATCTGTAAT	CTTGATCTCG	ACCTTTGCCC	180
	TCTCTGTAC	AAATCCCCTT	CATGAACTAA	AAGCAGCTGC	TTTCCCCCAG	ACCACTGAGA	240
	AAATTAGTCC	GAATGGGGAA	TCTGGCATTA	ATGTTGACTT	GGCAATTTCC	ACACGGCAAT	300
	ATCATCTACA	ACAGCTTTTC	TACCGCTATG	GAGAAATATA	TTCTTTGTCA	GTGGAAGGGT	360
	TCGAGAAATT	ACTTCAAAAT	ATAGGCATAG	ATAAGATTAA	AGAAATCCAT	ATACACCATG	420
	ACCAAGACCA	TCATCTCAGC	CACGAGCATC	ACTCAGACCA	TGAGCGTCAC	TCAGACCATG	480
10	AGCATCATCT	AGACCAAGAG	CATCACTCTG	ACCATGATCA	TCATCTCTAC	CATAATCATG	540
	CTGCTTCTGG	TAAATAAAG	CGAAAAGCTC	TTTGCCCGAG	CCATGACTCA	GATAGTTTCA	600
	GTAAAGATCC	TAGAAACAGC	CAGGGGAAAG	GAGCTCAACG	ACCAGAACAT	GCCAGTGGTA	660
	GAAGGAATGT	CAGGACAGT	GTTAGTGTCT	GTGAAGTGAC	CTCAACTGTG	TACAAACACTG	720
	TCCTCTGAAG	AACTCAGTTT	CTAGAGACAA	TAGAGACTCC	AAAGACTTGA	AAACTCTTCC	780
15	CCAAAGATGT	AGTCAGCTCC	ACTCCACCCG	GTGTCAATC	AAAGAGCCCG	GTGAGCCGGC	840
	TGGCTGATAG	GAATAACAA	GAATCTGTGA	GTGAGCCCGG	AAAGGCTTTC	ATGTTATCCA	900
	GAACACACAA	TGAATACTCT	CAGGAGTGT	TCAATGCATC	AAAGCTACTG	ACATCTCATG	960
	GCAATGGCAT	CCAGGTTCCG	CTGAATGCAA	CAGAGTTCAA	CTATCTCTGT	CCAGCCATCA	1020
	TCACCAAAAT	TGATGCTAGA	TCTTGTCTGA	TTCAATACAG	TGAAAGAAGG	GCTGAAATCC	1080
20	CTCCAAAGAC	CTATTCATTA	CAAAATAGCT	GGGTGTGTGG	TTTTATAGCC	ATTTCCATCA	1140
	TCAGTTTCTT	GTCTCTGTCT	GGGTTTATCT	TAGTGCCTCT	CATGAATCCG	GTGTTTTTCA	1200
	AAITTTCTCT	GATTTCTCTT	GTGGCACTGG	CCGTTGGGAC	TTTGTGTGGT	GATGCTTTTT	1260
	TACACTTCTT	TCTCATCTCT	CATGCAAGTC	ACCACCATAG	TCATAGCCAT	GAAGAACCAG	1320
	CAATGGAAAT	GAAGAAGAGG	CCACTTTTCA	GTCTCTGTCT	TTCTCAAAAC	ATAGAAGAAA	1380
25	GTGCTTATTT	TGATTCACAG	TGGAAGGGTC	TAACAGCTCT	AGGAGGCCCTG	TATTTCTATG	1440
	TTCTGTGTGA	ACATGTCTCT	ACATGTATCA	AACAATTTAA	AGATAAGAAG	AAAAAGAAAT	1500
	AGAAAGAAAC	TGAATACTCT	GATGATGTGG	AGATTAAGAA	GCAGTTGTCC	AAGTATGAAT	1560
	CTCAACTTTC	AACAAATGAG	GAGAAAGTAG	ATACAGATGA	TCGAACTGAA	GGCTATTTAC	1620
	GAGCAGACTC	ACAAGAGCCC	TCCCACTTTG	ATTCAGACGA	GCCTGCAATC	TTGGAAGAGG	1680
30	AAGAGGTGAT	TACTGCTCAT	GCTCATCCAC	AGGAAGTCTA	CAATGAATAT	GATACCCAGAG	1740
	GGTGCAAGAA	TAAATGCCAT	TCACATTTCC	ACGATACACT	CGGCCAGTCA	GACGATCTCA	1800
	TTCAACACCA	TCATGACTAC	CATCATATTC	TCCATCATCA	CCACCAACCA	AACCAACCAT	1860
	CTCAAGTCA	CAGCCAGCGC	TACTCTCGGG	AGGAGCTGAA	AGATGCCGGC	GTGCCCACCT	1920
	TGGCCTGGAT	GGTGATAATG	GGTGATGGCC	TGCACAAATT	CAGCGATGGC	CTAGCAATTC	1980
35	GTGCTGCTTT	TACTGAAGGC	TTATCAAGTG	GTTTAAGTAC	TTCTGTGTCT	GTGTTCTGTC	2040
	ATGATTTGCT	TCATGAATTA	GGTGACTTTG	CTGTCTTACT	AAAGGCTGGC	ATGACCGTTA	2100
	AGCAGGCTGT	CTTTTAAAT	GCAATGTCTG	CCATGCTGGC	GTATCTTGGA	ATGGCAACAG	2160
	GAATTTTCAT	TGGTCAATTA	GCTGAAATAG	TTTCTATGTG	GATATTTGCA	CTTACTGCTG	2220
	GCTTATTCAT	GTATGTGTCT	CTGGTTGATA	TGTTACCTGA	AAATGCTGCAC	AATGATGCTA	2280
40	GTGACCATGG	TGGAGACCCG	TGGGGGTAT	TCTTTTACCA	GAATGCTGGG	ATGCTTTTGG	2340
	GTITTTGGAAT	TATGTTACTT	ATTTCCATAT	TGGAACATAA	AAATCGTGTTC	CGTATAAAT	2400
	TCTAGTTAAG	GTTTAAATGC	TAGATAGCT	TAAAGAGTTG	TCATAGTTTC	AGTAGGTCTAT	2460
	AGGGAGATGA	GTTTGTATGC	TGTACTATGC	AGCGTTTAAA	GTTAGTGGGT	TTTGTGATTT	2520
	TTGTATTGAA	TATGTCTGTC	TGTTACAAAG	TCAGTTTAAAG	GTACGTTTAA	ATATTTAAGT	2580
45	TATTTATCT	TGGAGATAAA	ATCTGTATGT	GCAATTCACG	GATATTACCA	GTTTATTATG	2640
	TAAACAGAG	ATTGCGCATG	ACATGTTCTG	TATGTTTCAG	GGAAATATGT	CTTTAATGCT	2700
	TTTTCAGAA	CTTCAACATG	TATTCCTATA	CTGGATTTTA	GCTCTCTGAA	GAATGCTGAG	2760
	TTTTTAGGAA	TAGAAATGTG	CATGAAGCCT	AAAATACCAA	GAAAGCTTAT	ACITGAATTTA	2820
	AGCAAGAGAA	TAAAGAGGAA	AAAGAGAGAA	TCTGAGAAAT	GGGAGGCGAT	AGATTTCTTAT	2880
50	AAAAATCAAA	AAATTTGTTG	TAAATTAGAG	GGGAGAAATT	TAGAAATTAAG	TATAAAAAGG	2940
	CAGAAATAGT	ATAGAGTACA	TTCAATTAAC	ATTTTGTCTA	GGATTATTTC	CCGTAAAAAC	3000
	GTAGTACGCA	CTCTATATCA	CTAATTAGTG	TACATTTAAC	TTTGTATAAT	ACAGAAATCT	3060
	AAATATATTT	AATGAATTTA	AGCAATATAC	ACTTGAACCA	GAAATTTGAA	TTTCAAAATG	3120
	TTCTGTGGGG	TTATATATCA	GATGAGTACA	GTGAGTAGTT	TATGATTCAC	CAGACTGGGT	3180
55	TATTGCCAAG	TTATATATCA	CCAAAAGCTG	TATGACTGGA	TGTTCTGGTT	ACCTGGTTTA	3240
	CAAAATATAT	AGAGTAGTAA	AACTTTGATA	TATATAGGGA	TATTAATACT	ACACTAAGTA	3300
	TCATTTGATT	CGATTTCAAA	AGTACTTTGA	TATCTCTCAG	TGCTTCAGTG	CTATCATTTG	3360
	GAGCAATTTG	CTTTATATAC	GGTACTGTAG	CCATACTAGG	CCTGTCTGTG	GCATTTCTTA	3420
60	GATGTTTCTT	TTTACACAA	TAAATTCCTT	ATATCAGCTT	G		

AL21 PROTEIN SEQUENCE

Gene name:

LIV-1 protein, estrogen regulated

Unigene number:

Hs.79136

Protein Accession #:

NP_036451

Signal sequence:

1-21

Pfam domain:

Zip[591-743]

Transmembrane domains:

330-346, 352-368, 427-444, 663-679, 688-703, 730-745

Cellular Localization:

plasma membrane

70	1	11	21	31	41	51	
	MARKLSVILI	LTFALSVTNP	LEELKAAAFP	QTEKISPNW	BSGINVDLAI	STRQYHLQQL	60
	FKRYGNNNSL	SVGEPRKLLQ	NIGLDKIKRI	HIHHDHDS	DHEHSDHER	HSDHERSDH	120
75	EHHSDEHDS	HNHHAASGKN	KRKALCPDHD	SDSSGKDPHN	SQKGGAHRPE	HASGRNRVVD	180
	SVSASEVTST	VNTVSEGTG	FLETISTPRP	GKLFEPKDVSS	STPFSVTSSK	RVSRLAGRKT	240
	NEVSSEPRKG	PMYSRNTMEN	PQECFNASKL	LTSHGMIQV	PLNATEPNYL	CPALINQIDA	300
	RSCLHTSEK	KAEIIPKTYG	LQIAWVGCFI	AISII9FLSL	LGVILVPLMN	KVFVKFLLSF	360
	LVALAVGTLG	GDAPHLHLFH	SHASHHSHS	HEEPAMSKR	GPLFSELSSQ	NIEESAYFDS	420
80	TKBLTALGG	LYFMPLEVER	LTLIKQFDK	KKRNQKKPEN	DDVSEIKKQL	SKYESQLSTN	480
	REKVDVDDRT	EGYLRADSGE	PSHFDSQPPA	VLEEEBVMIA	HAHPQEVYNE	YVPRGCKNKC	540
	ESHHDVTLGQ	SDDLIEHHHD	YHHILHHHHH	QNHHPHSHSQ	KYSREELKDA	GVATLARMVI	600
	MGDGLHNFSD	GLAIGAAFTG	GLSSGLSTSV	AVFCHRLPHE	LQDFAVLLKA	GMTVKQAVLY	660
	NALSAMLAYL	GMAITGIFIGH	YAENVSMHIF	ALTAGLFMYV	ALVDMVPEML	HNDSADHGCS	720

RWGYFFLQNA GMLLFGGIML LISIFERKIV PRINT

5 A122 DNA SEQUENCE

Gene name: EGF-like-domain; multiple 6
 Unigene number: Hs.12844
 Probeset Accession #: N67551
 Nucleic Acid Accession #: NM_015507
 Coding sequence: 241-1902 (underlined sequences correspond to start and stop codons)

```

10      1      11      21      31      41      51
      |      |      |      |      |      |
15  CCGCAGAGGA GCGCTGGCCA GGCTAGCCAG GCGGCCGCCA GCGCCTCCCC AGGCCGCGAG 60
      |      |      |      |      |      |
      GCGCCCTGCC GCGGTGCTCG GCCTCCCTTC CCAGACTGCA GGGACAGCAC CCGGTAACCTG 120
      |      |      |      |      |      |
      CGAGTGGAGC GGAGGACCCG AGCGGCTGAG GAGAGAGGAG GCGGCGGCTT AGCTGCTACG 180
      |      |      |      |      |      |
      GGGTCCGGCC GCGCGCCTCC CGAGGGGGGG TCAGGAGGAG GAAGGAGGAC CCGTGCAGAG 240
      |      |      |      |      |      |
      ATGCTCTGCG CCGTGGAGCT TGCGCTCCCG CTGCTGCTCT CCTGGGTGGC AGGTGGTTTC 300
      |      |      |      |      |      |
      GGGAAACGCG CCACTGCAAG GCATCAGCGG TTGTTAGCAT GGGCAGCTCA GCCTGGGGTC 360
      |      |      |      |      |      |
      TGTCACTATG GAACATAACT GGCTGCTGTC TACGGCTGGA GAAGAAACAG CAAGGGAGTC 420
      |      |      |      |      |      |
      TGTGAAGCTA CATGCGAACC TGGATGTAAG TTTGGTGAAT GCGTGGGACC AAACAAATGC 480
      |      |      |      |      |      |
      AGATGCTTTC CAGGATACAC CGGGAAGAAC TGCAGTCAAG ATGTGAATGA GTGTGGAATGC 540
      |      |      |      |      |      |
      AAACCCCGGC CATGCCAACA CAGATGTGTG AATACACACG GAAGCTACAA GTGCTTTTGC 600
      |      |      |      |      |      |
      CTCAGTGGCC ACATGCTCAT GCCAGATGCT ACGTGTGTGA ACTCTAGBAC ATGTGCCATG 660
      |      |      |      |      |      |
      ATAACTGTC AGTACAGCTG TGAAGACACA GAAGAAGGGC CACAGTGCCT GTGTCCATCC 720
      |      |      |      |      |      |
      TCAGGACTCC GCGTGGCCCC AAATGGAAGA GACTGCTAG ATATTGAATG ATGTGCTCTC 780
      |      |      |      |      |      |
      GGTAAAGTCA TCTGTCCCTA CAATCGAAGA TGTGTGAACA CATTGGGAAG CTACTACTGC 840
      |      |      |      |      |      |
      AAATGTCACA TTGGTTTDTG ACTGCAATAT ATCAGTGGAC GATATGACTG TATAGATATA 900
      |      |      |      |      |      |
      AATGAATGTA CTATGGATAG CCATACCTGC AGCCAACATG CCAATGCTT CAATACCCAA 960
      |      |      |      |      |      |
      GGGTCTCTCA AGTGTAAATG CAAGCAGGGA TATAAAGGCA ATGGACTTCG GTGTCTGCTC 1020
      |      |      |      |      |      |
      ATCCCTGAAA ATCTGTGTGA GGAAGTCCCT AGAGCACCTG GTACCATCAA AGACAGAATC 1080
      |      |      |      |      |      |
      AAGAAGTTCG TTGCTCACAA AAACAGCATG AAAAAGAAGG CAAAATTAAT AAATGTTACC 1140
      |      |      |      |      |      |
      CCAGAACCCA CCAGCACTCC TACCCCTAAG GTGAACCTGC AGCCCTTCAA CTATGAAGAG 1200
      |      |      |      |      |      |
      ATAGTTTCCA GAGGCGGGAA CTCTCATGGA GGTAAAAAAG GGAATGAAGA GAAATGAAA 1260
      |      |      |      |      |      |
      GAGGGGCTTG AGGATGAGAA AAGAGAAGAG AAGCCCTGA AGAATGACAT AGAGGAGCGA 1320
      |      |      |      |      |      |
      AGCCTGCGAG GAGATGTGTT TTTCCCTAAG GTGAATGAAG CAGGTGAATT CGGCTTGATT 1380
      |      |      |      |      |      |
      CTGGTCCAAA GGAAGCGCTT AACCTCCAAA CTGGAACATA AAGATTTAAT TATCTCGGTT 1440
      |      |      |      |      |      |
      GACTGCAGCT TCAATGCTGG GATCTGTGAC TGGAAACAGG ATAGAGAAGA TGATTTTGAC 1500
      |      |      |      |      |      |
      TGGAACTCTG CTATGCGAGA TAATGCTATT GGCTTCTATA TGGCAGTTCC GGCCTTGCCA 1560
      |      |      |      |      |      |
      GGTACACAGA AAGACATTGG CCGATTGAAA CTTCTCTTAC CTGACCTGCA ACCCCAAAGC 1620
      |      |      |      |      |      |
      AACTCTGTGT TGCTCTTTGA TTACCGGCTG GCGGAGACA AAGTCGGGAA ACITCGAGTG 1680
      |      |      |      |      |      |
      TTTGTGAAAA ACAGTAACAA TGCCCTGGCA TGGGAGAGA CCACGAGTGA GGTGAAAAG 1740
      |      |      |      |      |      |
      TGGAAAGCAG GGAATAATCA GTTGTATCAA GGAACCTGATG CTACCAAAAG CATCATTTT 1800
      |      |      |      |      |      |
      GAAGCAGAAC GTGGCAAGGG CAAAACCGGC GAAATCGCAG TGGATGGCGT CTGCTTGTT 1860
      |      |      |      |      |      |
      TCAGGCCTAT GTCCAGATAG CCTTTTATCT GTGGATGACT GAAATGTAAT ATCTTTATAT 1920
      |      |      |      |      |      |
      TTAGACITTT ATGTGAGTTC CCTGGTTTTT TTGATATTGC ATCATAGGAC ATCTGGCATT 1980
      |      |      |      |      |      |
      TTAGAATTAC TAGCTGAAAA ATTGTAATGT ACCAACAGAA ATATTATTGT AAGATGCCTT 2040
      |      |      |      |      |      |
      TCTTGATATA GATATGCCAA TATTGTCTTT AAATATCATA TCACTGTATC TTCTCAGTCA 2100
      |      |      |      |      |      |
      TTTCTGAATC TTTCCATT ATATTATAAA ATATGGAAT GTGAGTTTAT CTCCCTCTCT 2160
      |      |      |      |      |      |
      CAGTATATCT GATTGTGATA AGTAAGTTGA TGAGCTTCTC TCTACACAT TTCTGAAAA 2220
      |      |      |      |      |      |
      TAGAAAAAAA AGCAGAGAGA AATGTTTAACT TGTTTGACTC TTATGATACT TCITGGAAAC 2280
      |      |      |      |      |      |
      TATGACATCA AAGATAGACT TTTGCCCTAAG TGGCTTAGCT GGGCTTTTCA TAGCCAAACT 2340
      |      |      |      |      |      |
      TGTATATTTA AATTCTTTGT AATAATAATA TCCAAATCAT CAAAAAATAA AAAAAAAA
  
```

55 A123 Protein sequence:

Gene name: EGF-like-domain; multiple 6
 Unigene number: Hs.12844
 Probeset Accession #: N67551
 Protein Accession #: NP_056322.2
 Signal sequence: 1-21
 Transmembrane domains: none found
 MAM domain: 402-546
 EGF domain: 80-259
 Cellular Localization: secreted

```

65      1      11      21      31      41      51
      |      |      |      |      |      |
      MPLPWSLALP LLLSWVAGGF GNAASARHGG LLASARQPGV CHYGTKLACC YGWRNRNSKGV 60
      |      |      |      |      |      |
      CEATCEPGCK FGECVGPKNK RCFFPGYTGT CSQDVNECGM KPRPCQHRCV NTHGSYKFC 120
      |      |      |      |      |      |
      LSGHMLPDA TCVNSRTCAM INCQYSCEDT EBGPOCLCPG SGLRLAPWGR DCILDIDECAS 180
      |      |      |      |      |      |
      GKVICPYNRR CVNTFGSYTC KCHIGFELQY ISGRYDCIDI NZCINDSHTC SHHANCFTNQ 240
      |      |      |      |      |      |
      GSPFKCKCKQG YKGNGLRCSA IPENSVKELV RAPGTTKDRI KLLLAHKNRM KKKAKIKNVT 300
      |      |      |      |      |      |
      PEPTRTPTPK VNLQPFNVSE IVSRGGNSHG GKKGNEEKKK EGLEDEKRES KALENDIEER 360
      |      |      |      |      |      |
      SLRGDVFFPK VMEAGEFLI LVQRKALTSK LEEKDLNIGV DCSFNGIGCD WKQDREDDFD 420
      |      |      |      |      |      |
      WNPADRDNAI GFYNAPVAPA GERKDIGRLK LLLFDLQPGS NFCLLFYDRL AGDKVGKLRV 480
      |      |      |      |      |      |
      FVKNRNALAL NKKTSSEDEK WKTGKIQLYQ GTDATKSIIF EAERGKGTG BIAVDGVLLV 540
      |      |      |      |      |      |
      SGLCPDLSLS VDD
  
```

80 A124 DNA SEQUENCE

Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)
 Unigene number: Hs.170195
 Probeset Accession #: BE616633
 Nucleic Acid Accession #: NM_001719

Coding sequence: 123-1418 (underlined sequences correspond to start and stop codons)

```

5 1      11      21      31      41      51
   |      |      |      |      |      |
GGGCGCAGCG GGGCCCGTCT GCAGCAAGTG ACCGACGGCC GGGACGGCCG CTGCCCCCT 60
CTGCCACCTG GGGCGGTGCG GGGCCCGGAGC CGGAGGCCCG GGTAGCGCGT AGAGCCGCG 120
CGATGCACCT GCGCTCACTG CGAGCTGCGG CGCCGCACAG CTTCGTGGCG CTCGGGCAC 180
CCCTGTTCTT GCTGCGCTCC GCCCTGGCCG ACTTCAGCCT GGAACAAGAG GTGCACTCGA 240
10 GCTTCATCCA CGGCGCGCTC CGCAGCCAGG AGCGGCGGGA GATGCAGCAG GAGATCTCT 300
CCATTTTGGG CTTCGCCACG CGCCCGCGCC CGCAGCTCCA GGGCAAGCAC AACTCGGCAC 360
CCATGTTTCT GCTGGAAGTG TACAACGCCA TGGCGGTGGA GGAGGGCGGC GGGCCCGCG 420
GCCAGGGCTT CTCTACCCCG TACAAGGCCG TCTTCAGTAC CCAGGGGCCG CCTCTGGCCA 480
GCCTGCAAGA TAGCCATTTC CTCACCGACG CCGACATGGT CATGAGCTTC GTCAACTCG 540
15 TCGAACATGA CAAGGAATTC TTCCACCCAC GCTACCACCA TCGAGAGTTC CGTTTGTATC 600
TTTCCAGAGT CCGAGAAGG GAGCTGTGTA CGGAGGCCGA ATTCCGATC TACAAGGACT 660
ACATCCGGGA ACGCTTCGAC AATGAGAAGT TCCGATCAG CGTTTATCAG GTGCTCCAG 720
AGCACTTGGG CAGGGAATCG GATCTCTTCC TGCTCGACAG CCGTACCTTC TGGGCTCGG 780
AGGAGGGCTG CTGCTGTGTT GACATCACAG CCACGAGCAA CCACTGGGTG GTCAATCCG 840
20 GGCACAACCT GGGCCTGCGC CTCTCGGTGG AGACGCTGGA TGGCAGAGC ATCAACCCCA 900
AGTTGGCGGG CCTGATTGGG CGGCACGGCG CCCAGAACAA CGAGCCCTTC ATGTTGGCT 960
TCTTCAAGCG CACGAGAGTC CACTTCCGCA GCATCCGCTC CACGGGAGC AAACAGCGCA 1020
GCCAGAACCG CTCACAGACG CCAAGAACCC AGGAAGCCCT CGCGATGGCC AACGTGGCAG 1080
AGAACAGCAG CAGCAGCCAG AGGCAAGGCT GTAGAAGCA CGAGCTGTAT GTCAGCTTCC 1140
25 GAGACCTGGG CTGCGAGGAC TGGATCATCG CGCTGAAGG CTACGCGGCC TACTACTGTG 1200
AGGGGAGTGG TGCCCTTCCC CTGAATCCTT ACATGAAGCG CACCAACCAT GCCATCGTGC 1260
AGACGCTGGT CCACTTCATC AACCCGGAAG CGGTGCCCAA GCCCTGCTGT GCGCCACGCG 1320
AGCTCAATGC CATCTCGTCC CTCTACTTCG ATGACAGCTC CAACGTCATC CTGAAGAAAT 1380
ACAGAAACAT GGTGGTCCGG GCTGTGGCTT GCCACTAGCT CCTCCAGAA TTCAGACCT 1440
30 TTGGGGCCAA GTTTTTCGGT ATCTCTCATT GCTCGCTTGG GCCAGGAACC AGCAGACCAA 1500
CTGCCCTTGG TGAAGACCTT CCTTCCCTAT CCCCACCTTT AAGGTGTGTA GAGTATTAG 1560
AAACATGAGC AGCATATGGC TTTTGTATCA TTTTTCAGTG GCAGCATCCA ATGAACAAGA 1620
TCTACAGAGC TGTGAGGACA AATCTAGACA GGAAGGAGAA ACAAGCATA AAGAAATAT 1680
GCGGGCCAGG GTCATTTGGT GGAAGTCTC AGCCATGCAC GGACTCGTTT CCAGAGGTAA 1740
35 TTATGAGCGC CTACAGCCCA GGCACCCAG CCGTGGGAGG AAGGGGGCGT GGCAGGGGGT 1800
GGGCACATTG GTGTCTGTGC GAAAGGAAAA TTGACCCGGA AGTTCCTGTA ATAAATGTCA 1860
CAATAAAACG AATGAATG

```

40 A125 Protein sequence:
 Gene name: bone morphogenetic protein 7 (osteogenic protein 1) (BMP7)
 Unigene number: Hs.170195
 Probeset Accession #: BB616633
 Protein Accession #: NP_001710.1
 45 Signal sequence: 1-30
 Pfam domains: TGF β propeptide [37-281]
 Transmembrane domains: none found
 Cellular Localization: secreted

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50 1      11      21      31      41      51
   |      |      |      |      |      |
MHVRSLEAAA PHSFVALMAP LFLRLSALAD FSLDNEVHSS FIHRLRSQGE RREMQRILS 60
ILGLPHERPR ELQGHNSAP MMLDLVYNA AVREGGSPGG QGFSTPYKAV FSTQGPPLAS 120
LQDSHPLTDA DMVMSFVNLV EHDKEFFHPR YHREPRFDL SKIPGEAVT AAEFRYKDY 180
IRERFDNETF RISVYQVLQE HLGRESDLFL LDRSLWASE ESWLVEDIYA TSNEWVWNP 240
HNLGLQLSVE TLGGQSLNPK LAGLGRHGP QNKQPPMVAF FKATEVHPRS IRTSGSKQRS 300
QNRSKTPKNS BALRMANVAE NSSSDQDQAC KHHELYVSEF DLGWQDWIIA PEGYAAATYC 360
60 GSCAFPLNSY MNAINHAIVQ TLVHFINPET VPKPCCAPTQ LNAISVLYFD DSSNVILAKY 420
RNMVVRACGC H

```

A126 DNA SEQUENCE
 Gene name: integrin, beta 8
 Unigene number: Hs.52620
 65 Probeset Accession #: AA479726
 Nucleic Acid Accession #: NM_002214
 Coding sequence: 680-2990 (underlined sequences correspond to start and stop codons)

```

70 1      11      21      31      41      51
   |      |      |      |      |      |
CCCAGAGCCG CTCCTCCCTG TTGCTGSCAT CCCGAGCTTC CTCCTTGCC AGCCAGGACG 60
CTGCCGACTT GTCTTTGCCG GCTGCTCCGC AGACGGGGCT GCAAAGCTGC AACTAATGGT 120
GTTGCCCTCC CTGCCACCTT GTGGAAGCAA CTGCGCTGAT TGATGGCCA CAGACTTTT 180
TCCCCTCGAC CTGCGCGGCG TACCCTCCCA CAGATCCAGC ATCACCAGT GAATGTACAT 240
75 TAGGGTGGTT TCCCTCCCGC CTTCGGGCTT TGTTTGGGTT TGATTGTGTT TGGCTCTTCG 300
CTAAGCTGAT TTATGCGGCA GAAGCCCCAC CGGCTGGAGA GAAACAAAG CTCTTTTCTT 360
TGTCCCGGAG CAGGCTGGCG AGCCCTTGCA GAGCCCTCTC TCAGTGGCC GCGGGGCCCT 420
TGGCCGTGGA AGGAGGTGCT TCTCGCGGAG ACCCGGGGAC CCGCGGTGCC GAGCGGGAG 480
GGCGGTAGGG GCGCTGAGAT GCGAGCGGCT GCGCGGGGCC GCTTACCTGC ACGCTTGCT 540
80 CCGAGCCGCG GCGTCCGCTT GCTAGGCCCT GCGAAADTCT CTTAGCGACA CTCGCTCCG 600
GCGCCCGAGG TCGCCCGGGA GCGCAGGCCC GCGTCCGAA GCGAGCCAG CCGCGGGCG 660
GGGGGGGGCT GTTTTGCAAT ATGTGCGGCT CGGCCCTGCG TTTTITTACC GCTGCATTG 720
TCTGCTGCA AATACGACCG CAGGCTCCCG CTCTGTTCTT CTGGGACGCT TGGGTGTTT 780

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5 CACTTGTCTT TGGACTGGGC CAAGGTGAAG ACAATAGATG TGCATCTTCA AATGCAGCAT 840
 CCTGTGCCAG GTGCCCTTGG CTGGGTCCAG AATGTGGATG GTGTGTTCAA GAGGATTTCA 900
 TTTTCAAGTG ATCAAGAAGT GAACGTGTGT ATATTGTTT CAATTAAATA AGCAAAGGCT 960
 GCTCAGTTGA TTCAATAGAA TACCATCTG TGCATGTTAT AATACCCACT GAAAATGAAA 1020
 TTAATACCCA GGTGACACCA GGAGAAGTGT CTATCCAGCT GCGTCCAGGA GCCGAAGCTA 1080
 ATTTTATGCT GAAAGTTCAT CCTCTGAAGA AATATCTTGT GGATCTTTAT TATCTTGTG 1140
 ATGTCTCAGC ATCAATGCAC AATAATATAG AAAAATTAAT TTCCGTTGGA AACGATTAT 1200
 CTAGAAAAAT GGCATTTTTC TCCGTTGACT TTGCTCTTGG ATTTGGCTCA TACGTTGATA 1260
 10 AAACAGTTTC ACCATACATF AGCATCCACC CCGAAGGAT TCATAATCAA TGCAGTGACT 1320
 ACAATTAGTA CTGCTATGCT CCCCATGGAT ACATCCATGT GCTGTCTTTG ACAGAGAACCA 1380
 TCACTGAGTT TGAGAAAGCA GTTCATAGAC AGAAGATCTC TGGAACATA GATACACCAG 1440
 AAGGAGGTTT TGACCGCATG CTTCAGGCAG CTGTCTGTGA AAGTCATATC GGTGCGGCAA 1500
 AAGAGGCTAA AAGATTGCTG CTGGTGTATG CAGATCAGAC GTCTCATCTC GCTCTTGATA 1560
 15 GCAAATTGGC AGGCATAGTG GTGCCAATG ACGGAACTG TCATCTGAAA AACACGTTCT 1620
 ACGTCAAATC GACAACCATG GAACACCCCT CACTAGGCCA ACTTTCAGAG AAATTAATAG 1680
 ACAACAACAT TAATGTCTAT TTTGCAGTTC AAGGAAACA ATTTCAFTGG TATAAGGATC 1740
 TTCTACCCCT TTGCCCATG ACCATTGCTG GTGAATAGA ATCAAAGGCT GCAAACCTCA 1800
 ATATTTGGT AGTGAAGCC TATCAGAAGC TCATTTCAGA AGTGAAGTT CAGGTGAAA 1860
 20 ACCAGGTACA AGGCATCTAT TTTAACATTA CCGCATCTG TCCAGATGGG TCCGAAAGC 1920
 AGGATGAGA AGGATGAGA AACGTGACGA GCATGATGA AGTTCTTTT AATGTAACAG 1980
 TTCAATAGAA AAAATGTGAT GTTCACAGAG GAAAAACTA TGCAATATC AAACCTATTG 2040
 GTTTAATGA TAGCGCTAAT ATTCATATAC ACAGAACTG CAGCTGTGAG TGTGAGGACA 2100
 ACAGAGGACC TAAAGGAAAG TGTGTAGATG AAACCTTTCT AGATTCCAAG TGTTTCCAGT 2160
 25 CTGATGAGA TAAATGTCTAT TTTGATGAG ATCAGTTTTC TTCTGAGAGT TGCAGTCACT 2220
 ACAGGATCA GCTGTGTTGC AGTGTCTGAG GAGTTTGTGT TTGTGGGAAA TGTTCATGTC 2280
 ACRAAATTA GCTTGGAAAA GTGTATGAAA AATACTGTGA AAGGATGAC TTTTCTTGTG 2340
 CATATACCA TGGAATCTG TGTGCTGGGC ATGGAGAGTG TGAAGCAGGC AGATGCCAAT 2400
 GCTTCAGTGG CTGGGAAGGT GATCGATGCC AGTGCCCTTC AGCAGCAGCC CAGCACTGTG 2460
 30 TCAATTCAAA GGGCCAAAGT TGCAGTGAA GAGGCACGTG TGTGTCTGGA AGGTGTGAGT 2520
 GCACCGATCC CAGGAGCATC GGCCGCTTCT GTGAACACTG CCCCACCTGT TATACAGCCT 2580
 GCAAGGAAAA CTGGAATGTG ATGCAATGCC TTACCCCTCA CAATTGTCT CAGGCTATAC 2640
 TTTATCAGTG CAAAACCTCA TGTGCTCTCA TGAACAACA GCATTATGTC GACCAAACTT 2700
 CAGAATGTTT CTCCAGCCCA AGCTACTTGA GAATATTTT CATCATTTT ATAGTTACAT 2760
 35 TCTGTGTTGG GTTGTCTAAA GTCCGTGATCA TTAGACAGGT GATACACAA TCGAATAGTA 2820
 ATAAATTAAT GTTCTATCA GATTACAGAG TGTCAAGCTC AAAAAAGGAT AGTTGATTC 2880
 TGCAAGTGTG TTGCACAGA GCAGTCACCT ACCGACGTGA GAAGCCTGAA GAAATAAAAA 2940
 TGGATATCAG CAAATTAAT GTCTATGAAA CTTTCAGGTG CAACTTCTAA AAAAAAGATT 3000
 TTAACACTT AATGGGAAAC TGGAAATGTT AATAATTGCT CCTAAAGATT AATATTTTAA 3060
 40 AAGTCACAGG AGGAGACAAA TTGCTCACGG TCATGCCAGT TGCTGTTGT ACATCGAAC 3120
 GAAGACTGAC AAGTATCCTC ATCATGATGT GACTCACATA GCTGCTGACT TTTTCAGAGA 3180
 AAAATGTGTC TTACTACTGT TTGAGACTAG TGTGTTGTA GCACCTTACT GTAATATATA 3240
 ACTTATTTAG ATCAGCATAG AATGTAGATC CTCTGAAGAG CACTGATTAC ACTTTACAGG 3300
 TACCTGTTAT CCTACGCTT CCGACAGAGA ACAATGCTGT GAGAGAGTTT AGCATTGTGT 3360
 45 CACTACAAGG GTACAGTAAT CCTGCACTG GACATGTGAG GAAAAAATA ATCTGGCAG 3420
 TATATTCFAA GGTGCCAAA CACTCAACA GTTGGTGGT GAATAGACAA GAACAGCTAG 3480
 ATGAATAAAT GATTCGTGTT TCACTCTTTC AAGAGGTGAA CAGATACAC CTTAATCTTA 3540
 AAAGATTATG GCTTTTAAAG GTGTGATGTT TTATGCATGT GTGTTTATGG TTTGCTTAT 3600
 TTTGCAAGAT GATACATAAT TCAGCATTC TCTCTCTT GCCTTTATGT TTTGTTTCT 3660
 50 TTTTACAGG ATAGTTTAT GTATGICACA GATGACTGGA TTAATTAAGT GCTAAGTTAC 3720
 TACTGCCATA AAAAATAAT AATACAATGT CACTTATCA GAATACTAGT TTTAAAGCT 3780
 GAATGTTAA

55 A127 Protein sequence:
 Gene name: Integrin, beta 8
 Unigene number: Ha.52620
 Probeset Accession #: AA479726
 Protein Accession #: NP_002205.1
 Signal sequence: 1-39
 60 Transmembrane domains: 682-704
 EGF domain: 552-584
 INB domain: 54-469
 Cellular Localization: plasma membrane
 65

1 11 21 31 41 51
 70 MCGSALAFFT AAFVCLQNR RGPASFLWAA NVFSLVLGLG QGEDNRCASS NAASCARCLA 60
 LGPECCWCQV EDFISGGERS ERCDIVENLI SKGCSVDSIE YPSVHVITPT ENHINTQVTF 120
 GEVSIQLRPG AERANFLKVH PLKXPVDLY YLVDVSASMH NMIEKLNSVG NDLSEKNAPF 180
 SRDFRLGPHS YVDKTVSPYI SIHFERIHNQ CSDYNLDOMP PHGYLIVLSL TENITEFEKA 240
 VHRQKISGNI DTPBSGGFAM LQAACVCESHI GWRKEAKRLI LVMTDQTSHL ALDSKLIV 300
 VPNDGMCHLK NNVVVKSTTM EHPSLGLSE KLIDNNINVI PAVQGEQPHW YKIDLLPLPG 360
 75 TINGEISSKA ANLNLVVEA YQKLISEVKV QVENQVQGIY FNITAICTPD SRKPGMEGCR 420
 NVTSNDVILF NVVTVMKKCD VTGKKNYALII KPIGFNETAK IHIERNCSCQ CEDNRGPKGK 480
 CVDETFLDSK CFQCDENKCH FDEQFSSSES CKSHKQDQVC SGRGVVCVCGK CSCHKIKLGE 540
 VYQKYCEKDD FSCPYHHEGML CAGHGECEAG RQCFSGWEG DRCCQPSAAA QSCVNSGQV 600
 80 CSGRGTCVCG KCECTDPRSI GRPCEHCPTC YTACKENWNC MQLIHPENLS QAILDQCKTS 660
 CALMEQQRHV DQTEBCFSSP SYLRIFFIIP IVTFLIGLLK VLIIRQVILQ NNSNKKIKSSS 720
 DYEVSASKD KLILQSVCTR AVTYRREKPE EIKMDISKIN AHETFRCMF

A128 DNA SEQUENCE

Gene name: G protein-coupled receptor 64

Unigene number: Hs.184942
 ProbeSet Accession #: AA435577
 Nucleic Acid Accession #: NM_005756
 Coding sequence: 73-3117 (underlined sequences correspond to start and stop codons)

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1      |      |      |      |      |
11     |      |      |      |      |
21     |      |      |      |      |
31     |      |      |      |      |
41     |      |      |      |      |
51     |      |      |      |      |
AGCCAGCCCG AGGACGCGAG CGGCAGGTGT GCACAGAGGT TCTCCACTTT GTTTTCTGAA 60
CTCGCGGTCA GGATGGTTTT CTCTGTGAGG CAGTGTGGCC ATGTTGGCAG AACGGAAGAA 120
GTTTTACTGA CGTTCAAGAT ATTCCTTGTC ATCATTTGTC TTCATGTGCT TCTGGTAACA 180
TCCCTGGAAG AAGATACTGA TAATTCCAGT TTGTCAACAC CACCTGCTAA ATTATCTGTT 240
GTCAGTTTTG CCCCTCCTCT CAATGAGGTT GAAACAACAA GCCTCAATGA TGTACTTTTA 300
AGCTTACTCC CTTCAAACGA AACAGAAAAA ACTAAAAACA CTATAGTAAA AACCTTCAT 360
GCTTCAGCGG TCAAAACCCA GAGAAATATC TGCATTTTGT CATCTATTGG CATGACTCA 420
GCATTTTITA GAGGTGAGAT CATGTTTCAA TATGATAAAG AAAGCACTGT TCCCAGAAAT 480
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GAGCTCAACA AAACCTCGCA AACCCTAAGT GAGACTTACT TTATAATGTG TGCTACAGCA 600
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TCCATCCCBG TGGTGCCTGG GGCACGTG TGCTTCCCBG TCCCAAAAGC TACCTCTTTT 900
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CCACAGTCTG AAACGATCTC TTCCCTATG CCCCCAACCC ATGTCTCCBG CACCCCACT 1080
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CAGGTGTTGC AGATGGAGAA GGCTCTGTCC TTGGGCAGCC TGGAGCCTAA CCTGCGAGGA 1260
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ACTATAAGTC TAACCTCCCC TTCTTGGCT CTGGCTGTGA TCAGAGTGAA TGCCAGTAGT 1440
TCAACACAA CTACCTTTGT GGCACAGAC CTGTCAATC TTCAAGTTTC TCTGGAAC 1500
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GTTGCAAAAC TGACCGTCAG GAACCTGACA AGAAACGTGA CAGTCACATT AAAGCACATC 1740
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GGCAGAGGAG GCTGTCTAGA CAATGGCTGC TGTGTCAAG ACAGGAGATT GAATGAAC 1860
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ATTTCAGTG AATGTTGGAT CTCAGACTAA CCATAGTAAT AATACACATT TCTGTGAGTG 4560

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CTGACTTGTC TTGCAATAT TTCTTTCTG ATTTATTTAA TTTTCTTGTA TTTATATGTT 4620
 AAAATCAAAA ATGTTAAAAA CAATGAAATA AATTTGCAGT TAAGA

A129 Protein sequence

Gene name: G protein-coupled receptor 64
 Unigene number: Hs.184942
 Protein Accession #: NP_005747.1
 Signal sequence: 1-38
 GPS domain: 564-615
 Transmembrane domains: 624-646, 660-682, 688-710, 733-755, 783-805, 828-850, 858-880
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 MVFSVRQCGH VGRTEEVLLT FKIFLVIIICL HVVLVTSLEE DTDNSSLSPF PAKLSVVSEFA 60
 PSSNEVETTS LMDVTLSELP SNETEKTKIT IVKTFNASGV KPQRNICMLS SICNDSEAFRR 120
 GEIMFYDYKE STVPQNHIT NGTLTGVLISL SELKRSELNK TLQTLSETYF IMCATAEAGS 180
 TLNCTFTIKL NMTMNAACAI AALERVKIRP MEHCCCSVRI PCPSSPEELG KLQCDLQDPI 240
 VCLADHPRGP PFSSSQSIFV VPRATVLSQV PKATSPAEPP DYSPVTHNVP SPIGSIQPLS 300
 PQSPAPIASS PAIDMPQSE TISSPMPTTH VSGTPPEVKA SFSSPTVSAP ANVNTTSAPP 360
 VQTDIVNTSS ISDLENQVLQ MEKALSLGSL EPNLAGEMIN QVSRLLHSPF DMLAPLAQRL 420
 LKVVDDIGLQ LNFSTTISL TSPSLALAVI RVNASSENTT TPVAQDEANL QVSLAQAPE 480
 NSIGTITLPS SIMMNLPAED MELASRVQFN EFETPALPQD PSENLGLIS YVSSSVANL 540
 TVRNLTRNVT VILKELNPSQ DELTVRCVFW DLGRNGGRGG WSDNGCEVED RRLNETICTC 600
 SHLTSPGVLN DLSRTSVLPA QMMALTFITY IGCGLSSIFL SVTLVITYLAF EKIRRDYPSK 660
 ILIQLCAALL LINLVFLDS WIALYKMQGL CISVAVFLHY FLLVSFTWNG LSAFMYLAL 720
 VKVENTYIRK YILKFCIVGW GVPVVVTII LTISPDNYGL GSYGKFPNGS PDDPCWIDNN 780
 AVFYITVVGY FCVIFLLNVS MFIVVLVQLC RIKKKKQLGA QRKTSIQDLR SIAGLTFLLG 840
 ITWGFAPFAW GPNVTFMYL FAIFNTLQGF FIFIPYCAK ENVRQWRRY LCCGLRLAE 900
 NSDWKTAATN GLKKQTIVNG VSSSSNSLQS SSSSTNSTTL LVNNDCEVHA SGNNGMASTER 960
 NGVSFSVQNG DVCLHDFTEK QHMFNEKEDS CNGKGRNALR RTSKRGSLHF IEQM

A130 DNA SEQUENCE

Gene name: G protein-coupled receptor 49 (GPR49) (HG38) (LGR5)
 Unigene number: Hs.285529
 ProbeSet Accession #: AA460530
 Nucleic Acid Accession #: NM_003667
 Coding sequence: 201-2924 (underlined sequences correspond to start and stop codons)

1 11 21 31 41 51
 GTGGCGGCAA CCGGCACCTC AGTCCCGGCC GCGCTTCTCC TCGCCGCCCA CCGCGTGGG 60
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 GGGCCCTCTAC TCGGGCACTC ATGGACACCT CCGGCTCGG TGTGCTCTCT TCCTTGCGTG 240
 TGCTGCTGCA CTGCGCGACC GGGGGCAGCT CTCCAGGTC TGGTGTGTG CTGAGGGGCT 300
 GCCCAACACA CTTCTATTGC GAGCCCGACG CAGAGATGTT GCTCAGGGTG GACTGCTCG 360
 ACCTGGGCGT CTGCGAGCTG CTTTCCAACT TCAGCGTCTT CAGCTCTTAC CTAGACCTCA 420
 GTATGAACAA CATCAGTCAG CTGCTGCCGA ATCCCTTACC CAGTCTCTCC TTCCTGGAG 480
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 AATTGTGTG GAGATCTGCT TTTCAACATT TACCTGAAT AAGAACACTG ACTCTGAATG 1140
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 CCGTTGCTT CTTATGATG ACCATTGCTT ACACCAAGCT CTACTGCAAT TTGGCAAGG 2460

5 GAGACCTGGA GAATATTGG GACTGCTCTA TGGTAAACA CATTGCCCTG TTGCTCTTCA 2520
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 10 AATGTTTTC AAGGTTGAGA ACCTGAAAAT GTGAGATTGA GTATATCAGA GCAGTAATTA 3000
 ATAAGAAGAG CTGAGGTGAA ACTCGGTTTA AA

A131 Protein sequence

15 Gene name: G protein-coupled receptor 49 (GPR49) (HG38) (IGR5)
 Unigene number: Hs.285529
 Protein Accession #: NP_003658.1
 Signal sequence: 1-22
 Transmembrane domains: 557-579, 596-618, 641-663, 687-709, 724-746, 770-792, 803-825
 20 Cellular Localization: plasma membrana

1 11 21 31 41 51
 25 MDTSRRLGVLL SLPVLLQLAT GSSSPRSGLV LRGCPTHCHC EPDGRMLLRV DCSDLGLSEL 60
 PSNLSEVTSY LLSMNNISQ LLLPNPLPSLR FLEELRLAGN ALTYIPKGAF TGLYSLKVLN 120
 LQNNQLRHVP TEALQNLRLS QSLRLDANHI SYVPPSCFSG LHSRLRLWLD DNALTEIPVQ 180
 AFRSLSAIQA MTLALNCKIH IVDYAFGNLS SLVVLHLENN RIHSLGKKCF DGLHSLLETID 240
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 30 FOHLPELRTL TLNGASQITE FPDLTGTANL ES/TLTGAQI SSLPQTVCNQ LPNLQVLDLS 360
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 LPFLIKLDLS SMLLSFPPT GLHGLTHLKL TGNHALQSLI SSENFFELKV IEMPYAYQCC 480
 AFGVCENAYK ISNQWNKGDN GEMDDLHKKD AGMFQAGDER DLEDPLDDE EDLKALESVQ 540
 CSPSPGPFKP CERLLDGLWL RIGVNTIAVL ALTCAALVTS TVPRSPLYIS PIKLLIGVIA 600
 35 AVNMLTGVS AVLAGVDAPT FGSFARHGAM WENGVGCEVI GFLSIFASES SVFLTLAAL 660
 ERGFSVKYSA KFETKAPFSS LKVIILLCAL LALTMAAVPL LGSSKYGASP LCLPLPFGER 720
 STMGYVALI LINSLCFLMM TIAYTKLYCN LDKGDLENIW DCSMVKHIAL LLFTNCILNC 780
 FVAFLSFSSL INLTIFISFEV IKFILLVVVP LPACLNPLLY ILFNPHFKEK LVSLRKQTYV 840
 40 WTRSKHPSLM SINSDDVERQ GCDSTQALVT FTSSSITYDL PPSVPSPAY PVTESCHLSS 900
 VAFVPCFL

A132 DNA SEQUENCE

45 Gene name: parathyroid hormone receptor 2
 Unigene number: Hs.159499
 Probeset Accession #: U25128
 Nucleic Acid Accession #: NM_005048
 Coding sequence: 143-1795 (underlined sequences correspond to start and stop codons)

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 55 GCTAATGCTC GGCAGCTGCC TCCTGGCCAG AGCCGACCTG GATCTGTATG GCACCATTAC 240
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 10 TTCTTTGTAA ACCATGTCAT GTGGAAAGAT TTCTCTAGT AGTGAGCTTG TGCTGCATA 2520
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 TTTAGCTGT TACTACATG TACATGGCAT GTGGGATCAA TTAATAATTT GTTTTAAAAA 2640
 T

15 A133 PROTEIN SEQUENCE

Gene name: parathyroid hormone receptor 2
 Unigene number: Hs.159499
 Protein Accession #: NP_005039.1
 Signal sequence: 1-25
 Pfam domain: 7tm_2 [141-420]
 20 Transmembrane domains: 177-197, 228-250, 253-275, 280-302, 320-342, 363-385, 398-419
 Cellular Localization: plasma membrane

25 1 11 21 31 41 51
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 MAGLGASLHV WGWLMLESCLE LARAQLDSGG TITIEBQIVL VLKAKVQCEL NITACLQEGE 60
 GNCFFPEWDGL ICWPRGTGKQ ISAVPCPPYI YDFNHKGVAF RHCNPNGTWD FMSLNKTWA 120
 NYSDDLRLFLQ PDISTGKQEF FERLYVMYTV GYSLSFGLA VAILLIGYFR RLECHRYNIH 180
 MHLFVSFMR LATSIPVKORV VHAHIGVKEL ESLIMQDDQ NSIEATSVDK SQYIGCKIAV 240
 30 VMFIYFLATN YXWILVEGLY LHNLIPIVAF SDTKYLWGF LIGWGFPAAF VAAWAVARAT 300
 LADARCWELS AGDIKIWIYA PILAAIGLNF ILFLNTVRVL ATKIWNENAV CHDTRKQYRK 360
 LAKSTLVVL VEGVYIVFV CLPHSFTGLG WIRMHCELF FNSFQGFVYS ILYCYNGEV 420
 QAEVKKMSR WNLSDVKKT PPGSRRRCS VLTITVTHST SQSQVAASR MVLISGKAAK 480
 35 IASRQPDSHI TLPGRVWNS BQDCLPSSFH ESTKEDSGRQ GDDILNEKPS RPESENPDTE 540
 GCGGETEDVL

40 A134 DNA sequence

Gene name: ESTs
 Unigene number: Hs.128899
 Probeset Accession #: AA983251
 Nucleic Acid Accession #: AA983251
 Coding sequence: 1-1749 (underlined sequences correspond to start and stop codons)

45 1 11 21 31 41 51
 | | | | | |
 ATGCTGTCTG GCTTCTGTAT GAGTCCAGT ACCAGCACA GAGCAGATA CACTCCCGGA 60
 GGAAGAAAC TTCCGTGGGA GGCITCCATC GGTGOGCACA CCTCOGAGG GCGAGGCAGC 120
 GACCGGAGA GGAAGAGCCG GCGGAGGCT GCGGGCTCC TGTGGACCG CACTGCAGCC 180
 GGGAGGCGG AGAAGGGGAA CCGGGGCGAG CGCGCGGCT GGATCGCGC CCAGCAGCAG 240
 50 CCGCGGCGGC CGCCAGCTGG GCAGGCTCCC GGGACTGCG CTTGGGGCGC GCAGGACTCT 300
 CGCTCTGCTC CTGGAGCTTC CGGGGGAGG GTCCGGTTGC CAGTGAACCC TCCAGAGGCT 360
 TCCGAGAGAC AGCCCCGGGG GCCTTCTGAC TGCAATCCGA GATTTCATC AGCAGGTGCA 420
 ACTCATAGG CAGTCCCTAA GGGGACCGGG CCACCGGCTG AGGACGGGA TGGCTTAGGA 480
 GCTCTCGGAC CTAGGGCCCG GCGTCTGTCG CTCTGCGCG TCGCGCAGA GGGAGTGGC 540
 55 CCGCGCGGAA AGCGCCCGCG GACAGTCAGT GACGAGGCC GGGGGTCCG GGGGCCAGG 600
 CTTCCTCGAG ACCGTCTGCG GCTCTCTGGA GAGCGGCTGT CCGCGCCAG GGTGGTCCCA 660
 TGTGGGGCGC TGCCGCTCTG TCCGTCTCT CATCTGGA GCGCCCTTC CTCTGCGAG 720
 TGCTGTCTGC TCGCTGCTG GCGCGGGGG CGAGGGCCCA GCGGGGAGTA CTGCCAGCGC 780
 TGGCTGGAAG CCGAGGCGT CTGGCGCATC GCTTCCAGT GTCCGAGCG CTTCCAGCGC 840
 60 GGCAGCGCCA CCATCTGCTG CCGCAGCTGC GCGTTGCGCT ACTGCTGCTC CAGCGCCGAG 900
 GCGCGCCTGG ACCAGGCGCG CTGCGCAAT GACCGCCAGC AGGGCGCTGG CGAGCCTGGC 960
 CCGCGCGACA AAGACCGGCC CCGACGGCTC GCGAGGCTT CATGCTTAG GGGTACCCAA 1020
 GGAGACCGCG AGGGTTCGCC CCACCCCGTG AGGGCCTGGC AGCGGTGCTC CCTGGAAGGC 1080
 65 TCCCGGAAAG GAAGGCAGCT CCTCAGGGCT TTCCCGGGG TGTGCCCCG TGCAGACGC 1140
 CGCGGATCC CATCTTCTCC AGCGGGCGGC CCTCTCCCC TGCAGCGGCC CGCTTGCCTC 1200
 ATCTACGTGC CGTTCCTCAT TGTGGCTCC GTGTTGTGCG CTTTATCAT CTGGGGTCC 1260
 CTGTTGGCAG CTGTGTGCTG CAGATGTCTC CGGCTTAGC AGGATCCCA GCAGAGCCGA 1320
 GCGCCAGGGG GTAAACGCTT GATGGAGACC ATCCCATGA TCCCGAGTC CAGCACTCC 1380
 CGGGGGTCTG CTACAGCCA GTCCAGCACA GCTGCCAGT CCAGCTCCAG CGCCACTCC 1440
 70 GGGGCCCGGG CGCCCCAAC AAGGTCACAG ACCAACTGTT GCTTCCCGA AGGAGCATG 1500
 AACAACTGT ATGTACACAT GCGCACAAAT TTCTGTGTC TGAACGTGA GCAGGCCACC 1560
 CAGATTGTGC CACATCAAGG GCAGTATCTG CATCCCATCATCGTGGTA CACGCTGAC 1620
 CACGACTCTG TGCCCATGAC AGCTGTGCCA CCTTTCATGG ACGGCTGCA GCTGGCTAC 1680
 75 AGGCAGATT AGTCCCGCTT CCCTCACACC AACAGTGAAC AGAAGATGA CCCAGCGGTG 1740
 ACTGTATAAC CAGAGTCTAC TGGTGGGTTT CTTTACTGAA GGGAGACGAA GGCAGGGGTG 1800
 GATTCTCGAG GTGGAAGTCC GCACATGTCT GTGGTATTTA TGGCAGGAT CCTTTGGATG 1860
 GCTTCATTG CCCCCAGACT GTATGAAGAC ATCTCGAAT TAGCATTTCT GATATGTTT 1920
 CATCCAGGAT ATCATTGATT TATGATGGAA AAGCGGCTC AGCTGGAGAT GACTGTGATG 1980
 80 TTGCTGATG TGTGATAACA AATGCTTGAG TCCGAAGTGC CCTTGAGATA TGGTTGAGCA 2040
 AAGAAATTTA TAAACTGATA AATTAAAGAT TTTTATTATG TTGTTATTAT TATTTCTTTT 2100
 TTGTTGTTGA CTGCACAGGA TCAAAATGCC TGTATATCTC CTTTTACTGG GACTTTTTTT 2160
 TTTTCTTTT TTTTCTTTAA TCAGACAGGG TCTTGTCTG TTGCCAGGC TGGAGTGCAG 2220
 TGGTGGATC TCGGCTCACT GCAACTTCA GCTCTGTGAT TCAGGCAACA CTCTGCCCTC 2280
 AGCTCCACAG GTGCTGGGA TTACAGGTGC CTGCCCATAT GGCATATTTT TGTATTTT 2340

5 TGATAGAGATG GGGTTTCACC ATGTTGGCTG GGCTGGTCTC ACTCTCCTGA CCTCAAGCAA 2400
 TCTGCTGTCT TCAGCCTTCC AAAGTGCTGG GATTACAGGC GTGAGCCACC GCCCCAGCC 2460
 TGAGCCTTTT TTTTTCCTTA ATGCATCCAA GGTAAAGGGG AAGACGCCAA TAACAGGACT 2520
 ATTCATAAAG GAACCTGCTT TGAACCTGTG GAGATCAGTC ATCAGTCACA GTATCCACA 2580
 GGCACACCTT AATTTCATTG TAAAAAGATA TATATATTTT GTCTATTTT GTGCTTTTGG 2640
 GGGCTATTTT TGTGCTTTT TACCTTATGT AGAGATCTTA TTACAAAGTG ATTTTCTACA 2700
 TAAAAAAGAG ACTGAATAAA ATTGTATAGT TACTTAACCTA ATGAAGACAT TTCAGAACTC 2760
 TGGGATGATT TTAATCTTGA AGTAGTAGGT GGTATAGTCA TAAACCAATT CATCCCCCTC 2820
 10 TTGATTGTAT CTTAATTTTC TGGCTTTAAG GTGACATCTG AGAGGTAATG CATTCTTTT 2880
 TATATTGAAA TCATAAACTA TCACCGCTG CTCTCTGAG TTACTTTTAA TTTTGCCTTG 2940
 TGGTATAGT TTTGCGTTTC CTCTGTTTGT GTTTTCAGAG CCCCATGTCT ATATAGTCCT 3000
 GAGTCAAGT AATTACTATA CTGTAAATG AAGATCAGTA TTTCTGCCCTA GATCTGATAA 3060
 AAAAAATTTT TGTCTTAGT TATAAAAAAT CAAAGAAATG TGTACAAAG ATACTTAGTA 3120
 TAGCTCCTCA GCCATAACCT GAGACTTGGG ATGAAATTTA AACCAATAC GATTACTTT 3180
 15 GCAGATCATA AGGCTTTTAA TACTCTTGT ATCAAAATGG CTTATTTTTC AGGCCTAAG 3240
 GATTGTTAAG AGAAAGCTT TTCAACGAG GATTGCCTTT CTCTCCAC ACTGTTCTTG 3300
 ATTTCTCTC TCTTCTAGGC CTCAACAGGC ACTGTATTCA TTGCCAATGT TCCAAATTAT 3360
 CAAATTCAG TGAATTTATT TGTGTGTCT TACTTATAT AAAAAAGAT AACTTTAAGG 3420
 20 ATGTGCAAGT ACATTTTCAA CTCTAGCAC AACCAATTTT TTGTAATTA ACAATTCGT 3480
 GTATGGTATG GTCTCTTACA CATTATGTC TATAGATATC TATGATCAT CTTTCTATT 3540
 TGTTCATGA CTGAATAATG TAAACCAAG GTTGGCAATT GGTATCATCA ATGATACTCA 3600
 TTTTAAATA ACCAAAGCA GGGGAAATC ATTTTACTTA TTAATAAATA TTTTATGAT 3660
 TGAATAAATA AAAAAAATA AAAAAAATA

25 A135 Protein sequence
 Gene name: ESTs
 Unigene number: Hs.128899
 Protein Accession #: none found
 30 Signal sequence: 1-11
 Transmembrane domains: 402-424
 Cellular Localization: not determined

35 1 11 21 31 41 51
 | | | | | |
 MLGGFLMSPS TQHRAYTPG GKLLPWEASI GAHTSRGRGS DRERESRFEA AGLLWDRAAA 60
 GEAEKGNRGE PFAWIRAQQQ PRPPAGQAP GTAAGGAQDP RLPRGRERGR VRLPVKFEPA 120
 SGRQFRGPD CTFEPFASA THKAVPKGTG PPAEDGDGLG APGPRARRRR LLGVAABEGSG 180
 PRGKRRGTYS DEARGSPGFR LLGDRPALSG DALSAPEVVP CGALAARPSF HPGTPLRSCS 240
 40 COWLRQWRG RGPSPGYCHG WLDAQGVNRI GFQCPERFDG GDATICCGSC ALRYCCSSAE 300
 ARLDQGGCDN DRQQGAGEFG RADKDGPRRL GRASCLRGTQ GDGEGAPPVW RAWQRCSPRG 360
 SPFGQLLRA PFGLLFRARR RGPSSPRGG PSLQRPALP IYVPLIVGS VFVAFILGS 420
 LVAACCCRCCL RPKQDPQGR APGGNRLMET IPMIPSASTS RGSSSRQSSST AASSSSSANS 480
 GARAPPTRSQ TNCCLPEBTM NNVVVDMPTN FSVLNCQQAT QIVPHQGGYL HPPVIVGTVQ 540
 45 HDSVEMTAVP PFMDGLQPGY RQIQSPFFHT NSEQKMPAV TV

A136 DNA SEQUENCE
 Gene name: selectin E (endothelial adhesion molecule 1)
 50 Unigene number: Hs.89546
 ProbeSet Accession #: M24736
 Nucleic Acid Accession #: NM_000450
 Coding sequence: 1-1833 (underlined sequences correspond to start and stop codons)

55 1 11 21 31 41 51
 | | | | | |
 ATGATTGCTT CACAGTTTCT CTGAGCTCTC ACTTTGGTGC TTCTCATTAAGAGAGTGA 60
 GCCTGGTCTT ACACACCTTC CACGGAAGCT ATGACTATG ATGAGGCCAG TGCTTATGT 120
 CAGCAAGGT ACACACACCT GGTTCGAATT CAAACCAAG AAGAGATTGA GTACCTAAC 180
 TCCATATTGA GCTATTTCAC AAGTTATTAC TGGATTGGAA TCAGAAAGT CAACAATGT 240
 60 TGGGTCTGGG TAGGAACCCA GAAACCTCTG ACAGAAAGAG CCAGAACCTG GCTCCAGGT 300
 GAACCCACCA ATAGGCAAAA AGATGAGGAC TCGTGGAGA TCTACATCAA GAGAGAAAA 360
 GATGTGGGCA TGTGGAAATGA TGAGAGGTGC AGCAAGAAGA AGCTTGCCCT ATGCTACACA 420
 GCTGCCTGTA CCAATACATC CTGCACTGGC CACGGTGAAT GTGTAGAGAC CATCAATAAT 480
 TACTACTTGA AGTGTCAACC TGGCTTCAGT GGACTCAAGT GTGAGCAAAAT TGTGAACGT 540
 65 ACAGCCCTGG AATCCCTTGA GCATGGAAGC CTGGTTTCCA GTCAACCACT GGGAAACTTC 600
 AGCTACAAAT CTCTCTGCTC TATCAGCTGT GATAGGGGTT ACCTGCCAAG CAGCATGGAG 660
 ACCATGCAGT GTATGTCTTC TGGAGAATGG AGTGTCTCTA TTCCAGCCTG CAATGTGGTT 720
 GAGTGTGATG CTGTGACAAA TCCAGCCAAT GGGTTCGTGG AATGTTTCCA AAACCTTGA 780
 AGCTTCCAT GGAACACAACT CAGTACATT GACTGTGAAG AAGGATTGA ACTAATGGGA 840
 70 GCGCAGAGCC TTCAGTGTAC CTCATCTGGG AATTGGGACA ACAGAAAGCC AACGTGTAAA 900
 GCTGTGACAT GCAGGGCCGT CCGCCAGCCT CAGAAATGGCT CTGTGAGGTG CAGCCATTCC 960
 CCTGCTGGAG AGTTCGACCT CAAATCATCC TGCAACTTCA CCTGTGAGGA AGGCTTCATG 1020
 TTGCAAGGAG CAGCCAGGT TGAATGCACC ACTCAAGGAC AGTGGACACA GCAATCCCA 1080
 GTTGTGAAG CTTCCTCAGT CACAGCCTTG TCCAACCCG AGCGAGGCTA CATGAATTGT 1140
 75 CTCTCTAGTG CTCTCTGAG TTTCCGTAT GGGTCCAGCT GTGAGTCTCT CTGTGAGCAG 1200
 GGTTTTGTGT TGAAAGGATC CAAAGGCTC CAATGTGGCC CCACAGGGGA GTGGGACAA 1260
 GAGAAAGCCA CAGTGAAGC TGTGAGATGC GATGCTGTCC ACCAGCCCCC GAAGGTTTGT 1320
 GTGAGGTGTG CTATTTCCCC TATTGGAGAA TTCACCTACA AGTCCCTCTG TGCCTTACGC 1380
 TGTGAGGAGG GATTGAAAT ATATGATCA ACTCAACTTG AGTGCACAT TCAGGACAA 1440
 80 TGGACAGAG AGGTTCCTTC CTGCCAAGTG GTAAATGTT CAAGCCTGGC AGTTCGGGA 1500
 AAGATCAACA TGAGCTGAGC TGGGGAGGCC GTGTTTGCCA CTGTGTGCA GTTCCGCTGT 1560
 CCGAAGGAT GAGCTCTCAA TGGCTCTGCA GCTCGGACAT GTGGAGCCAC AGGACACTGG 1620
 TCTGGCCTGC TACCTACCTG TGAAGCTCCC ACTGAGTCCA ACATTCCCTT GGTAGCTGGA 1680
 CTTCTGCTG CTGACTCTC CTTCTCTGCA TTAGACCAT TTCTCTCTG GCTTCGGAAA 1740

TGCTTACGGA AAGCAAAGAA ATTTGTTCTT GCCAGCAGCT GCCAAAGCCT TGAATCAGAC 1800
GGAAGCTACC AAAAGCCTTC TTACATCCTT TAA

5 **A137 Protein sequence:**
Gene name: Selectin E (endothelial adhesion molecule 1)
Unigene number: Hs.89546
Probeset Accession #: M24736
Protein Accession #: NP_000441
10 Signal sequence: 1-22
Transmembrane domains: 555-573
C-lectin domain: 23-139
Cellular Localization: plasma membrane

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1 11 21 31 41 51
| | | | |
MIASQFLSAL TLVLLIKESG AWSYNTSTEA MTYDEASAYC QQRVTHLVAI QNKKEIEYLN 60
SILSYSPSYI WIGIRKVMNV NVWVGTQKPL TEEAKNWAPG EPNNRQKDED CVRIYIKREK 120
20 DVGWMDEREC SKKKLALCYT AACTINTSCSG HGECVETINN YTCKCDPGFS GLKCEQIVNC 180
TALESPEHGS LVCSHPLGNF SYNSSCSISC DRGYLPSSMS TMQCMSSGSEW SAPIPACNVV 240
ECDAVTNPAN GFVECFQNEG SFPWNTTCTF DCEBGFELMG AQSLQCTSSG NWDNEKPTCK 300
AVTCRAVRQP QNGSVRCSHS PAGEFTFKSS CNFTCEEFGM LQGPAAQVECT TOGOWTQQIP 360
VCEAFQCTAL SNPERGYMNC LPSASGSEFY GSSCBFSCEQ GFVLKGSKRL QCGPTGEWON 420
25 EKPTCEAVRC DAVHQPPEGL VRCASPIGE PTYKSSCAPS CEQGEZLYGS TQLECTSQSQ 480
WTEEVPSQVY VKCSSLAVFG KINMSCSGEP VFGTVCKFAC PEGWTLNGSA ARTCGATGRW 540
SGLLPTCEAP TESNIPLVAG LSAAGLSLLT LAPFLNLRLK CLRKAKKFVP ASSCQSLBSN 600
GSYQKPSYIL

30 **A138 DNA SEQUENCE:**
Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
Unigene number: Hs.100686
Probeset Accession #: AA487468
Nucleic Acid Accession #: AA487468
35 Coding sequence: 55-555 (underlined sequences correspond to start and stop codons)

40 1 11 21 31 41 51
| | | | |
CGGCACCAAG AGCACTGGCC AAGTCAGCIT CTCTGAGAG AGTCTCTAGA AGACATGATG 60
CTACACTCAG CTTTGGGTCT CTGCCTCTTA CTGCTCACAG TTCTCTCCAA CCTTGCCATT 120
GCATATAAAA AGGAAAAGAG GCCTCCTCAG ACACCTCTCA GAGGATGGGG AGATGACATC 180
ACTTGGGTAC AAACCTATGA AGAAGGTCTC TTTTATGCTC AAAAAAGTAA GAGGCCATTA 240
ATGGTTATTC ATCACTCTGA GGATTGTCAA TACTCTCAAG CACTAAGAA AGTATTGGCC 300
45 CAAATGAAG AATACAAGA AATGGCTCAG AATAAGTICA TCATGCTAAA CCTTATGCAT 360
GAAACCACTG ATAAGAATT ATCACTGAT GGGCAATATG TGCTTAGAAT CATGTTTGTA 420
GACCTTCTT TAACAGTTAG AGCTGACATA GCTGGAAGAT ACTCTAACAG ATTGFACACA 480
TATGAGCCTC GGGATTATCC CCTATTGATA GAAAACATGA AGAAGCAATT AAGACTTATT 540
50 CAGTCAGAGC TATAAGAGAT GATAGAAAAA AGCCTTCACT TCAAGAAAGT CAAATTTTAT 600
GAAGAAAACC TCTGGCACAT TGACAAATAC TAAATGTGCA AGTATATAGA TTTTGTAAAT 660
TTACTATTTA GTTTTTTTAA TGTGTTTGCA ATAGTCTTAT TAAATAAAT GTTTTTTAAA 720
TCTGAAAAAA AAAAAAAA AAAAAAAA

55 **A139 Protein sequence:**
Gene name: ESTs, Weakly similar to JE0350 Anterior gradient-2 [H.sapiens]
Unigene number: Hs.100686
Probeset Accession #: AA487468
Protein Accession #: none found
60 Signal sequence: 1-23
Transmembrane domains: none found
Cellular Localization: secreted

65 1 11 21 31 41 51
| | | | |
MMLHSALGLC LLLVTVSSNL AIAIKKEKRP PQTLSRGWGD DIIVVQTYEE GLFYAQSKSK 60
PLMVEHLED CQYSQALKKV PAQNEEIQEM AQNKFIMLNL MBETTDKNLS EDGQVYPRIM 120
70 FVDPSLTVRA DIAGRYSMRL YTYEPDPLP LIENMKKALR LIQSEL

75 **A140 DNA SEQUENCE**
Gene name: TMPS33a
Unigene number: Hs.298241
Probeset Accession #: AI538613
Nucleic Acid Accession #: AB038157
Coding sequence: 202-1566 (underlined sequences correspond to start and stop codons)

80 1 11 21 31 41 51
| | | | |
ACCGGGCACC GGACGGCTCG GTTACTTTCG TTCTTAATTA GGTCAATGCC GTGTGAGCCA 60
GGAAGGGCT GTGTTTATGG GAGCCAGTA ACACGTGGGC CTACTATCTC TTCCGTGGTG 120
CCATCTACAT TTTTGGGACT CGGGAATTAT GAGGTAGAGC TGGAGCGGGA GCCGGATGTC 180
AGAGGTCTCT AATAGTCAC CATGGGGGAA AATGATCCGC CTGCTGTGTA ACCCCCTTC 240

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TCATTCCGAT CGCTTTTGG CCITGATGAT TTGAAATAA GTCCGTGTGC ACCAGATGCA 300
GATGCTGTG CTGCACAGAT CCTGTCACTG CTGCCATTGA AGTFTTTTCC AATCATCGTC 360
ATTGGGATCA TTGCATTGAT ATTAGCACTG GCCATTGCTC TGGGCATCCA CTTCGACTGC 420
TCAGGGAAGT ACAGATGTG CTGATCCTTT AAGTGTATCG AGCTGATAGC TCGATGTGAC 480
GGAGTCTCGG ATTGCAAGA OGGGGAGGAC GAGTACCGCT GTGTCCGGGT GGGTGGTCAG 540
AATGCCGTGC TCCAGGTGTT CACAGCTGCT TCGTGAAGA CCATGTGCTC CGATGACTGG 600
AAGGCTCACT ACGCAATGT TGCCTGTGCC CAACGGGTT TCCCAAGCTA TGTGAGTTCA 660
GATAACCTCA GAGTGAGCTC GCTGGAGGGG CAGTTCCGGG AGGAGTTTGT GTCCATCGAT 720
CACCTCTTGC CAGATGACAA GGTGACTGCA TTACACACT CAGTATATGT GAGGGAGGGA 780
TGTGCTCTG GCCAGTGGT TACCTTGAG TGACAGCCT GTGGTCATAG AAGGGGCTAC 840
AGCTCACGCA TCGTGGGTG AAAACATGTC TTGCTCTGCG AGTGGCCCTG GCAGGCCAGC 900
CTTCAGTTCC AGGCTTACCA CCTGTGCGGG GGCTCTGTCA TCACGCCCTT GTGGATCATC 960
ACTGTGTCAC ACTGTGTTA TGACTGTAC CTCCCAAGT CATGGAACAT CCAGGTGGGT 1020
CTAGTTTCC TGTGGACAA TCCAGCCCCA TCCCACTGG TGGAGAAGAT TGTCTACAC 1080
AGCAAGTACA AGCCAAAGAG GCTGGGCAAT GACATGSCC TTATGAAGCT GCGCGGCCA 1140
CTCACGTTCA ATGAAATGAT CCAGCCTGTG TGCCTGCCCA ACTCTGAAGA GAACCTCCCC 1200
GATGGAAGA TGTCTGGAC GTGAGGATGG GGGGCCACAG AGGATGGAG AGGTGACGCC 1260
TCCCTGTGCC TGAACCAAGC GCGCGTCCCT TTGATTCCA ACAAGATCTG CAACCAAGG 1320
GACGTGTAG GTGGCATCAT CTCCTCTCC ATGCTCTGCG CGGGCTACCT GACGGTGGC 1380
GTGGACAGCT GCCAGGGGA CAGCGGGGG CCCTGTGTGT GTCAAGAGAG GAGGCTGTGG 1440
AAGTTAGTGG GAGCGACCG CTTTGGCATC GGCTGGCAG AGGTGAACAA GCCTGGGGTG 1500
TACACCGTGG TCCAGCTCTT OCTGGACTGG ATCCAGAGC AGATGGAGAG AGACCTAAAA 1560
ACCTGAAGAG GAGGGGACA AGTAGCCACC TGAGTTCTG AGGTGATGAA GACAGCCGGA 1620
TCTCTCCCTG GACTCCGTG TAGGAACCTG CACACGAGCA GACACCTTG GAGCTCTGAG 1680
TTCCGGCACC AGTAGCAGGC CCGAAGAGG CACCTTCCA TCTGATTCCA GCACAACCTT 1740
CAAGCTGCTT TTTGTTTTT GTTTTTTTGA GGTGGAGTCT CGCTCTGTG CCCAGGCTGG 1800
AGTGAGTGG CSAAATCCCT GCTCACTGCA GCCTCGCTT CCTGTGTTCA AGCGATTCTC 1860
TTCCCTCAGC TTCCCCAGTA GCTGGGACCA CAGGTGCCCG CCACCAACCC CAACCTAATT 1920
TTGTATTTT GTAGAGACA GGGTTTCACT ATGTGGCCA GGCTGCTCTC AAACCCCTGA 1980
CCTCAATGA TGTGCTGCT TCAGCCTCCC ACAGTGTGCG GATTACAGGC ATGGGCCACC 2040
ACGCCTAGCC TCACGCTCCT TTCTGATCTT CACTAAGAAC AAAAGAAGCA GCACTTGCA 2100
AGGGCGGCTT TTCCACTGG TCCATCTGCT TTCTCTCCA GGGGTCTGC AAAATTCTG 2160
ACGAGATAAG CAGTATATG ACCTCAGGTG CAAAGCCACC AACAGCCACT CAGAAAAGAC 2220
GCACCAAGCC AGAAGTGCAG AACTGCAGTC ACTGCAGTT TTCATCTCTA GGGACCAAA 2280
CCAAACCCAC CCTTCTACT TCAGAGACTT ATTTTCACAT GTGGGAGGT TAATCTAGGA 2340
ATGACTGCTT TAAGGCTAT TTTTCATGAT TCTTTGTAGC ATTTGGTGTG TGAAGTATTA 2400
TTGTCTTTG ATTCCAAATA ATATGTTTCC TTCCCTCAA AAAAAAATA AAAAAAATA 2460
AAAAAATA
  
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A141 Protein sequence:

Gene name: TMPS93a
 Unigene number: Hs.298241
 Probeset Accession #: AI538613
 Protein Accession #: BAB20077
 Signal sequence: none found
 Transmembrane domains: 43-65, 239-261
 Tryp_SPC domain: 216-444
 Cellular Localization: plasma membrane

1 11 21 31 41 51
 | | | | |
 MGENDPPAVE APFSFRSLFG LDDLKISFVA EDADAVAAQI LSLPLKFFP IIVIGIALI 60
 LALAIGLQIH FDCSGKRCR SSFKCIELIA RCDGVSDCKD GEDEYRCVRV GGQNAVQLQVF 120
 TAASWKTMCS DDWKGHYANV ACAQLFPSPY VSSDNLRVSS LESQFREEPV SIDHLLPDDK 180
 VTALHESVYV RRGCSAGHVV TLQCTACGHR RGYSSRIVGG NMSLLSQWPN QASLOFQGYH 240
 LCGGSVITPL NIKTAARCVY DLYLPKSWTI QVGLVSLDN PAFSELVEKI VYHSKYKPKR 300
 LGNDIALMKL AGPLTFMEMI QPVCLFENSE NFPDGKVCWT SGWGATEDGA GDASPVLNHA 360
 AVPLISNKKC NHRDVGII SPSMLCAGYL TGGVDSQGD SGGPLVCQER RLWLKLVGATS 420
 RGIGCAEVNK PGVYTRVTSF LDWIEHQMER DLKT

A142 DNA SEQUENCE

Gene name: ESTs; Weakly similar to LITHOSTATHINE 1 BETA PRECURSOR [H.sapiens]
 Unigene number: Hs.105484
 Probeset Accession #: AA314779
 Nucleic Acid Accession #: none found
 Coding sequence: 103-579 (underlined sequences correspond to start and stop codons)

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1 11 21 31 41 51
| | | | |
CCAAACAGAT TTGCAGATCA AGGAGAACCC AGGAGTTTCA AAGAAGCGCT AGTAAGGTCT 60
CTGAGATCCT TGCATAGCT ACATCTCTAG GGTAGGAGGA AGATGGCTTC CAGAAGCATG 120
CGGCTGCTCC TATGTCTGAG CTGCTGCGCC AAAACAGGAG TCTTGGGTGA TATCATCATG 180
AGACCCAGCT TGCTCTCTG ATGGTITTAC CACAAGTCCA ATTGCTATGG TTACTTCAGG 240
AAGCTGAGGA ACTGGTTCTG TCCGAGCTC GAGTGTCACT CTTACGAAA CGGAGCCAC 300
CTGGCATCTA TCTTGAGTTT AAAGGAAGCC AGCAACATAG CAGAGTACAT AAGTGCTAT 360
CAGAAAGCC AGCGATATG GATTGGCTG CACGACCCAC AGAAGAAGCA GCAGTGGCAG 420
TGGATTGATG GGGCCATGTA TCTGTACAGA TCTTGGTCTG GCAAGTCCAT GGGTGGGAAC 480
AAGCACTGTG CTGAGATGAG CTCCAATAAC AACTTTTAA CTTGGAGCAG CAACGAATGC 540
AACAGCGGCC AACACTTCTT GTGCAGTAC CGAOCATAGA GCAGAAATCA AGATTCTGCT 600
AACTCTGCA CCAGCCCCGT CCTTCTCTT TCTGCTAGCC TGGCTAAATC TGCTCATTAT 660
TTCAGAGGGG AAACCTAGCA AACTAAGAGT GATAAGGCC CTACTACACT GCCTTTTTTA 720
  
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A143 Protein sequence:

Gene name: ESTs; Weakly similar to LITHEOSTATHINE 1 BETA PRECURSOR [H.sapiens]
 Unigene number: Hs.105484
 Probeset Accession #: RA314779
 Protein Accession #: none found
 Signal sequence: 1-22
 Transmembrane domains: none found
 C-type lectin domain: 47-156
 Cellular Localization: secreted

1 11 21 31 41 51
 NASRSMRLLL LLSCLAKTGV LGLDIIMRPSG APGNFYHKSN CYGYFRKLRY WSDAELECSQ 60
 YNGAEELAS LSLKEASTIA EYISGVQORSQ PINIGLHDPQ KRQWQWIDG AMYLRSWSG 120
 KSMGGNKRCA EMSSNNNFLT WSSNEBCNKRQ HFLCKYRP

A144 DNA SEQUENCE

Gene name: Cadherin 3, P-cadherin (placental)
 Unigene number: Hs.2877
 Probeset Accession #: X63629
 Nucleic Acid Accession #: X63629
 Coding sequence: 54-2543 (start and stop codons are underlined)

1 11 21 31 41 51
 GGGGAACACC GGGCCGCGGT GGGGCGAGCT GCTTCACCCC TCTCTCTGCA GCCATGGGGC 60
 TCCCTCGTGG ACCCTCTCGCG TCTCTCTCTCC TTCTCCAGGT TTGCTGGCTG CAGTSCGCGG 120
 CCTTCGAGGC GTGCGCGGGG GTCTTCAGGG AGGCTGAAGT GACCTTGGAG GCGGAGGGGG 180
 CGGAGCAGGA GCCCGGCCAG GCGCTGGGGA AGGTATTCTAT GGGCTGCCCT GGCACAGAGC 240
 CAGCTCTGTT TAGCACTGAT AATGATGACT TCACTGTGGG GAATGGCGAG ACAGTCCAGG 300
 AAGAAAGGTC ACTGAAGGAA AGGAATCCAT TGAAGATCTT CCCATCCAAA CGTATCTTAC 360
 GAGACACAAA GAGAGATTGG CTGGTTGCTC CAATATCTGT CCTGAAAAT GGCAGGGGTC 420
 CCTTCCCCCA GAGACTGAAT CAGCTCAAGT CTAATAAAGA TAGAGACACC AAGATTTTCT 480
 ACAGCATCAC GGGGCGGGGG GCAGACAGCC CCCCTGAGGG TGTCTCTGCT GTAGAGAAGG 540
 AGACAGGCTG GTTGTGTGTT AATAGGCCAC TGGACCGGGA GGAGATTGCC AAGTATGAGC 600
 TCCTTGGCCA CGCTGTGTCA GAGAATGGTG CCTCAGTGGA GGACCCCATC AACATCTCCA 660
 TCATCTGTAC GCACAGAAAT GACCAACAGC CCAAGTTTAC CCAAGACACC TTCGAGGGGA 720
 GTGTCTTAGA GGGAGTCTTA CCAGGTACTT CTGTGATGCA GGTGACAGCC ACAGATGAGG 780
 ATGATGCCAT CTATACCTTAC AATGGGGTGG TTGCTTACTC CATCATAGC CAAGAACCMA 840
 AGGACCCACA GCACCTCATG TTCACATTC ACCGGAGCAC AGGCACATC AGCGTCATCT 900
 CCAGTGGCCT GACACGGGAA AAGTTCCTTC AGTACACACT GACCATCCAG GCCACAGACA 960
 TGGATGGGGA CGGCTCCACC ACCACGGCAG TGGCAGTAGT GGAGATCCTT GATGCCAATG 1020
 ACAATGCTCC CATGTTTGAAC CCCACAGAAT ACCGAGGCCA TGTGCTGAG AATGCACTGG 1080
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